



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 189458

TO: Bao-Qun Li
Location: REM-3D24/3C18
Art Unit: 1648
Wednesday, May 17, 2006
Case Serial Number: 10/764985

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: (571)272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2523

This Page Blank (uspto)



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact*:

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg.



This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein^t protein search, using sw model

Run on: May 17, 2006, 06:11:57 ; Search time 232 Seconds
(without alignments)
17.737 Million cell updates/sec

Title: US-10-764-985-2

Perfect score: 9

Sequence: 1 KVDDTFFVY 9

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2520123

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_8.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*
- 10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	100.0	9	8	Adr12417 Vaccinia
2	9	100.0	150	8	Adj66069 MVA C7L e
3	8	88.9	9	8	Adr12435 Vaccinia
4	8	88.9	9	8	Adr12433 Vaccinia
5	8	88.9	9	8	Adr12434 Vaccinia
6	6	66.7	9	8	Adr12442 Vaccinia
7	6	66.7	9	8	Adr12437 Vaccinia
8	6	66.7	9	8	Adr12438 Vaccinia
9	6	66.7	9	8	Adr12444 Vaccinia
10	6	66.7	9	8	Adr12436 Vaccinia
11	6	66.7	9	8	Adr12443 Vaccinia
12	6	66.7	231	6	AAO29584
13	6	66.7	267	8	Adt56958 Ricordea
14	6	66.7	326	3	AAO42271
15	6	66.7	329	3	AAO4698
16	6	66.7	331	6	ABU28452
17	6	66.7	331	6	ABU31900
18	6	66.7	382	7	ABO64234
19	6	66.7	399	6	ABU33347
20	6	66.7	399	9	ABP33625
21	6	66.7	400	6	ABP78086
22	6	66.7	400	6	ABU37336
23	6	66.7	400	6	ABU37892 Protein e

24	6	66.7	405	9	AEb36203
25	6	66.7	409	6	ABU41410
26	6	66.7	479	8	ADY24554
27	6	66.7	485	3	AAO4697
28	6	66.7	485	8	ADN72665
29	6	66.7	496	3	AAO4696
30	6	66.7	500	3	AAO42270
31	6	66.7	500	5	ABP92358
32	6	66.7	510	3	AAO42269
33	6	66.7	510	8	ADN48028
34	6	66.7	800	4	ABP59871
35	6	66.7	900	4	ABP71398
36	6	66.7	1136	8	ADN21456
37	5	55.6	21	5	AAU89238
38	5	55.6	21	6	ADA04060
39	5	55.6	21	7	ADH95273
40	5	55.6	21	8	ADL67964
41	5	55.6	21	8	ADN37809
42	5	55.6	27	6	ADA04794
43	5	55.6	27	7	ADH96007
44	5	55.6	27	8	ADL68698
45	5	55.6	27	8	ADM38543
46	5	55.6	59	8	ABO57827
47	5	55.6	62	4	AAU44424
48	5	55.6	62	6	ABM40943
49	5	55.6	74	8	ADM97962
50	5	55.6	74	8	ADM97960
51	5	55.6	74	8	ADM97963
52	5	55.6	74	9	AEAS1017
53	5	55.6	74	9	AEAS1019
54	5	55.6	74	9	AEAS1020
55	5	55.6	78	7	ADC88085
56	5	55.6	80	7	ADC88093
57	5	55.6	109	4	ABG28513
58	5	55.6	110	8	ADN92114
59	5	55.6	118	7	ADM05832
60	5	55.6	118	9	AEC88762
61	5	55.6	119	2	AAW13923
62	5	55.6	126	2	AAW11635
63	5	55.6	127	6	ABU07100
64	5	55.6	128	9	AEA24151
65	5	55.6	134	5	ABG94245
66	5	55.6	134	5	ABG80557
67	5	55.6	138	7	ADG62328
68	5	55.6	146	4	AAU19377
69	5	55.6	152	3	ABP53696
70	5	55.6	157	7	AE339932
71	5	55.6	157	7	ADJ26813
72	5	55.6	159	4	ABP70518
73	5	55.6	166	2	AAW31742
74	5	55.6	170	4	ABP70366
75	5	55.6	173	8	ADY05039
76	5	55.6	177	4	AAO82719
77	5	55.6	182	8	ADY11020
78	5	55.6	182	8	ADY11256
79	5	55.6	189	6	ABU30050
80	5	55.6	201	4	ABG10671
81	5	55.6	202	7	ADC94805
82	5	55.6	211	4	AAO96683
83	5	55.6	230	2	AAO29015
84	5	55.6	230	7	ADG17081
85	5	55.6	235	3	ABP25468
86	5	55.6	238	9	ADY64614
87	5	55.6	240	8	ADN70680
88	5	55.6	244	3	ADG28321
89	5	55.6	245	4	ADM20093
90	5	55.6	254	6	AE37328
91	5	55.6	254	6	AE37328
92	5	55.6	254	6	AE37328
93	5	55.6	254	6	AE37328
94	5	55.6	254	6	AE37328
95	5	55.6	259	9	AEA24176

Aeb36203 L. pneumo
 AbU41410 Protein e
 ADY24554 Plant ful
 Aag04697 Arabidops
 Adn72665 Thale cre
 Aag04696 Arabidops
 Aag42270 Arabidops
 Abp92358 Herbicida
 Aag42269 Arabidops
 Adm48028 Polypepti
 Abp59871 Drosophil
 Abp71398 Drosophil
 Adn21456 Bacterial
 Aau89238 Insulin i
 Ada04060 Insulin r
 Adh95273 Insulin r
 Adl67964 IGF-1R/IR
 Adm37809 Anti-IR f
 Ada04794 IGF-1R bi
 Adh96007 Insulin g
 Adl68698 IGF-1R/IR
 Adm38543 Insulin a
 Abo57827 Human gen
 Aau44424 Propionib
 Abm40943 Propionib
 Adm97962 Vetispira
 Adm97960 5-epi-Ari
 Adm97963 Vetispira
 Aea51017 Tobacco S
 Aea51019 Potato ve
 Aea51020 Hyoscyamu
 Adc88085 Ribosomal
 Adc88093 Ribosomal
 Abg28513 Novel hum
 Adx92114 Plant ful
 Adm05832 Human pro
 Aec88762 Human cdn
 Aaw13923 Heavy cha
 Aaw11635 Human ant
 AbU07100 Maize Sta
 Aea24151 Anti-HAHA
 Abg94245 Apis cera
 Abg80557 Bee phosp
 Ade62328 Rat Prote
 Aau19377 Human G p
 Aab53696 Human col
 Aae39932 Corn phos
 Adj26813 Corn phos
 Abb70518 Drosophil
 Aaw31742 Canine ob
 Abb70366 Drosophil
 Ady05039 Plant ful
 Aag82719 S. epider
 Ady11020 Plant ful
 Ady11256 Plant ful
 AbU30050 Protein e
 Ady10671 Plant ful
 Abg1277 Novel hum
 Adc94805 E. faeciu
 Aab96683 Putative
 Aau29015 T. gondii
 Aau25486 T. gondii
 Adg17081 T. gondii
 Aab25468 Pinus rad
 Adq66091 Novel hum
 Ady64614 S. manso
 Adx70680 Plant ful
 Adx70680 Plant ful
 Aag28321 Arabidops
 Adm20093 Bacterial
 Aes37328 Protein e
 Adx74695 Plant ful
 Aea24176 Anti-HAHA

97	5	55.6	266	7	ADJ11794	Adj11794 Rice prot	170	5	55.6	451	4	AAG89796	Aag89796 C glutami
98	5	55.6	267	7	ADJ11440	Adj11440 Rice prot	171	5	55.6	451	9	AEb15157	Aeb15157 C glutami
99	5	55.6	268	7	ABM88716	Abm88716 Rice abio	172	5	55.6	452	3	AAy74388	Aay74388 Neisseria
100	5	55.6	280	6	ABU43599	Abu43599 Protein e	173	5	55.6	452	3	AAy74386	Aay74386 Neisseria
101	5	55.6	285	7	ABO82245	AbO82245 Pseudomon	174	5	55.6	452	3	AAy90302	Aay90302 1-2-rhamn
102	5	55.6	297	8	ADR46377	Adr46377 Human End	175	5	55.6	452	6	ABU38141	Abu38141 Protein e
103	5	55.6	297	8	ABM81069	Abm81069 Tumour-as	176	5	55.6	453	8	ADT56183	Adt56183 Plant pol
104	5	55.6	299	7	ADT70043	C. neofor	177	5	55.6	455	3	AAy74387	Aay74387 Neisseria
105	5	55.6	300	8	ADT58018	Plant pol	178	5	55.6	465	6	ABU44153	Abu44153 Protein e
106	5	55.6	301	6	ADA35398	Acinetoba	179	5	55.6	468	8	ADN22809	Adn22809 Bacterial
107	5	55.6	302	3	AAG20740	Aag20740 Arabidops	180	5	55.6	470	7	ABM87867	Abm87867 Rice abio
108	5	55.6	306	8	ADN21573	Bacterial	181	5	55.6	475	2	AAW11641	Aaw11641 Human ant
109	5	55.6	307	3	AAG51074	Aag51074 Arabidops	182	5	55.6	475	5	ABM92034	Abm92034 Herbicida
110	5	55.6	307	3	AAG14587	Aag14587 Arabidops	183	5	55.6	476	7	ABM87991	Abm87991 Rice abio
111	5	55.6	308	9	AEA20222	Novel hum	184	5	55.6	479	5	ABF39590	Abf39590 Staphyloc
112	5	55.6	311	3	AAG20739	Aag20739 Arabidops	185	5	55.6	479	8	ADN05581	Adn05581 Staphyloc
113	5	55.6	311	8	ADT55972	Plant pol	186	5	55.6	483	2	AAW07445	Aaw07445 Represibl
114	5	55.6	313	5	ABB49170	Abb49170 Listeria	187	5	55.6	484	7	ADJ69412	Adj69412 Human hea
115	5	55.6	313	8	ADN99771	Novel hum	188	5	55.6	486	6	AAO26537	Aao26537 Soybean h
116	5	55.6	316	3	AAG14586	Aag14586 Arabidops	189	5	55.6	487	3	AEF16012	Aef16012 Glycine m
117	5	55.6	316	3	AAG51073	Aag51073 Arabidops	190	5	55.6	487	3	AAG53798	Aag53798 Arabidops
118	5	55.6	316	4	ADM19847	Adm19847 Protein e	191	5	55.6	497	5	ABP29237	Abp29237 Streptoco
119	5	55.6	317	4	ABB68103	Abb68103 Drosophil	192	5	55.6	497	6	AAO26536	Aao26536 Rice high
120	5	55.6	322	4	ABB60330	Abb60330 Drosophil	193	5	55.6	497	10	ADR83912	Adr83912 S. pyogen
121	5	55.6	323	8	ADY25260	Ady25260 Plant ful	194	5	55.6	504	8	ADJ49082	Adj49082 Oil-assoc
122	5	55.6	326	3	AAG20738	Aag20738 Arabidops	195	5	55.6	508	9	ABE26749	Abe26749 Consensus
123	5	55.6	328	6	ABR57463	AbR57463 AcC fami	196	5	55.6	518	8	ADN25097	Adn25097 Bacterial
124	5	55.6	329	3	AAG51072	Aag51072 Arabidops	197	5	55.6	523	9	ABE27210	Abe27210 Pinus rad
125	5	55.6	329	6	ABR52858	AbR52858 Protein s	198	5	55.6	526	4	AAW93809	Aaw93809 Human pol
126	5	55.6	329	7	ADK62318	Adk62318 Disease t	199	5	55.6	526	8	ADL31820	Adl31820 Human pro
127	5	55.6	329	8	ADs43699	AdS43699 Bacterial	200	5	55.6	528	8	ADN23692	Adn23692 Bacterial
128	5	55.6	329	8	ADT87145	Adt87145 Yeast Str	201	5	55.6	535	6	ABU21542	Abu21542 Protein e
129	5	55.6	330	6	ABU44842	Abu44842 Protein e	202	5	55.6	545	9	ABE26744	Abe26744 Tomato sh
130	5	55.6	330	6	ABU50533	Abu50533 Protein e	203	5	55.6	547	7	ABO68617	AbO68617 Pseudomon
131	5	55.6	331	3	AAG14585	Aag14585 Arabidops	204	5	55.6	548	3	AAy90836	Aay90836 Tobacco s
132	5	55.6	331	6	ABU47384	Abu47384 Protein e	205	5	55.6	548	3	AAy90831	Aay90831 Tobacco s
133	5	55.6	331	6	ABU15092	Abu15092 Protein e	206	5	55.6	548	3	AAy90833	Aay90833 Tobacco s
134	5	55.6	337	6	ABU21270	Abu21270 Protein e	207	5	55.6	548	3	AAy90832	Aay90832 Tobacco s
135	5	55.6	347	3	AAG53800	Aag53800 Arabidops	208	5	55.6	548	3	AAy90834	Aay90834 Tobacco s
136	5	55.6	348	8	ADN00790	Adn00790 Mycobacte	209	5	55.6	550	2	AAW01637	Aaw01637 Tobacco e
137	5	55.6	368	3	AAG28320	Aag28320 Arabidops	210	5	55.6	550	2	AAW01637	Aaw01637 Tobacco e
138	5	55.6	370	3	ADG28319	Adg28319 Arabidops	211	5	55.6	551	8	ADP21177	Adp21177 Potato ve
139	5	55.6	370	7	ADH87165	Adh87165 Enterococ	212	5	55.6	551	8	ADP21177	Adp21177 Potato ve
140	5	55.6	373	3	ABO8467	AbO8467 Amino aci	213	5	55.6	555	3	AAW48733	Aaw48733 Tobacco D
141	5	55.6	378	7	ADD02198	Add02198 B2L viral	214	5	55.6	556	3	AAy90843	Aay90843 Potato ve
142	5	55.6	378	7	ADD02200	Add02200 B2L viral	215	5	55.6	566	6	ADA54977	Ada54977 Human pro
143	5	55.6	378	7	ADJ63965	Adj63965 Parapox v	216	5	55.6	567	9	ABM92568	Abm92568 M. xanthu
144	5	55.6	378	7	ADJ63963	Adj63963 Parapox v	217	5	55.6	569	9	ABE26745	Abe26745 Tobacco s
145	5	55.6	378	8	ADG46065	Adg46065 Parapoxvi	218	5	55.6	575	6	AAO23887	Aao23887 Phi-29 DN
146	5	55.6	378	8	ADG46067	Adg46067 Parapoxvi	219	5	55.6	575	6	AAO23887	Aao23887 Phi-29 DN
147	5	55.6	378	8	ADK01348	Adk01348 D1701 B2L	220	5	55.6	575	6	AAO23894	Aao23894 Phi-29 DN
148	5	55.6	378	8	ADK01346	Adk01346 Envelope	221	5	55.6	575	6	AAO23898	Aao23898 Phi-29 DN
149	5	55.6	378	8	ADT99512	Adt99512 Parapox o	222	5	55.6	575	6	AAO23899	Aao23899 Phi-29 DN
150	5	55.6	378	8	ADT99514	Adt99514 Parapox o	223	5	55.6	575	6	AAO23911	Aao23911 Phi-29 DN
151	5	55.6	387	3	AAy99482	Aay99482 Tojoba ac	224	5	55.6	575	6	AAO23887	Aao23887 Native ph
152	5	55.6	389	6	ABW67123	Abw67123 Phototrab	225	5	55.6	575	6	AAO23894	Aao23894 Phi-29 DN
153	5	55.6	400	8	ADS43420	AdS43420 Bacterial	226	5	55.6	575	6	AAO23878	Aao23878 Phi-29 DN
154	5	55.6	408	3	AAy95855	Aay95855 Autoantig	227	5	55.6	575	6	AAO23889	Aao23889 Phi-29 DN
155	5	55.6	413	6	ABG74936	Abg74936 A. gossyp	228	5	55.6	575	6	AAO23897	Aao23897 Phi-29 DN
156	5	55.6	426	6	ADU26778	Adu26778 Protein e	229	5	55.6	575	6	AAO23881	Aao23881 Phi-29 DN
157	5	55.6	428	2	AAy35302	Aay35302 Amino aci	230	5	55.6	575	6	AAO23885	Aao23885 Phi-29 DN
158	5	55.6	428	5	ABP74064	Abp74064 Candida a	231	5	55.6	575	6	AAO23885	Aao23885 Phi-29 DN
159	5	55.6	431	9	AEb41590	Aeb41590 L. pneumo	232	5	55.6	575	6	AAO23898	Aao23898 Phi-29 DN
160	5	55.6	435	8	ADS27786	AdS27786 Bacterial	233	5	55.6	575	6	AAO23899	Aao23899 Phi-29 DN
161	5	55.6	436	9	ABE38420	Abe38420 L. pneumo	234	5	55.6	575	6	AAO23900	Aao23900 Phi-29 DN
162	5	55.6	436	6	ABP80582	Abp80582 N. gonorr	235	5	55.6	575	6	AAO23910	Aao23910 Phi-29 DN
163	5	55.6	436	6	ABU37208	Abu37208 Protein e	236	5	55.6	575	6	AAO23877	Aao23877 Native ph
164	5	55.6	438	8	ADX90021	Adx90021 Plant ful	237	5	55.6	575	6	AAO23883	Aao23883 Phi-29 DN
165	5	55.6	440	2	AAE11515	Aae11515 Soybean c	238	5	55.6	575	6	AAO23891	Aao23891 Phi-29 DN
166	5	55.6	441	9	ADY58797	Ady58797 Tobacco e	239	5	55.6	575	6	AAO23896	Aao23896 Phi-29 DN
167	5	55.6	447	8	ADN00792	Adn00792 Mycobacte	240	5	55.6	575	6	AAO23896	Aao23896 Phi-29 DN
168	5	55.6	449	9	AEA49233	Aea49233 L. rhamno	241	5	55.6	575	6	AAO23907	Aao23907 Phi-29 DN
169	5	55.6	449	9	AED03641	Aed03641 L. rhamno	242	5	55.6	575	6	AAO23909	Aao23909 Phi-29 DN

243	5	55.6	316	Rao23913	Phi-29	DN	316	5	55.6	1308	3	AAB18167	Aab18167	Plasmodiu
244	5	55.6	317	Rao23905	Phi-29	DN	317	5	55.6	1361	6	ABR53440	AbR53440	Protein s
245	5	55.6	318	Rao23892	Phi-29	DN	318	5	55.6	1361	7	ADK64644	AdK64644	Disease t
246	5	55.6	319	Rao23908	Phi-29	DN	319	5	55.6	1499	9	ADV16756	AdV16756	E faecal
247	5	55.6	320	Rao23895	Phi-29	DN	320	5	55.6	1679	8	ADs43650	AdS43650	Bacterial
248	5	55.6	321	Rao23888	Phi-29	DN	321	5	55.6	1788	4	AU000016	Au000016	Human Ple
249	5	55.6	322	Rao23901	Phi-29	DN	322	5	55.6	1903	9	ADW23580	AdW23580	Lactobaci
250	5	55.6	323	Rao23880	Phi-29	DN	323	5	55.6	1903	9	ADW23577	AdW23577	Lactobaci
251	5	55.6	324	Rao23882	Phi-29	DN	324	5	55.6	1903	9	ADW23578	AdW23578	Lactobaci
252	5	55.6	325	Rao23903	Phi-29	DN	325	5	55.6	1903	9	ADW23579	AdW23579	Lactobaci
253	5	55.6	326	Rao23890	Phi-29	DN	326	5	55.6	1903	9	ADW23480	AdW23480	Lactobaci
254	5	55.6	327	Rao23879	Phi-29	DN	327	5	55.6	1903	9	ADW23581	AdW23581	Lactobaci
255	5	55.6	328	Rao23884	Phi-29	DN	328	5	55.6	1915	4	ABBS2635	AbBS2635	Escherich
256	5	55.6	329	Rao23886	Phi-29	DN	329	5	55.6	3871	8	ADN23885	AdN23885	Bacterial
257	5	55.6	330	Rao23902	Phi-29	DN	330	5	55.6	3871	8	ADN23886	AdN23886	Bacterial
258	5	55.6	331	Rao23914	Phi-29	DN	331	5	55.6	4313	7	ADJ95084	AdJ95084	Novel NOV
259	5	55.6	332	Rao23904	Phi-29	DN	332	5	55.6	44.4	4	AAB48494	Aab48494	Antifibri
260	5	55.6	333	Rao23906	Phi-29	DN	333	4	44.4	6	4	AAB82642	Aab82642	All-D pep
261	5	55.6	334	ADA8084	Rice	prot	334	4	44.4	6	5	AU96830	Au96830	Amyloid t
262	5	55.6	335	ADA8740	Rice	prot	335	4	44.4	6	5	AU11669	Au11669	Peptide #
263	5	55.6	336	ABM93080	M. xanthu		336	4	44.4	6	6	AAB35456	Aae35456	Abeta pep
264	5	55.6	337	Aau87287	Novel	cen	337	4	44.4	6	6	ABP66377	AbP66377	Human RSV
265	5	55.6	338	ADI54602	Novel	hum	338	4	44.4	6	8	ADQ37310	AdQ37310	Antifibri
266	5	55.6	339	ADY70698	Human	BAC	339	4	44.4	6	8	ADQ37333	AdQ37333	Antifibri
267	5	55.6	340	ABBS9507	Drosophi		340	4	44.4	6	8	ADQ37281	AdQ37281	Vaccine a
268	5	55.6	341	AAB95404	Human	pro	341	4	44.4	6	9	AAE10573	Aae10573	Humanised
269	5	55.6	342	ABB83435	Human	Gol	342	4	44.4	7	5	ABP66377	AbP66377	Human RSV
270	5	55.6	343	ADA48005	Human	Pro	343	4	44.4	7	5	ABP66453	AbP66453	Human RSV
271	5	55.6	344	ADG2508	Human	Pro	344	4	44.4	7	5	ABP66444	AbP66444	Human RSV
272	5	55.6	345	ADD48003	Rat	Prote	345	4	44.4	7	5	ABE28032	Aae28032	Human mod
273	5	55.6	346	ADD48007	Rat	Prote	346	4	44.4	7	6	ABU69240	AbU69240	Respirato
274	5	55.6	347	ADD48009	Human	Pro	347	4	44.4	7	6	ABU69307	AbU69307	Respirato
275	5	55.6	348	ADE62512	Human	Pro	348	4	44.4	7	6	ABU69316	AbU69316	Respirato
276	5	55.6	349	ADE62506	Rat	Prote	349	4	44.4	7	6	ADBS3735	AdB3735	SYNAGIS a
277	5	55.6	350	ADBE62510	Rat	Prote	350	4	44.4	7	7	ADBS3811	AdB3811	SYNAGIS a
278	5	55.6	351	ABM81668	Tumour-as		351	4	44.4	7	7	ADBS3802	AdB3802	SYNAGIS a
279	5	55.6	352	ADW23911	Pea	NFRIB	352	4	44.4	7	8	ADI56897	AdI56897	RSV antib
280	5	55.6	353	ADI28012	ECMCD	pr	353	4	44.4	7	8	ADI56964	AdI56964	RSV antib
281	5	55.6	354	ABU16681	Protein	e	354	4	44.4	7	8	ADI56973	AdI56973	RSV antib
282	5	55.6	355	AED03440	5-keto-D-		355	4	44.4	7	8	ADT89220	AdT89220	Humanised
283	5	55.6	356	ABG67779	Drosophi		356	4	44.4	7	8	ADT97652	AdT97652	Low molec
284	5	55.6	357	ADZ10388	P. gingiv		357	4	44.4	7	9	ADW19877	AdW19877	RSV antig
285	5	55.6	358	ADN27338	Bacterial		358	4	44.4	7	9	ADW19944	AdW19944	RSV antig
286	5	55.6	359	ADN18994	Human	dis	359	4	44.4	7	9	ADW19953	AdW19953	RSV antig
287	5	55.6	360	ADP23526	Pro	polyp	360	4	44.4	7	9	AEBO6926	AeBO6926	RSV-speci
288	5	55.6	361	AEE87026	Human	che	361	4	44.4	7	9	AEBO6859	AeBO6859	RSV-speci
289	5	55.6	362	ABBS9658	Drosophi		362	4	44.4	7	9	AEBO6935	AeBO6935	RSV-speci
290	5	55.6	363	ADL04598	M. catarr		363	4	44.4	7	9	AEC76654	Aec76654	SYNAGIS-d
291	5	55.6	364	ADP98960	C. albica		364	4	44.4	7	9	AEC76721	Aec76721	SYNAGIS-d
292	5	55.6	365	AA373330	Chlamydia		365	4	44.4	7	9	AEC76730	Aec76730	SYNAGIS-d
293	5	55.6	366	ADN74391	Thale	cre	366	4	44.4	7	10	ABF31692	AeF31692	Human cor
294	5	55.6	367	ABG24930	Novel	hum	367	4	44.4	8	6	ABB99493	AbB99493	Internal
295	5	55.6	368	ABO61952	Klebsiell		368	4	44.4	8	8	AUK03917	AdK03917	Hepatitis
296	5	55.6	369	ABG21280	Novel	hum	369	4	44.4	8	10	AEF43715	AeF43715	Inland ta
297	5	55.6	370	ABU41607	Protein	e	370	4	44.4	9	2	AA47053	AaY47053	Immunogen
298	5	55.6	371	ABU41607	Protein	e	371	4	44.4	9	3	AB445572	Aab445572	Human B99
299	5	55.6	372	ADH74937	A. gossyp		372	4	44.4	9	5	ABP55767	AbP55767	B15 class
300	5	55.6	373	ADH87167	Enterococ		373	4	44.4	9	5	ABP55860	AbP55860	B15 class
301	5	55.6	374	ADV16755	E. faecal		374	4	44.4	9	5	ABP55860	AbP55860	B15 class
302	5	55.6	375	ADH86812	Enterococ		375	4	44.4	9	5	ABG96712	AbG96712	Human leu
303	5	55.6	376	ABBS9609	Herbicida		376	4	44.4	9	5	ABG96907	AbG96907	Human leu
304	5	55.6	377	ADJ49062	Oil-associ		377	4	44.4	9	5	ABG96578	AbG96578	Human leu
305	5	55.6	378	ABM88365	Rice	abio	378	4	44.4	9	5	ABG97076	AbG97076	Human leu
306	5	55.6	379	ADJ49651	Oil-associ		379	4	44.4	9	6	ABP99187	AbP99187	Erbb2 cel
307	5	55.6	380	ABP27157	Streptoco		380	4	44.4	9	6	ABR75537	AbR75537	Liver res
308	5	55.6	381	ABU46770	Protein	e	381	4	44.4	9	7	ADL98379	AdL98379	Human leu
309	5	55.6	382	ADD43930	Chlamydia		382	4	44.4	9	7	ADL98740	AdL98740	Human leu
310	5	55.6	383	Aea19222	Chlamydia		383	4	44.4	9	7	ADL98911	AdL98911	Human leu
311	5	55.6	384	ADG62226	Novel	hum	384	4	44.4	9	7	ADL98420	AdL98420	Human leu
312	5	55.6	385	ABM68350	Phototrab		385	4	44.4	9	7	ADL98529	AdL98529	Human leu
313	5	55.6	386	ABO79230	Pseudomon		386	4	44.4	9	7	ADN07535	AdN07535	Liver res
314	5	55.6	387	ADR86509	Aspergill		387	4	44.4	9	8	ADK03918	AdK03918	Hepatitis
315	5	55.6	388	AAB18244	Plasmodiu		388	4	44.4	9	8	ADP26067	AdP26067	Plasmodiu

389	4	44.4	9	8	ADR12440	Adrl2440 Vaccinia	462	4	44.4	15	9	ABD21559	Aed21559 Mycobacte
390	4	44.4	9	8	ADR12441	Adrl2441 Vaccinia	463	4	44.4	15	9	ABD21560	Aed21560 Mycobacte
391	4	44.4	9	8	ADR12439	Adrl2439 Vaccinia	464	4	44.4	15	9	ABD21558	Aed21558 Mycobacte
392	4	44.4	9	8	ADR12445	Adrl2445 Vaccinia	465	4	44.4	16	2	AAR49461	Aar49461 HLA-A30 p
393	4	44.4	9	9	ADZ37248	Adz37248 Human CKI	466	4	44.4	16	8	ADK69565	Adk69565 Epitope 1
394	4	44.4	9	10	ABE25636	Aef25636 RANKL pre	467	4	44.4	16	8	ADU80761	Adu80761 Staphyloc
395	4	44.4	9	10	ABF95893	Aef95893 Soluble M	468	4	44.4	16	10	ABF32533	Aef32533 Human cor
396	4	44.4	9	10	ABF96030	Aef96030 Soluble M	469	4	44.4	17	2	AAR49398	Aar49398 HLA-Cw9 p
397	4	44.4	9	10	ABF96536	Aef96536 SHLA-BL5	470	4	44.4	17	2	AAR49387	Aar49387 HLA-A2 po
398	4	44.4	10	2	AAR79781	Aar79781 Rabbit te	471	4	44.4	17	2	AAW39861	Aaw39861 Heavy cha
399	4	44.4	10	2	AAR79782	Aar79782 Rabbit te	472	4	44.4	17	3	AAW39861	Aaw39861 Heavy cha
400	4	44.4	10	2	AAW42663	Aaw42663 Antigenic	473	4	44.4	17	3	AAW39861	Aaw39861 Heavy cha
401	4	44.4	10	2	AAW42662	Aaw42662 Antigenic	474	4	44.4	17	4	AAU16718	Aau16718 Peptide E
402	4	44.4	10	2	AAV30139	Aav30139 Peptide t	475	4	44.4	17	5	ABJ00248	Abj00248 Human IgE
403	4	44.4	10	4	ABG66237	Abg66237 Saccharom	476	4	44.4	17	9	ADY26785	Ady26785 Human ant
404	4	44.4	10	4	AAW42842	Aaw42842 Mycoplasma	477	4	44.4	17	9	ADY26791	Ady26791 Human ant
405	4	44.4	10	6	ABU090819	Abu090819 Peptide #	478	4	44.4	17	10	ABE97404	Aee97404 Phox-spec
406	4	44.4	10	8	ADK03915	Adk03915 Hepatitis	479	4	44.4	17	10	ABF32554	Aef32554 Human cor
407	4	44.4	11	4	AAU25284	Aau25284 Schizophr	480	4	44.4	18	5	AAR49396	Aar49396 HLA-Cw9 p
408	4	44.4	11	4	AAU15628	Aau15628 Schizophr	481	4	44.4	18	5	AAO22320	Aao22320 Anti-CD14
409	4	44.4	11	5	ABG96938	Abg96938 Human leu	482	4	44.4	18	6	ABP82344	Abp82344 G protein
410	4	44.4	11	5	ABG96579	Abg96579 Human leu	483	4	44.4	18	6	ABP82344	Abp82344 G protein
411	4	44.4	11	5	ABG97251	Abg97251 Human leu	484	4	44.4	18	10	ADV12667	Adv12667 Human pho
412	4	44.4	11	5	ABG96723	Abg96723 Human leu	485	4	44.4	18	10	AEF01963	Aef01963 Ii-key/H
413	4	44.4	11	5	ABR58835	AbR58835 Alzheimer	486	4	44.4	19	2	AAR49395	Aar49395 HLA-C pos
414	4	44.4	11	6	ADL98772	Adl98772 Human leu	487	4	44.4	19	2	AAR49384	Aar49384 HLA-A2 po
415	4	44.4	11	7	ADL98421	Adl98421 Human leu	488	4	44.4	19	3	AAV69298	Aav69298 Expressed
416	4	44.4	11	7	ADL99087	Adl99087 Human leu	489	4	44.4	19	3	AAV69298	Aav69298 Expressed
417	4	44.4	11	7	ADL98540	Adl98540 Human leu	490	4	44.4	19	3	AAV69298	Aav69298 Expressed
418	4	44.4	11	8	ADL35803	Adh35803 Kininogen	491	4	44.4	20	2	AAW45459	Aaw45459 Peptide f
419	4	44.4	11	8	ADN32062	Adn32062 Human Alz	492	4	44.4	20	2	AAW82296	Aaw82296 Dynamin 4
420	4	44.4	11	8	ADW78895	Adw78895 Schizophr	493	4	44.4	20	2	AAW82295	Aaw82295 Dynamin 4
421	4	44.4	11	9	ADW56518	Adw56518 Cardioras	494	4	44.4	20	3	AAV57072	Aav57072 Neglected
422	4	44.4	11	10	ABF95894	Aef95894 Soluble M	495	4	44.4	20	3	ADG15779	Adg15779 Rv3879c-d
423	4	44.4	11	10	ABF96041	Aef96041 Soluble M	496	4	44.4	20	7	ADG15778	Adg15778 Rv3879c-d
424	4	44.4	12	9	ADY52295	Ady52295 SP-3b1 he	497	4	44.4	20	7	ADW33877	Adw33877 HLA bindi
425	4	44.4	13	2	AAW64576	Aaw64576 Human fac	498	4	44.4	20	7	ADW33877	Adw33877 HLA bindi
426	4	44.4	13	5	ABE27772	Aae27772 Human bet	499	4	44.4	21	2	AAW49393	Aaw49393 HLA-C pos
427	4	44.4	13	5	ABE27774	Aae27774 Human bet	500	4	44.4	21	2	AAW49393	Aaw49393 HLA-C pos
428	4	44.4	13	5	ABE27773	Aae27773 Human bet	501	4	44.4	21	2	AAW49393	Aaw49393 HLA-C pos
429	4	44.4	13	5	ABE27775	Aae27775 Human bet	502	4	44.4	21	7	ADW35108	Adw35108 HLA bindi
430	4	44.4	13	5	ABE27771	Aae27771 Human bet	503	4	44.4	21	7	ADW33874	Adw33874 HLA bindi
431	4	44.4	13	5	ADG66069	Adg66069 Human bet	504	4	44.4	21	7	ADW33875	Adw33875 HLA bindi
432	4	44.4	13	5	ADG66237	Adg66237 Human pro	505	4	44.4	21	7	ADW33876	Adw33876 HLA bindi
433	4	44.4	13	5	ADG66071	Adg66071 Human bet	506	4	44.4	21	7	ADW33877	Adw33877 HLA bindi
434	4	44.4	13	5	ADG66236	Adg66236 Human pro	507	4	44.4	21	7	ADW33879	Adw33879 HLA bindi
435	4	44.4	13	5	ADG66238	Adg66238 Human pro	508	4	44.4	21	7	ADW35109	Adw35109 HLA bindi
436	4	44.4	13	5	ADG66070	Adg66070 Human bet	509	4	44.4	21	9	ADV56589	Adv56589 G protein
437	4	44.4	13	5	ADG66068	Adg66068 Human bet	510	4	44.4	21	9	ADV57274	Adv57274 G protein
438	4	44.4	13	5	ADG66072	Adg66072 Human bet	511	4	44.4	21	9	ADY38489	Ady38489 Antigenic
439	4	44.4	13	5	ADG66235	Adg66235 Human pro	512	4	44.4	22	2	AAW00599	Aaw00599 Heparan s
440	4	44.4	13	7	ADM75453	Adm75453 Potential	513	4	44.4	22	2	AAW42690	Aaw42690 Peptide G
441	4	44.4	13	7	ADM75188	Adm75188 Potential	514	4	44.4	22	8	ADU07977	Adu07977 Dentin ma
442	4	44.4	13	7	ADM74924	Adm74924 Potential	515	4	44.4	22	8	ADU07977	Adu07977 Dentin ma
443	4	44.4	13	7	ADM75718	Adm75718 Potential	516	4	44.4	23	2	AAW10791	Aaw10791 Interphot
444	4	44.4	13	7	ADM74923	Adm74923 Potential	517	4	44.4	23	2	AAW49391	Aaw49391 HLA-C pos
445	4	44.4	13	7	ADM75189	Adm75189 Potential	518	4	44.4	23	2	AAW49485	Aaw49485 HLA-A2 po
446	4	44.4	13	9	ADM03565	Adm03565 Human RIN	519	4	44.4	23	2	AAW82310	Aaw82310 Transport
447	4	44.4	13	10	ABF02153	Aef02153 Ii-key hy	520	4	44.4	23	3	AAW82310	Aaw82310 Transport
448	4	44.4	14	1	APB83024	Aap83024 Shiga tox	521	4	44.4	23	6	ABO12608	Abol2608 Human sec
449	4	44.4	14	2	AAV41869	Aav41869 Rheumatoid	522	4	44.4	23	6	ABO12608	Abol2608 Human sec
450	4	44.4	14	5	ABB74800	Abb74800 Nuclear p	523	4	44.4	23	7	ADJ94225	Adj94225 Interphot
451	4	44.4	14	7	ADD23197	Add23197 Breast ca	524	4	44.4	24	4	AAW87096	Aaw87096 Human TAN
452	4	44.4	14	7	ADD23836	Add23836 Breast ca	525	4	44.4	24	4	AAW87096	Aaw87096 Human TAN
453	4	44.4	14	8	ADR15907	Adr15907 Transferr	526	4	44.4	27	5	AAU89414	Aau89414 Insulin/i
454	4	44.4	14	8	ADR15967	Adr15967 Transferr	527	4	44.4	27	8	ABO57756	Abos7756 Human gen
455	4	44.4	14	8	ADU13243	Adu13243 Human rhe	528	4	44.4	28	2	AAW42765	Aaw42765 Peptide o
456	4	44.4	14	9	ADU17313	Adu17313 Human ser	529	4	44.4	29	10	ABE36919	Aee36919 Human ser
457	4	44.4	14	9	ADW56868	Adw56868 Cardioras	530	4	44.4	30	4	AAW54339	Aaw54339 Human bra
458	4	44.4	14	9	ADW56827	Adw56827 Human con	531	4	44.4	30	4	ABG36393	Abg36393 Human pep
459	4	44.4	15	8	ADR97649	Adr97649 Low molec	532	4	44.4	31	4	ABB03246	Abb03246 Human mus
460	4	44.4	15	9	ADW77852	Adw77852 Human can	533	4	44.4	31	6	ABU12540	Abu12540 Novel hum
461	4	44.4	15	9	ADY39841	Ady39841 Human pla	534	4	44.4	31	8	ADJ28566	Adj28566 Human mus

535	44.4	31	9	ADY30798	Ady30798 Human epi	608	44.4	45	5	ABB79951	Abb79951 Human pro
536	44.4	31	9	ADY30797	Ady30797 Human epi	609	44.4	45	5	ABB79950	Abb79950 Human pro
537	44.4	31	10	AEF32082	Aef32082 Human cor	610	44.4	45	5	ABB79947	Abb79947 Human pro
538	44.4	32	10	ABE38354	Abe38354 Human ser	611	44.4	45	7	ADB71159	Adb71159 Human pro
539	44.4	33	5	ABG99540	Abg99540 Conus sp	612	44.4	45	7	ADB71155	Adb71155 Human pro
540	44.4	33	5	ABG99548	Abg99548 Conus sp	613	44.4	46	2	AAW60934	Aaw60934 Streptoco
541	44.4	33	5	ABG99686	Abg99686 Conus sp	614	44.4	46	2	AAW65444	Aaw65444 Lebetin d
542	44.4	33	7	ABO23567	AbO23567 Helicobac	615	44.4	46	4	AAW21521	Aaw21521 Peptide #
543	44.4	34	2	AAO23567	AAO23567 Helicobac	616	44.4	46	4	ABW43867	Abw43867 Peptide #
544	44.4	34	6	AAW5095	Aaw5095 Rat SIII	617	44.4	46	4	AAW37782	Aaw37782 Peptide #
545	44.4	34	10	AEF38056	Aef38056 Human ser	618	44.4	46	4	ABW26792	Abw26792 Protein #
546	44.4	35	10	AEF13661	Aef13661 Human MBL	619	44.4	46	4	AAW77593	Aaw77593 Human bon
547	44.4	36	4	ABW37297	Abw37297 Peptide #	620	44.4	46	4	AAW64850	Aaw64850 Human bra
548	44.4	36	4	AAW88075	Aaw88075 Human imm	621	44.4	46	4	ABG59242	Abg59242 Human liv
549	44.4	36	4	AAE03915	Aae03915 Human gen	622	44.4	46	4	ADG50557	Adg50557 Staphyloc
550	44.4	36	4	ABG28481	Abg28481 Novel hum	623	44.4	47	2	AAW36149	Aaw36149 Mutant N.
551	44.4	36	8	ADK01635	Adk01635 Hepatitis	624	44.4	47	2	AAW36150	Aaw36150 Wild type
552	44.4	36	8	ADS93011	Ads93011 Human alp	625	44.4	47	2	AAW11508	Aaw11508 Human 5'
553	44.4	37	2	AAW65450	Aaw65450 Lebetin d	626	44.4	47	2	AAW07778	Aaw07778 Human sec
554	44.4	37	3	AAW45168	Aaw45168 Human sec	627	44.4	47	2	ADY27478	Ady27478 Amino aci
555	44.4	37	4	AAW91020	Aaw91020 Human imm	628	44.4	47	9	ADX83802	Adx83802 Human cor
556	44.4	37	4	AAW64430	Aaw64430 Human sec	629	44.4	47	9	ADZ59262	Adz59262 Bidentate
557	44.4	37	6	ABW72198	Abw72198 Staphyloc	630	44.4	48	2	AAW13552	Aaw13552 Human c-I
558	44.4	37	8	ABO57148	AbO57148 Human gen	631	44.4	48	2	AAW13551	Aaw13551 Human c-I
559	44.4	38	2	AAW37637	Aaw37637 Peptide c	632	44.4	48	4	ABW41156	Abw41156 Peptide #
560	44.4	38	2	AAW65449	Aaw65449 Lebetin d	633	44.4	48	4	AAW34934	Aaw34934 Peptide #
561	44.4	38	4	ABB39710	Abb39710 Peptide #	634	44.4	48	4	ABW25192	Abw25192 Peptide #
562	44.4	38	4	AAW33287	Aaw33287 Peptide #	635	44.4	48	4	AAW74818	Aaw74818 Human bon
563	44.4	38	4	AAW73068	Aaw73068 Human bon	636	44.4	48	4	AAW62016	Aaw62016 Human bra
564	44.4	38	4	AAW60428	Aaw60428 Human bra	637	44.4	48	4	ABG56599	Abg56599 Human liv
565	44.4	38	4	ABG4782	Abg4782 Human liv	638	44.4	48	5	ABG44605	Abg44605 Human pep
566	44.4	38	5	AAU87968	Aau87968 Human WW	639	44.4	49	4	AAW14643	Aaw14643 Peptide #
567	44.4	38	5	ABG42912	Abg42912 Human pep	640	44.4	49	4	ABW40367	Abw40367 Peptide #
568	44.4	38	5	ADH32374	Adh32374 Yeast smo	641	44.4	49	4	ABW33803	Abw33803 Peptide #
569	44.4	38	7	ADW49229	Adw49229 Novel hum	642	44.4	49	4	ABW27062	Abw27062 Peptide #
570	44.4	38	9	ABW94521	Abw94521 M. xanthu	643	44.4	49	4	ABW28422	Abw28422 Peptide #
571	44.4	38	10	AEF43788	Aef43788 Lebetin 2	644	44.4	49	4	ABW19058	Abw19058 Protein #
572	44.4	39	8	ABO55221	AbO55221 Human gen	645	44.4	49	4	AAW66777	Aaw66777 Human bon
573	44.4	39	9	ADV13140	Adv13140 Human pho	646	44.4	49	4	AAW73891	Aaw73891 Human bon
574	44.4	41	2	AAW11905	Aaw11905 Protein C	647	44.4	49	4	AAW54376	Aaw54376 Human bra
575	44.4	41	2	AAW14037	Aaw14037 Repeat se	648	44.4	49	4	ABG55642	Abg55642 Human liv
576	44.4	41	3	ABG05922	Abg05922 Arabidops	649	44.4	49	4	ABG48445	Abg48445 Human liv
577	44.4	41	4	AAW84382	Aaw84382 Human imm	650	44.4	49	4	AAW02368	Aaw02368 Peptide #
578	44.4	41	6	ABR83861	AbR83861 Caenorhab	651	44.4	49	5	ABG36432	Abg36432 Human pep
579	44.4	42	6	ABR57036	AbR57036 Regulator	652	44.4	49	5	ABG43779	Abg43779 Human pep
580	44.4	42	7	ADP69907	Adp69907 Acma-type	653	44.4	49	9	ABG30857	Abg30857 Pertussis
581	44.4	42	8	ADP79566	Adp79566 Human MAD	654	44.4	50	4	ABG22352	Abg22352 Novel hum
582	44.4	43	2	AAW82294	Aaw82294 Dynamin 4	655	44.4	50	6	ABP99632	Abp99632 Human sec
583	44.4	43	4	ABG22764	Abg22764 Novel hum	656	44.4	50	6	ABR01112	AbR01112 Human gen
584	44.4	43	6	ABU19571	Abu19571 Protein e	657	44.4	50	8	ADU79164	Adu79164 Human pro
585	44.4	43	9	ADY20643	Ady20643 PRO polyp	658	44.4	50	8	ADU79178	Adu79178 Human pro
586	44.4	44	2	AAW18297	Aaw18297 Modified	659	44.4	51	2	AAW19528	Aaw19528 Amino aci
587	44.4	44	2	AAW18300	Aaw18300 Modified	660	44.4	51	3	AAW45159	Aaw45159 Human sec
588	44.4	44	2	AAW18307	Aaw18307 Modified	661	44.4	51	3	AAW61663	Aaw61663 Arabidops
589	44.4	44	2	AAW18299	Aaw18299 Modified	662	44.4	51	3	ABP35025	Abp35025 Human ORF
590	44.4	44	2	AAW18301	Aaw18301 Modified	663	44.4	51	5	ADK35859	Adk35859 Novel hum
591	44.4	44	2	AAW18309	Aaw18309 Modified	664	44.4	52	4	AAW74895	Aaw74895 Human col
592	44.4	44	2	AAW18298	Aaw18298 Modified	665	44.4	52	4	AAU65249	Aau65249 Propionib
593	44.4	44	2	AAW18303	Aaw18303 Human pro	666	44.4	52	5	ABP07470	Abp07470 Human ORF
594	44.4	44	4	AAW36402	Aaw36402 Human pro	667	44.4	52	5	ABP34254	Abp34254 Human gly
595	44.4	44	7	ADW50094	Adw50094 Human vit	668	44.4	52	6	ABW61768	Abw61768 Propionib
596	44.4	44	7	ADP69958	Adp69958 Acma-type	669	44.4	52	8	ADM01104	Adm01104 Legume le
597	44.4	44	8	ABO57670	AbO57670 Human gen	670	44.4	52	8	ADL95705	Adl95705 Legume le
598	44.4	44	8	ADQ26900	Adq26900 Human pro	671	44.4	53	8	ADX80309	Adx80309 Plant ful
599	44.4	44	9	ADZ14055	Adz14055 Human pro	672	44.4	53	8	ABM93561	Abm93561 M. xanthu
600	44.4	44	9	ADZ14076	Adz14076 Human pro	673	44.4	54	3	AAW49275	Aaw49275 Arabidops
601	44.4	44	9	ADZ14077	Adz14077 Human pro	674	44.4	54	6	ABP76021	Abp76021 Human GEN
602	44.4	45	2	AAW75710	Aaw75710 Partial h	675	44.4	54	6	ABP76023	Abp76023 Human GEN
603	44.4	45	4	AAW33007	Aaw33007 Peptide #	676	44.4	54	6	ABP76177	Abp76177 Human GEN
604	44.4	45	4	AAW87412	Aaw87412 Human imm	677	44.4	54	6	ABP76022	Abp76022 Human GEN
605	44.4	45	4	ABG23395	Abg23395 Novel hum	678	44.4	55	4	AAU50923	Aau50923 Propionib
606	44.4	45	5	ABW79946	Abw79946 Human pro	679	44.4	55	4	AAU44636	Aau44636 Propionib
607	44.4	45	5	ABB79949	Abb79949 Human pro	680	44.4	55	5	ABP31524	Abp31524 Human gly

681	4	44.4	55	6	ABM411155	Abm411155 Propionib	754	4	44.4	62	6	ABM64244	Abm64244 Propionib
682	4	44.4	55	6	ABM47442	Abm47442 Propionib	755	4	44.4	63	3	AAQ42912	AaQ42912 Arabidops
683	4	44.4	56	2	AAr11103	Aar11103 Propione bo	756	4	44.4	63	3	AAQ09746	AaQ09746 Arabidops
684	4	44.4	56	2	AAr11102	Aar11102 Human bon	757	4	44.4	63	4	AAU55093	AaU55093 Propionib
685	4	44.4	56	2	AAQ00446	AaQ00446 Human sec	758	4	44.4	63	6	ABM51612	Abm51612 Propionib
686	4	44.4	57	4	AAm17778	Aam17778 Peptide #	759	4	44.4	63	8	ADL69531	AdL69531 Insulin-1
687	4	44.4	57	4	AAm30288	Aam30288 Peptide #	760	4	44.4	64	3	AAQ01175	AaQ01175 Human gen
688	4	44.4	57	4	AAm86357	Aam86357 Human imm	761	4	44.4	64	4	AAE03973	AaE03973 Human gen
689	4	44.4	57	4	ABG51646	AbG51646 Human liv	762	4	44.4	64	5	ABP10905	AbP10905 Human ORF
690	4	44.4	57	5	ABP02961	AbP02961 Human ORF	763	4	44.4	65	3	AAQ32879	AaQ32879 Zea may
691	4	44.4	57	8	ADX92199	AdX92199 Plant ful	764	4	44.4	65	3	AAU52432	AaU52432 Propionib
692	4	44.4	58	2	AAr48161	Aar48161 BPTI (11D	765	4	44.4	65	4	ABG13119	AbG13119 Novel hum
693	4	44.4	58	2	AAr48170	Aar48170 BPTI (11P	766	4	44.4	65	5	ABP04984	AbP04984 Human ORF
694	4	44.4	58	2	AAr48177	Aar48177 BPTI (11T	767	4	44.4	65	6	ABM48951	Abm48951 Propionib
695	4	44.4	58	2	AAr48174	Aar48174 BPTI (11P	768	4	44.4	65	8	ADU98759	Adu98759 Borrelia
696	4	44.4	58	2	AAr48181	Aar48181 BPTI (11E	769	4	44.4	66	6	ABU19955	AbU19955 Protein e
697	4	44.4	58	2	AAr48198	Aar48198 BPTI (11E	770	4	44.4	67	4	AAm21412	Aam21412 Peptide #
698	4	44.4	58	2	AAr48193	Aar48193 BPTI (11L	771	4	44.4	67	4	AAQ74748	AaQ74748 Human col
699	4	44.4	58	2	AAr48166	Aar48166 BPTI (11S	772	4	44.4	67	4	ABB43752	AbB43752 Peptide #
700	4	44.4	58	2	AAr48169	Aar48169 BPTI (11S	773	4	44.4	67	4	ABB26695	AbB26695 Protein #
701	4	44.4	58	2	AAr48175	Aar48175 BPTI (11A	774	4	44.4	67	4	AAm64714	Aam64714 Human bra
702	4	44.4	58	2	AAr48180	Aar48180 BPTI (11P	775	4	44.4	67	4	ABG59124	AbG59124 Human liv
703	4	44.4	58	2	AAr48197	Aar48197 BPTI (8S,	776	4	44.4	67	9	ABE42462	Aeb42462 L. pneumo
704	4	44.4	58	2	AAW80030	Aaw80030 Bovine pa	777	4	44.4	68	2	AAU20813	AaU20813 Human neu
705	4	44.4	58	2	AAW80033	Aaw80033 Bovine pa	778	4	44.4	68	4	AAU41313	AaU41313 Propionib
706	4	44.4	58	2	AAW80036	Aaw80036 Bovine pa	779	4	44.4	68	4	ABG02152	AbG02152 Novel hum
707	4	44.4	58	2	AAW80069	Aaw80069 Bovine pa	780	4	44.4	68	5	ABP00072	AbP00072 Human ORF
708	4	44.4	58	2	AAW80003	Aaw80003 Bovine pa	781	4	44.4	68	6	ABM37832	Abm37832 Propionib
709	4	44.4	58	2	AAW80039	Aaw80039 Bovine pa	782	4	44.4	68	7	ADB61816	Adb61816 Human inh
710	4	44.4	58	2	AAW80068	Aaw80068 Bovine pa	783	4	44.4	68	7	ADB61813	Adb61813 Human inh
711	4	44.4	58	2	AAW80057	Aaw80057 Bovine pa	784	4	44.4	68	8	ADK48020	AdK48020 Streptoco
712	4	44.4	58	2	AAW80001	Aaw80001 Bovine pa	785	4	44.4	68	8	ADR94505	Adr94505 Novel S.
713	4	44.4	58	2	AAW80127	Aaw80127 Bovine pa	786	4	44.4	68	9	AEA58375	Aea58375 Streptoco
714	4	44.4	58	2	AAW80004	Aaw80004 Bovine pa	787	4	44.4	69	2	AAQ72540	AaQ72540 ADP-ribos
715	4	44.4	58	2	AAW80035	Aaw80035 Bovine pa	788	4	44.4	69	2	AAU41811	AaU41811 Escherich
716	4	44.4	58	2	AAW80080	Aaw80080 Bovine pa	789	4	44.4	69	2	AAW95221	AaW95221 Verotoxin
717	4	44.4	58	2	AAW80085	Aaw80085 Bovine pa	790	4	44.4	69	2	AAU43008	AaU43008 Mutant Sh
718	4	44.4	58	2	AAW80013	Aaw80013 Bovine pa	791	4	44.4	69	2	AAU43001	AaU43001 Mutant Sh
719	4	44.4	58	2	AAW80056	Aaw80056 Bovine pa	792	4	44.4	69	2	AAU43003	AaU43003 Mutant Sh
720	4	44.4	58	2	AAW80075	Aaw80075 Bovine pa	793	4	44.4	69	2	AAU43005	AaU43005 Mutant Sh
721	4	44.4	58	2	AAW80126	Aaw80126 Bovine pa	794	4	44.4	69	2	AAU43007	AaU43007 Mutant Sh
722	4	44.4	58	2	AAW80078	Aaw80078 Bovine pa	795	4	44.4	69	2	AAU43010	AaU43010 Mutant Sh
723	4	44.4	58	2	AAW80090	Aaw80090 Bovine pa	796	4	44.4	69	2	AAU43012	AaU43012 Mutant Sh
724	4	44.4	58	2	AAW80123	Aaw80123 Bovine pa	797	4	44.4	69	2	AAU43015	AaU43015 Mutant Sh
725	4	44.4	58	2	AAW80070	Aaw80070 Bovine pa	798	4	44.4	69	3	AAU68360	AaU68360 Verotoxin
726	4	44.4	58	2	AAW80071	Aaw80071 Bovine pa	799	4	44.4	69	3	AAQ22733	AaQ22733 Zea may
727	4	44.4	58	2	AAW80093	Aaw80093 Bovine pa	800	4	44.4	69	3	AAQ22733	AaQ22733 Zea may
728	4	44.4	58	2	AAW80095	Aaw80095 Bovine pa	801	4	44.4	69	4	AAW92284	AaW92284 Human dig
729	4	44.4	58	2	AAW80040	Aaw80040 Bovine pa	802	4	44.4	69	4	ABB14787	Abb14787 Human ner
730	4	44.4	58	2	AAW80058	Aaw80058 Bovine pa	803	4	44.4	69	4	AAE66234	Aae66234 E. coli he
731	4	44.4	58	2	AAW80081	Aaw80081 Bovine pa	804	4	44.4	69	8	ADF39753	AdF39753 E. coli he
732	4	44.4	58	2	AAW80089	Aaw80089 Bovine pa	805	4	44.4	69	8	ADX89931	AdX89931 Plant ful
733	4	44.4	58	2	AAW80128	Aaw80128 Bovine pa	806	4	44.4	70	9	ADV34850	Adv34850 Shiga tox
734	4	44.4	58	2	AAW80055	Aaw80055 Bovine pa	807	4	44.4	70	6	ABP78501	AbP78501 N. gonorr
735	4	44.4	58	2	AAW80094	Aaw80094 Bovine pa	808	4	44.4	70	7	ABO77947	AbO77947 Pseudomon
736	4	44.4	58	2	AAW80090	Aaw80090 Bovine pa	809	4	44.4	70	8	ADX95352	AdX95352 Plant ful
737	4	44.4	58	2	AAW80002	Aaw80002 Bovine pa	810	4	44.4	70	9	ABM94713	Abm94713 M. xanthu
738	4	44.4	58	2	AAW80054	Aaw80054 Bovine pa	811	4	44.4	71	4	AAE50535	Aae50535 Rat C-CAM
739	4	44.4	58	2	AAW80084	Aaw80084 Bovine pa	812	4	44.4	71	5	ABE53126	AbE53126 Human ORF
740	4	44.4	58	2	AAW80122	Aaw80122 Bovine pa	813	4	44.4	71	7	ADF07705	AdF07705 Bacterial
741	4	44.4	58	4	AAW86826	Aaw86826 Human imm	814	4	44.4	71	8	ABO56689	AbO56689 Human gen
742	4	44.4	59	5	ABP00924	AbP00924 Yeast ORF	815	4	44.4	72	3	AAW71701	AaW71701 Truncated
743	4	44.4	60	2	AAU08823	AaU08823 Yeast Ynu	816	4	44.4	72	3	AAU90847	AaU90847 Cotton de
744	4	44.4	60	2	AAU08795	AaU08795 Yeast Nup	817	4	44.4	72	5	ABR01785	AbR01785 Human bre
745	4	44.4	60	5	ABP09967	AbP09967 Human ORF	818	4	44.4	72	9	ADY51931	AdY51931 Phage SPO
746	4	44.4	60	10	AAE91657	Aae91657 HLA-B*400	819	4	44.4	73	4	AAU62590	AaU62590 Propionib
747	4	44.4	60	10	AAE91655	Aae91655 HLA-B*400	820	4	44.4	73	4	AAE50534	Aae50534 Mouse C-C
748	4	44.4	60	10	AAE91656	Aae91656 HLA-B*400	821	4	44.4	73	6	ABM59109	Abm59109 Propionib
749	4	44.4	61	4	AAW84043	Aaw84043 Human imm	822	4	44.4	73	7	ABM74310	Abm74310 DNA clone
750	4	44.4	62	2	AAW27868	Aaw27868 Staphyloc	823	4	44.4	74	3	AAW42911	AaW42911 Arabidops
751	4	44.4	62	3	AAE38599	Aae38599 Human sec	824	4	44.4	74	4	AAW43511	AaW43511 Human pol
752	4	44.4	62	4	AAU67725	AaU67725 Propionib	825	4	44.4	74	8	ADM24532	Adm24532 Human PRO
753	4	44.4	62	6	ADA05627	Ada05627 IGF-1R ag	826	4	44.4	74	8	ADM97961	Adm97961 5-epi-Ari

[illegible]

973 4 44.4 90 9 AD285745 Adz85745 Human leu
974 4 44.4 91 3 AAG53511 Aag53511 Arabidops
975 4 44.4 91 5 AA017189 Aa017189 Human sec
976 4 44.4 91 5 AA017222 Aa017222 Human sec
977 4 44.4 91 5 ABG64786 Abg64786 Human alb
978 4 44.4 91 5 ABG64788 Abg64788 Human alb
979 4 44.4 91 5 ABP51250 Abp51250 Human MDD
980 4 44.4 91 6 ADB07134 Adb07134 Alloiococ
981 4 44.4 91 8 ADL78053 Adl78053 Albumin f
982 4 44.4 91 8 ADL78055 Adl78055 Albumin f
983 4 44.4 91 10 AEF79706 Aef79706 E. coli a
984 4 44.4 92 4 AAO06285 Aao06285 Human pol
985 4 44.4 92 5 AAU79450 Aau79450 HLA-G alp
986 4 44.4 92 7 ADG15775 Aag15775 Rv3879c 8
987 4 44.4 92 7 ABO65306 Abo65306 Klebsiell
988 4 44.4 93 2 AAW82562 Aaw82562 Corn glyc
989 4 44.4 93 3 AAY64754 Aay64754 Human 5,
990 4 44.4 93 4 AAE05243 Aae05243 Corn glyc
991 4 44.4 93 4 AAM90556 Aam90556 Human inm
992 4 44.4 93 5 ABP01546 Abp01546 Human ORF
993 4 44.4 93 5 AAU76197 Aau76197 Corn glyc
994 4 44.4 93 6 ABO00505 Abo00505 Novel hum
995 4 44.4 93 7 AAE38777 Aae38777 Corn glyc
996 4 44.4 93 8 ADU72318 Adu72318 Signal pe
997 4 44.4 93 8 ADV89101 Adv89101 Streptoco
998 4 44.4 93 8 ADV80354 Adv80354 Streptoco
999 4 44.4 93 8 ADV82466 Adv82466 Streptoco
1000 4 44.4 93 9 ADZ73309 Adz73309 Human inc

ALIGNMENTS

RESULT 1
ADRI2417
ID ADRI2417 standard; peptide; 9 AA.
XX
AC ADRI2417;
XX
DT 04-NOV-2004 (first entry)
XX
XX Vaccinia virus immunisation peptide 165.
XX
XX virucide; vaccine; immunisation; vaccinia; variola; immune response.
XX
XX Vaccinia virus; strain Ankara.
XX
XX WO2004067032-A2.
XX
XX 12-AUG-2004.
XX
XX 26-JAN-2004; 2004WO-US002141.
XX
XX 24-JAN-2003; 2003US-0442846P.
XX
XX (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
XX
XX Terajima M, Cruz J, Ennis FA;
XX
XX WPI; 2004-594031/57.
XX
XX Immunizing an individual against infection by vaccinia and/or variola
PT virus comprises inducing an immune response against a polypeptide
PT comprising peptide 74A or 165.
XX
XX Claim 19; SEQ ID NO 2; 32pp; English.
XX
XX The invention relates to a method of immunizing an individual against
CC infection by vaccinia and/or variola virus by inducing an immune response
CC against a polypeptide comprising peptide 74A or 165, or its immunogenic
CC fragments or mutants. The method is useful for immunizing an individual
CC against infection by vaccinia and/or variola virus. This sequence
CC represents a vaccinia virus peptide used in the method of the invention.

XX
SQ Sequence 9 AA;
XX
Query Match 100.0%; Score 9; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDTFYYV 9
|||||
Db 1 KVDDTFYYV 9
|||||
RESULT 2
ADJ66069
ID ADJ66069 standard; protein; 150 AA.
XX
AC ADJ66069;
XX
DT 06-MAY-2004 (first entry)
XX
DE MVA C7L encoded amino acid sequence, seq id 1.
XX
KW Virucide; vaccine; virus; Vaccinia virus; host range gene; avipoxvirus;
avian.
XX
OS Vaccinia virus (strain Ankara).
XX
XX WO2004015118-A1.
XX
XX 19-FEB-2004.
XX
XX 29-JUL-2003; 2003WO-EP008359.
XX
XX 07-AUG-2002; 2002DK-00001189.
XX
XX (BAVA-) BAVARIAN NORDIC AS.
XX
XX Howley P, Meisinger C;
XX
XX WPI; 2004-180680/17.
XX
XX N-PSDB; ADJ66068.
XX
XX New avipoxvirus comprising in the viral genome a Vaccinia virus host
PT range gene or a homologue of the host range gene, useful for the
PT preparation of a medicament or as a vaccine for affecting immunological
PT response in human.
XX
XX Disclosure; SEQ ID NO 2; 53pp; English.
XX
XX The invention relates to a new avipoxvirus comprising in the viral
CC genome, a Vaccinia virus host range gene or a homologue of the host range
CC gene, provided that the host range gene is not the E3L gene if the
CC avipoxvirus is a recombinant Canary poxvirus comprising in the viral
CC genome the Vaccinia virus K3L gene as well as expression cassettes for
CC HIV gag-pro, gp120/TM and a Nef/Pol poly-epitope string, respectively.
CC The virus is useful for the preparation of a medicament or as a vaccine.
CC The composition or the vaccine is useful as a drug for affecting,
CC preferably inducing immunological response in a living animal, including
CC a human. The Vaccinia virus host range gene or its homologue, preferably
CC a host range gene is useful to increase the titer of avipoxviruses
CC produced from avian cells after infection of the cells with the
CC avipoxvirus, where the host range gene is expressed in the cells. The
CC current sequence represents the amino acid sequence encoded by the C7L
CC (host range gene) region of modified Vaccinia Ankara.
XX
XX Sequence 150 AA;
XX
Query Match 100.0%; Score 9; DB 8; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDTFYYV 9
|||||

Db 74 KVDDTFYV 82

RESULT 3
ADRI2435
ID ADR12435 standard; peptide; 9 AA.
XX AC ADR12435;
XX DT 04-NOV-2004 (first entry)
XX DE Vaccinia virus immunisation peptide 165 variant #3.
XX KW virucide; vaccine; immunisation; vaccinia; variola; immune response.
XX OS Vaccinia virus; strain Ankara.
XX PN WO2004067032-A2.
XX PD 12-AUG-2004.
XX PF 26-JAN-2004; 2004WO-US002141.
XX PR 24-JAN-2003; 2003US-0442846P.
XX PA (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
XX PI Terajima M, Cruz J, Ennis FA;
XX DR WPI; 2004-594031/57.
XX PT Immunizing an individual against infection by vaccinia and/or variola virus comprises inducing an immune response against a polypeptide comprising peptide 74A or 165.
XX PS Disclosure; SEQ ID NO 21; 32pp; English.
XX CC The invention relates to a method of immunizing an individual against infection by vaccinia and/or variola virus by inducing an immune response against a polypeptide comprising peptide 74A or 165, or its immunogenic fragments or mutants. The method is useful for immunizing an individual against infection by vaccinia and/or variola virus. This sequence represents a vaccinia virus peptide used in the method of the invention.
XX SQ Sequence 9 AA;
Query Match 88.9%; Score 8; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTFYV 9
Db |||||
2 VDDTFYV 9

RESULT 4
ADRI2433
ID ADR12433 standard; peptide; 9 AA.
XX AC ADR12433;
XX DT 04-NOV-2004 (first entry)
XX DE Vaccinia virus immunisation peptide 165 variant #1.
XX KW virucide; vaccine; immunisation; vaccinia; variola; immune response.
XX OS Vaccinia virus; strain Ankara.
XX PN WO2004067032-A2.
XX PD 12-AUG-2004.
XX PF 26-JAN-2004; 2004WO-US002141.
XX PR 24-JAN-2003; 2003US-0442846P.
XX PA (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
XX PI Terajima M, Cruz J, Ennis FA;
XX DR WPI; 2004-594031/57.
XX PT Immunizing an individual against infection by vaccinia and/or variola virus comprises inducing an immune response against a polypeptide comprising peptide 74A or 165.
XX PS Disclosure; SEQ ID NO 21; 32pp; English.
XX CC The invention relates to a method of immunizing an individual against infection by vaccinia and/or variola virus by inducing an immune response against a polypeptide comprising peptide 74A or 165, or its immunogenic fragments or mutants. The method is useful for immunizing an individual against infection by vaccinia and/or variola virus. This sequence represents a vaccinia virus peptide used in the method of the invention.
XX SQ Sequence 9 AA;
Query Match 88.9%; Score 8; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTFYV 9
Db |||||
2 VDDTFYV 9

PF 26-JAN-2004; 2004WO-US002141.
XX
PR 24-JAN-2003; 2003US-0442846P.
XX
PA (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
XX
PI Terajima M, Cruz J, Ennis FA;
XX
DR WPI; 2004-594031/57.
XX
PT Immunizing an individual against infection by vaccinia and/or variola virus comprises inducing an immune response against a polypeptide comprising peptide 74A or 165.
XX
PS Disclosure; SEQ ID NO 19; 32pp; English.
XX
CC The invention relates to a method of immunizing an individual against infection by vaccinia and/or variola virus by inducing an immune response against a polypeptide comprising peptide 74A or 165, or its immunogenic fragments or mutants. The method is useful for immunizing an individual against infection by vaccinia and/or variola virus. This sequence represents a vaccinia virus peptide used in the method of the invention.
XX
SQ Sequence 9 AA;
Query Match 88.9%; Score 8; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTFYV 9
Db |||||
2 VDDTFYV 9

RESULT 5
ADRI2434
ID ADR12434 standard; peptide; 9 AA.
XX
AC ADR12434;
XX
DT 04-NOV-2004 (first entry)
XX
DE Vaccinia virus immunisation peptide 165 variant #2.
XX
KW virucide; vaccine; immunisation; vaccinia; variola; immune response.
XX
OS Vaccinia virus; strain Ankara.
XX
PN WO2004067032-A2.
XX
PD 12-AUG-2004.
XX
PF 26-JAN-2004; 2004WO-US002141.
XX
PR 24-JAN-2003; 2003US-0442846P.
XX
PA (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
XX
PI Terajima M, Cruz J, Ennis FA;
XX
DR WPI; 2004-594031/57.
XX
PT Immunizing an individual against infection by vaccinia and/or variola virus comprises inducing an immune response against a polypeptide comprising peptide 74A or 165.
XX
PS Disclosure; SEQ ID NO 20; 32pp; English.
XX
CC The invention relates to a method of immunizing an individual against infection by vaccinia and/or variola virus by inducing an immune response against a polypeptide comprising peptide 74A or 165, or its immunogenic fragments or mutants. The method is useful for immunizing an individual against infection by vaccinia and/or variola virus. This sequence represents a vaccinia virus peptide used in the method of the invention.
XX
SQ Sequence 9 AA;
Query Match 88.9%; Score 8; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTFYV 9
Db |||||
2 VDDTFYV 9

CC represents a vaccinia virus peptide used in the method of the invention.
 XX Sequence 9 AA;

Query Match 88.9%; Score 8; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFYVV 9
 |||||
 Db 2 VDDTFYVV 9

RESULT 6

ADRI2442
 ID ADRI2442 standard; peptide; 9 AA.

XX AC

XX ADR12442;

XX 04-NOV-2004 (first entry)

XX Vaccinia virus immunisation peptide 165 variant #10.

XX virucide; vaccine; immunisation; vaccinia; variola; immune response.

XX Vaccinia virus; strain Ankara.

XX WO2004067032-A2.

XX 12-AUG-2004.

XX 26-JAN-2004; 2004WO-US002141.

XX 24-JAN-2003; 2003US-0442846P.

XX (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.

XX Terajima M, Cruz J, Ennis FA;

XX WPI; 2004-594031/57.

XX Immunizing an individual against infection by vaccinia and/or variola
 PT virus comprises inducing an immune response against a polypeptide
 PT comprising peptide 74A or 165.

XX Disclosure; SEQ ID NO 28; 32pp; English.

XX The invention relates to a method of immunizing an individual against
 CC infection by vaccinia and/or variola virus by inducing an immune response
 CC against a polypeptide comprising peptide 74A or 165, or its immunogenic
 CC fragments or mutants. The method is useful for immunizing an individual
 CC against infection by vaccinia and/or variola virus. This sequence
 CC represents a vaccinia virus peptide used in the method of the invention.

XX Sequence 9 AA;

Query Match 66.7%; Score 6; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTF 6
 |||||
 Db 1 KVDDTF 6

RESULT 7

ADRI2437
 ID ADRI2437 standard; peptide; 9 AA.

XX AC

XX ADR12437;

XX 04-NOV-2004 (first entry)

XX Immunizing an individual against infection by vaccinia and/or variola

DE Vaccinia virus immunisation peptide 165 variant #5.
 XX virucide; vaccine; immunisation; vaccinia; variola; immune response.

XX Vaccinia virus; strain Ankara.

XX WO2004067032-A2.

XX 12-AUG-2004.

XX 26-JAN-2004; 2004WO-US002141.

XX 24-JAN-2003; 2003US-0442846P.

XX (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.

XX Terajima M, Cruz J, Ennis FA;

XX WPI; 2004-594031/57.

XX Immunizing an individual against infection by vaccinia and/or variola
 PT virus comprises inducing an immune response against a polypeptide
 PT comprising peptide 74A or 165.

XX Disclosure; SEQ ID NO 23; 32pp; English.

XX The invention relates to a method of immunizing an individual against
 CC infection by vaccinia and/or variola virus by inducing an immune response
 CC against a polypeptide comprising peptide 74A or 165, or its immunogenic
 CC fragments or mutants. The method is useful for immunizing an individual
 CC against infection by vaccinia and/or variola virus. This sequence
 CC represents a vaccinia virus peptide used in the method of the invention.

XX Sequence 9 AA;

Query Match 66.7%; Score 6; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVV 9
 |||||
 Db 4 DTFYVV 9

RESULT 8

ADRI2438
 ID ADRI2438 standard; peptide; 9 AA.

XX AC

XX ADR12438;

XX 04-NOV-2004 (first entry)

XX Vaccinia virus immunisation peptide 165 variant #6.

XX virucide; vaccine; immunisation; vaccinia; variola; immune response.

XX Vaccinia virus; strain Ankara.

XX WO2004067032-A2.

XX 12-AUG-2004.

XX 26-JAN-2004; 2004WO-US002141.

XX 24-JAN-2003; 2003US-0442846P.

XX (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.

XX Terajima M, Cruz J, Ennis FA;

XX WPI; 2004-594031/57.

XX Immunizing an individual against infection by vaccinia and/or variola

PT virus comprises inducing an immune response against a polypeptide
 PT comprising peptide 74A or 165.

FS Disclosure; SEQ ID NO 24; 32pp; English.

XX The invention relates to a method of immunizing an individual against
 CC infection by vaccinia and/or variola virus by inducing an immune response
 CC against a polypeptide comprising peptide 74A or 165, or its immunogenic
 CC fragments or mutants. The method is useful for immunizing an individual
 CC against infection by vaccinia and/or variola virus. This sequence
 CC represents a vaccinia virus peptide used in the method of the invention.

XX Sequence 9 AA;

Query Match 66.7%; Score 6; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
 |||||
 Db 4 DTFYV 9

RESULT 9

ID ADR12444 standard; peptide; 9 AA.
 AC ADR12444;

XX 04-NOV-2004 (first entry)
 DT Vaccinia virus immunisation peptide 165 variant #12.

DE virucide; vaccine; immunisation; vaccinia; variola; immune response.
 KW Vaccinia virus; strain Ankara.

OS WO2004067032-A2.

PN 12-AUG-2004.

XX 26-JAN-2004; 2004WO-US002141.

PF 24-JAN-2003; 2003US-0442846P.

PR (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
 PA Terajima M, Cruz J, Ennis FA;
 XX WPI; 2004-594031/57.

XX Immunizing an individual against infection by vaccinia and/or variola
 PT virus comprises inducing an immune response against a polypeptide
 PT comprising peptide 74A or 165.

PS Disclosure; SEQ ID NO 30; 32pp; English.

XX The invention relates to a method of immunizing an individual against
 CC infection by vaccinia and/or variola virus by inducing an immune response
 CC against a polypeptide comprising peptide 74A or 165, or its immunogenic
 CC fragments or mutants. The method is useful for immunizing an individual
 CC against infection by vaccinia and/or variola virus. This sequence
 CC represents a vaccinia virus peptide used in the method of the invention.

XX Sequence 9 AA;

Query Match 66.7%; Score 6; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
 |||||
 Db 4 DTFYV 9

RESULT 10
 ADR12436

ID ADR12436 standard; peptide; 9 AA.

XX ADR12436;

AC 04-NOV-2004 (first entry)

DT Vaccinia virus immunisation peptide 165 variant #4.

DE virucide; vaccine; immunisation; vaccinia; variola; immune response.

XX Vaccinia virus; strain Ankara.

OS WO2004067032-A2.

PN 12-AUG-2004.

XX 26-JAN-2004; 2004WO-US002141.

PF 24-JAN-2003; 2003US-0442846P.

PR (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.

PA Terajima M, Cruz J, Ennis FA;
 XX WPI; 2004-594031/57.

DR Immunizing an individual against infection by vaccinia and/or variola
 XX virus comprises inducing an immune response against a polypeptide
 PT comprising peptide 74A or 165.

PT Disclosure; SEQ ID NO 22; 32pp; English.

PS The invention relates to a method of immunizing an individual against
 CC infection by vaccinia and/or variola virus by inducing an immune response
 CC against a polypeptide comprising peptide 74A or 165, or its immunogenic
 CC fragments or mutants. The method is useful for immunizing an individual
 CC against infection by vaccinia and/or variola virus. This sequence
 CC represents a vaccinia virus peptide used in the method of the invention.

XX Sequence 9 AA;

Query Match 66.7%; Score 6; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
 |||||
 Db 4 DTFYV 9

RESULT 11
 ADR12443

ID ADR12443 standard; peptide; 9 AA.

XX ADR12443;

AC 04-NOV-2004 (first entry)

DT Vaccinia virus immunisation peptide 165 variant #11.

DE virucide; vaccine; immunisation; vaccinia; variola; immune response.

XX Vaccinia virus; strain Ankara.

OS WO2004067032-A2.

PN 12-AUG-2004.

XX 26-JAN-2004; 2004WO-US002141.

CC plant with a recombinant DNA construct comprising a promoter region
 CC functional in a plant cell operably joined to a polynucleotide encoding a
 CC polypeptide associated with the property, and growing the transformed
 CC plant. The property is selected from improving plant cold tolerance, for
 CC manipulating growth rate in plant cells by modification of the cell cycle
 CC pathway, for improving plant drought tolerance, for providing increased
 CC resistance to plant disease, for galactomannan production, for production
 CC of plant growth regulators, for improving plant heat tolerance, for
 CC improving plant tolerance to herbicides, for increasing the rate of
 CC homologous recombination in plants, for lignin production, for improving
 CC plant tolerance to extreme osmotic conditions, for improving plant
 CC tolerance to pathogens or pests, for yield improvement by modification of
 CC photosynthesis, for modifying seed oil yield and/or content, for
 CC modifying seed protein yield and/or content, for yield improvement by
 CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake
 CC and for yield improvement by providing improved plant growth and
 CC development under at least one stress condition. The polynucleotide may
 CC also encode a plant transcription factor. The methods and compositions of
 CC the present invention are useful in the field of biochemistry and
 CC genetics, in particular for producing transgenic plants with improved
 CC biological characteristics such as increased yield, improved nitrogen
 CC flow, increasing plant tolerance to cold or heat, improving plant
 CC tolerance to extreme osmotic and drought conditions, and improving plant
 CC tolerance to plant pests or pathogens. They can also be used in physical
 CC arrays of molecules, plant breeding markers, computer-based storage and
 CC analysis systems. The present sequence is one of the 5544 plant protein
 CC sequences of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20040216190.

XX Sequence 267 AA;

Query Match 66.7%; Score 6; DB 8; Length 267;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFFY 8
 DB 21 DDTFFY 26
 |||||

RESULT 14

AAG42271 AAG42271 standard; protein; 326 AA.

XX AC AAG42271;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 52697.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0123180P.

XX PR 09-MAR-1999; 99US-0123548P.

XX PR 23-MAR-1999; 99US-0125788P.

XX PR 29-MAR-1999; 99US-0126264P.

XX PR 25-MAR-1999; 99US-0126785P.

XX PR 01-APR-1999; 99US-0127462P.

XX PR 06-APR-1999; 99US-0128234P.

XX PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.
 PR 19-APR-1999; 99US-0130077P.
 PR 21-APR-1999; 99US-0130449P.
 PR 23-APR-1999; 99US-0130510P.
 PR 23-APR-1999; 99US-0130891P.
 PR 28-APR-1999; 99US-0131449P.
 PR 30-APR-1999; 99US-0132048P.
 PR 30-APR-1999; 99US-0132407P.
 PR 04-MAY-1999; 99US-0132484P.
 PR 05-MAY-1999; 99US-0132485P.
 PR 06-MAY-1999; 99US-0132486P.
 PR 06-MAY-1999; 99US-0132487P.
 PR 07-MAY-1999; 99US-0132863P.
 PR 11-MAY-1999; 99US-0134256P.
 PR 11-MAY-1999; 99US-0134218P.
 PR 14-MAY-1999; 99US-0134219P.
 PR 14-MAY-1999; 99US-0134221P.
 PR 14-MAY-1999; 99US-0134370P.
 PR 18-MAY-1999; 99US-0134768P.
 PR 19-MAY-1999; 99US-0134941P.
 PR 20-MAY-1999; 99US-0135124P.
 PR 21-MAY-1999; 99US-0135353P.
 PR 24-MAY-1999; 99US-0135629P.
 PR 25-MAY-1999; 99US-0136021P.
 PR 27-MAY-1999; 99US-0136392P.
 PR 28-MAY-1999; 99US-0136782P.
 PR 01-JUN-1999; 99US-0137222P.
 PR 03-JUN-1999; 99US-0137528P.
 PR 04-JUN-1999; 99US-0137502P.
 PR 07-JUN-1999; 99US-0137724P.
 PR 08-JUN-1999; 99US-0138094P.
 PR 10-JUN-1999; 99US-0138540P.
 PR 10-JUN-1999; 99US-0138847P.
 PR 14-JUN-1999; 99US-0139119P.
 PR 16-JUN-1999; 99US-0139452P.
 PR 16-JUN-1999; 99US-0139453P.
 PR 17-JUN-1999; 99US-0139492P.
 PR 18-JUN-1999; 99US-0139454P.
 PR 18-JUN-1999; 99US-0139455P.
 PR 18-JUN-1999; 99US-0139456P.
 PR 18-JUN-1999; 99US-0139457P.
 PR 18-JUN-1999; 99US-0139458P.
 PR 18-JUN-1999; 99US-0139459P.
 PR 18-JUN-1999; 99US-0139460P.
 PR 18-JUN-1999; 99US-0139461P.
 PR 18-JUN-1999; 99US-0139462P.
 PR 18-JUN-1999; 99US-0139463P.
 PR 18-JUN-1999; 99US-0139750P.
 PR 18-JUN-1999; 99US-0139763P.
 PR 21-JUN-1999; 99US-0139817P.
 PR 22-JUN-1999; 99US-0139899P.
 PR 23-JUN-1999; 99US-0140353P.
 PR 23-JUN-1999; 99US-0140354P.
 PR 24-JUN-1999; 99US-0140695P.
 PR 28-JUN-1999; 99US-0140823P.
 PR 29-JUN-1999; 99US-0140991P.
 PR 30-JUN-1999; 99US-0141287P.
 PR 01-JUL-1999; 99US-0141842P.
 PR 01-JUL-1999; 99US-0142154P.
 PR 02-JUL-1999; 99US-0142055P.
 PR 06-JUL-1999; 99US-0142390P.
 PR 08-JUL-1999; 99US-0142803P.
 PR 09-JUL-1999; 99US-0142920P.
 PR 12-JUL-1999; 99US-0142977P.
 PR 13-JUL-1999; 99US-0143542P.
 PR 14-JUL-1999; 99US-0143624P.
 PR 15-JUL-1999; 99US-0144005P.
 PR 16-JUL-1999; 99US-0144085P.
 PR 16-JUL-1999; 99US-0144086P.
 PR 19-JUL-1999; 99US-0144325P.
 PR 19-JUL-1999; 99US-0144331P.
 PR 19-JUL-1999; 99US-0144332P.
 PR 19-JUL-1999; 99US-0144333P.

PR 19-JUL-1999;	99US-0144334P.
PR 19-JUL-1999;	99US-0144335P.
PR 20-JUL-1999;	99US-0144352P.
PR 20-JUL-1999;	99US-0144332P.
PR 20-JUL-1999;	99US-0144884P.
PR 21-JUL-1999;	99US-0144814P.
PR 21-JUL-1999;	99US-0145086P.
PR 21-JUL-1999;	99US-0145088P.
PR 22-JUL-1999;	99US-0145085P.
PR 22-JUL-1999;	99US-0145087P.
PR 22-JUL-1999;	99US-0145089P.
PR 22-JUL-1999;	99US-0145192P.
PR 23-JUL-1999;	99US-0145145P.
PR 23-JUL-1999;	99US-0145218P.
PR 23-JUL-1999;	99US-0145218P.
PR 23-JUL-1999;	99US-0145224P.
PR 26-JUL-1999;	99US-0145276P.
PR 27-JUL-1999;	99US-0145913P.
PR 27-JUL-1999;	99US-0145918P.
PR 27-JUL-1999;	99US-0145919P.
PR 28-JUL-1999;	99US-0145951P.
PR 02-AUG-1999;	99US-0146386P.
PR 02-AUG-1999;	99US-0146388P.
PR 02-AUG-1999;	99US-0146389P.
PR 03-AUG-1999;	99US-0147038P.
PR 04-AUG-1999;	99US-0147204P.
PR 04-AUG-1999;	99US-0147302P.
PR 05-AUG-1999;	99US-0147192P.
PR 05-AUG-1999;	99US-0147260P.
PR 06-AUG-1999;	99US-0147303P.
PR 06-AUG-1999;	99US-0147416P.
PR 09-AUG-1999;	99US-0147493P.
PR 09-AUG-1999;	99US-0147935P.
PR 10-AUG-1999;	99US-0148171P.
PR 11-AUG-1999;	99US-0148319P.
PR 12-AUG-1999;	99US-0148341P.
PR 13-AUG-1999;	99US-0148565P.
PR 13-AUG-1999;	99US-0148684P.
PR 16-AUG-1999;	99US-0149368P.
PR 17-AUG-1999;	99US-0149175P.
PR 18-AUG-1999;	99US-0149426P.
PR 20-AUG-1999;	99US-0149722P.
PR 20-AUG-1999;	99US-0149723P.
PR 20-AUG-1999;	99US-0149929P.
PR 23-AUG-1999;	99US-0149902P.
PR 23-AUG-1999;	99US-0149930P.
PR 25-AUG-1999;	99US-0150566P.
PR 26-AUG-1999;	99US-0150884P.
PR 27-AUG-1999;	99US-0151065P.
PR 27-AUG-1999;	99US-0151066P.
PR 27-AUG-1999;	99US-0151080P.
PR 30-AUG-1999;	99US-0151303P.
PR 31-AUG-1999;	99US-0151438P.
PR 01-SEP-1999;	99US-0151930P.
PR 07-SEP-1999;	99US-0152363P.
PR 10-SEP-1999;	99US-0153070P.
PR 13-SEP-1999;	99US-0153758P.
PR 15-SEP-1999;	99US-0154018P.
PR 16-SEP-1999;	99US-0154039P.
PR 20-SEP-1999;	99US-0154779P.
PR 22-SEP-1999;	99US-0155139P.
PR 23-SEP-1999;	99US-0155486P.
PR 24-SEP-1999;	99US-0155659P.
PR 28-SEP-1999;	99US-0156458P.
PR 29-SEP-1999;	99US-0156596P.
PR 04-OCT-1999;	99US-0157117P.
PR 05-OCT-1999;	99US-0157753P.
PR 06-OCT-1999;	99US-0157865P.
PR 07-OCT-1999;	99US-0158029P.
PR 08-OCT-1999;	99US-0158232P.
PR 12-OCT-1999;	99US-0158369P.
PR 13-OCT-1999;	99US-0158293P.
PR 13-OCT-1999;	99US-0159294P.
PR 13-OCT-1999;	99US-0159295P.
PR 14-OCT-1999;	99US-0159329P.
PR 14-OCT-1999;	99US-0159330P.
PR 14-OCT-1999;	99US-0159331P.
PR 14-OCT-1999;	99US-0159637P.
PR 14-OCT-1999;	99US-0159638P.
PR 18-OCT-1999;	99US-0159584P.
PR 21-OCT-1999;	99US-0160741P.
PR 21-OCT-1999;	99US-0160767P.
PR 21-OCT-1999;	99US-0160768P.
PR 21-OCT-1999;	99US-0160770P.
PR 21-OCT-1999;	99US-0160814P.
PR 22-OCT-1999;	99US-0160815P.
PR 22-OCT-1999;	99US-0160980P.
PR 22-OCT-1999;	99US-0160981P.
PR 22-OCT-1999;	99US-0160981P.
PR 25-OCT-1999;	99US-0161404P.
PR 25-OCT-1999;	99US-0161405P.
PR 25-OCT-1999;	99US-0161406P.
PR 26-OCT-1999;	99US-0161359P.
PR 26-OCT-1999;	99US-0161360P.
PR 26-OCT-1999;	99US-0161361P.
PR 28-OCT-1999;	99US-0161920P.
PR 28-OCT-1999;	99US-0161992P.
PR 28-OCT-1999;	99US-0161993P.
PR 29-OCT-1999;	99US-0162142P.
Query Match 66.7%; Score 6; DB 3; Length 326;	
Best Local Similarity 100.0%; Pred. No. 37;	
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 4 DTFYV 9	
Db 168 DTFYV 173	
RESULT 15	
AAG04698	
ID AAG04698 standard; protein; 329 AA.	
XX AAG04698;	
DT 17-OCT-2000 (first entry)	
XX Arabidopsis thaliana protein fragment SEQ ID NO: 824.	
DE Arabidopsis thaliana protein fragment SEQ ID NO: 824.	
XX Protein identification; signal transduction pathway; metabolic pathway;	
KW hybridisation assay; genetic mapping; gene expression control; promoter;	
KW termination sequence.	
XX Arabidopsis thaliana.	
XX EP1033405-A2.	
PD 06-SEP-2000.	
XX 25-FEB-2000; 2000EP-00301439.	
XX 25-FEB-1999; 99US-0121825P.	
PR 05-MAR-1999; 99US-0123180P.	
PR 09-MAR-1999; 99US-0123548P.	
PR 23-MAR-1999; 99US-0125788P.	
PR 25-MAR-1999; 99US-0126264P.	
PR 29-MAR-1999; 99US-0126785P.	
PR 01-APR-1999; 99US-0127462P.	
PR 06-APR-1999; 99US-0128234P.	
PR 08-APR-1999; 99US-0128714P.	
PR 16-APR-1999; 99US-0129845P.	
PR 19-APR-1999; 99US-0130077P.	
PR 21-APR-1999; 99US-0130449P.	
PR 23-APR-1999; 99US-0130510P.	
PR 23-APR-1999; 99US-0130891P.	
PR 28-APR-1999; 99US-0131449P.	
PR 30-APR-1999; 99US-0132048P.	

PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134376P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 21-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.

PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 05-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 11-AUG-1999; 99US-0148171P.
PR 12-AUG-1999; 99US-0148319P.
PR 13-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 16-AUG-1999; 99US-0148684P.
PR 17-AUG-1999; 99US-0149368P.
PR 18-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 23-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 25-AUG-1999; 99US-0149930P.
PR 26-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 30-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151338P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152263P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 22-SEP-1999; 99US-0154779P.
PR 23-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159291P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.

```

PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 66.7%; Score 6; DB 3; Length 329;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
Db 171 DTFYV 176

RESULT 16
ABU28452
ID ABU28452 standard; protein; 331 AA.
XX AC ABU28452;
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #13979.
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Enterobacter cloacae.
XX PN WO200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI Wall D, Zwick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX PR WPI; 2003-029926/02.
XX DR N-PSDB; ACA32322.
XX PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids, required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX PS Claim 25; SEQ ID NO 56376; 1766pp; English.
XX CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense

```

```

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway; (8)
CC required for proliferation, or that inhibits cellular proliferation; (9)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 331 AA;

Query Match 66.7%; Score 6; DB 6; Length 331;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
Db 179 DTFYV 184

RESULT 17
ABU31900
ID ABU31900 standard; protein; 331 AA.
XX AC ABU31900;
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #17427.
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Klebsiella pneumoniae.
XX PN WO200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI Wall D, Zwick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX PR WPI; 2003-029926/02.
XX DR N-PSDB; ACA35770.
XX PT New antisense nucleic acids, useful for identifying proteins or screening

```


PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 59824; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 331 AA;

Query Match 66.7%; Score 6; DB 6; Length 331;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVY 9
 |||||
 Db 179 DTFYVY 184

RESULT 18
 ABO64234
 ID ABO64234 standard; protein; 382 AA.

XX AC ABO64234;

XX DT 29-JUL-2004 (first entry)

XX DE Klebsiella pneumoniae polypeptide seqid 10751.

XX KW Recombinant expression vector; transcription regulatory element;
 KW Klebsiella pneumoniae protein; antibacterial; Vaccine.

XX OS Klebsiella pneumoniae.

XX PN US6610836-B1.

XX PD 26-AUG-2003.

XX PF 27-JAN-2000; 2000US-00489039.

XX PR 29-JAN-1999; 99US-0117747P.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX

PI Breton GL, Osborne M;
 XX WPI; 2003-895346/82.
 DR N-PSDB; ACH97785.
 XX

PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 PT preparing a vaccine composition against Klebsiella pneumoniae.

XX Disclosure; SEQ ID NO 10751; 932pp; English.

CC The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a
 CC Klebsiella pneumoniae polypeptide of the invention

SQ Sequence 382 AA;

Query Match 66.7%; Score 6; DB 7; Length 382;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVY 9
 |||||
 Db 230 DTFYVY 235

RESULT 19
 AB033347
 ID AB033347 standard; protein; 399 AA.

XX AC AB033347;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #18874.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Legionella pneumophila.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX DR N-PSDB; ACA37217.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 61271; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway; (8)
 CC required for proliferation, or that inhibits cellular proliferation; (9)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 399 AA;

Query Match 66.7%; Score 6; DB 6; Length 399;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
 Db 186 VDDTFY 191
 |||||

RESULT 20
 AEB39625
 ID AEB39625 standard; protein; 399 AA.
 AC AEB39625;
 XX
 DT 08-SEP-2005 (first entry)
 XX
 DE L. pneumophila protein SEQ ID NO 3957.
 XX
 KW detection; infection; Antibacterial; Vaccine.
 XX Legionella pneumophila.
 OS
 XX WO2005049642-A2.
 PN
 XX 02-JUN-2005.
 PD
 XX 23-SEP-2004; 2004WO-IB003578.
 PF
 XX 21-NOV-2003; 2003FR-00013687.
 PR
 XX (INSP) INST PASTEUR.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (UVLY-) UNIV LYON 1 BERNARD CLAUDE.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 CC Buchsieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;
 PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
 PI Jarraud S;
 XX
 DR WPI; 2005-388305/40.
 XX
 PT New genome of *Legionella pneumophila* Paris strain and derived

PT polypeptides, useful for detection or identification of the strain and
 PT for treatment and prevention of infections.
 XX
 PS Claim 3; SEQ ID NO 3957; 660pp; English.
 XX
 CC The invention relates to an isolated or purified nucleotide sequences (I)
 CC from *Legionella pneumophila* Paris strain. (I), and their related
 CC sequences or fragments, are useful as primers and probes for detection
 CC and amplification, including differentiation between the Paris and
 CC Philadelphia strains of *Legionella pneumophila* and to prepare recombinant
 CC (hybrid) polypeptides (II). (II) are also useful for preparation of
 CC specific antibodies (Ab), also used for detection/identification of
 CC *Legionella*, and some (I), specifically those involved in synthesis of
 CC surface proteins, are targets for identification of inhibitors. (II), or
 CC vectors that contain (I), are useful as vaccines and immunogenic
 CC compositions, for treatment and prevention of infections by L.
 CC pneumophila. The present sequence represents the amino acid sequence of a
 CC L. pneumophila protein.
 XX
 SQ Sequence 399 AA;

Query Match 66.7%; Score 6; DB 9; Length 399;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
 Db 186 VDDTFY 191
 |||||

RESULT 21
 ABP78086
 ID ABP78086 standard; protein; 400 AA.
 XX
 AC ABP78086;
 XX
 DT 07-MAR-2003 (first entry)
 XX
 DE N. gonorrhoeae amino acid sequence SEQ ID 2702.
 XX
 KW Antibacterial; infection; vaccine; gene therapy.
 XX
 OS *Neisseria gonorrhoeae*.
 XX
 PN WO200279243-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 12-FEB-2002; 2002WO-IB002069.
 XX
 PR 12-FEB-2001; 2001GB-00003424.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Fontana MR, Pizza M, Masignani V, Monaci E;
 XX
 DR WPI; 2003-058415/05.
 DR N-PSDB; ABZ39056.
 XX
 PT New protein from *Neisseria gonorrhoeae*, useful for the manufacture of a
 PT medicament for treating or preventing N. gonorrhoeae infection.
 XX
 PS Disclosure; Page 385; 815pp; English.
 XX
 CC The present invention relates to proteins from *Neisseria gonorrhoeae*.
 CC Also disclosed are the nucleic acid molecules encoding the proteins and
 CC antibodies that specifically bind to the proteins. The composition
 CC comprising the protein, nucleic acid or antibody is useful for the
 CC manufacture of a medicament for treating or preventing N. gonorrhoeae
 CC infection, this may be in the form of a vaccine or gene therapy.
 CC Sequences given in records ABP76736-ABP81046 represent nucleic acid
 CC molecules of the invention
 XX

SQ Sequence 400 AA;

Query Match 66.7%; Score 6; DB 6; Length 400;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
 |||||
 Db 186 VDDTFY 191

RESULT 22
 ABU37336
 ID ABU37336 standard; protein; 400 AA.
 XX
 AC ABU37336;
 XX
 DT 23-OCT-2003 (revised)
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #22863.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Neisseria gonorrhoeae.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACA41206.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 65260; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation or the activity of a gene in an operon required for
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 400 AA;
 Query Match 66.7%; Score 6; DB 6; Length 400;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
 |||||
 Db 186 VDDTFY 191

RESULT 23
 ABU37892
 ID ABU37892 standard; protein; 400 AA.
 XX
 AC ABU37892;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #23419.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Neisseria meningitidis.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACA41762.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 65816; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 400 AA;

Query Match 66.7%; Score 6; DB 6; Length 400;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
 DB 186 VDDTFY 191
 |||||

RESULT 24
 AEB36203
 ID AEB36203 standard; protein; 405 AA.
 XX
 AC AEB36203;
 XX
 DT 08-SEP-2005 (first entry)
 XX
 DE L. pneumophila protein SEQ ID NO 535.
 XX
 KW detection; infection; Antibacterial; Vaccine.
 XX
 OS Legionella pneumophila.
 XX
 XX WO2005049642-A2.
 XX
 XX 02-JUN-2005.
 XX
 XX 23-SEP-2004; 2004WO-IB003578.
 XX
 XX 21-NOV-2003; 2003FR-00013687.
 XX
 XX (INSP) INST PASTEUR.
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
 XX (CNRS) CNRS CENT NAT RECH SCI.
 XX Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;
 PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
 PI Jarraud S;
 XX
 XX WPI; 2605-388305/40.
 XX
 XX New genome of *Legionella pneumophila* Paris strain and derived
 PT polypeptides, useful for detection or identification of the strain and
 PT for treatment and prevention of infections.
 XX
 XX Claim 3; SEQ ID NO 535; 660pp; English.
 XX
 XX The invention relates to an isolated or purified nucleotide sequences (I)

CC from *Legionella pneumophila* Paris strain. (I), and their related
 CC sequences or fragments, are useful as primers and probes for detection
 CC and amplification, including differentiation between the Paris and
 CC Philadelphia strains of *Legionella pneumophila* and to prepare recombinant
 CC (hybrid) polypeptides (II). (II) are also useful for preparation of
 CC specific antibodies (Ab), also used for detection/identification of
 CC *Legionella*, and some (I), specifically those involved in synthesis of
 CC surface proteins, are targets for identification of inhibitors. (II), or
 CC vectors that contain (I), are useful as vaccines and immunogenic
 CC compositions, for treatment and prevention of infections by L.
 CC pneumophila. The present sequence represents the amino acid sequence of a
 CC L. pneumophila protein.
 XX
 XX Sequence 405 AA;

Query Match 66.7%; Score 6; DB 9; Length 405;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
 DB 192 VDDTFY 197
 |||||

RESULT 25
 ABU41410
 ID ABU41410 standard; protein; 409 AA.
 XX
 AC ABU41410;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #26937.

XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Pseudomonas syringae.
 XX
 XX WO200277183-A2.
 XX
 XX 03-OCT-2002.
 XX
 XX 21-MAR-2002; 2002WO-US009107.
 XX
 XX 21-MAR-2001; 2001US-00815242.
 XX 06-SEP-2001; 2001US-00948993.
 XX 25-OCT-2001; 2001US-0342923P.
 XX 08-FEB-2002; 2002US-00072851.
 XX 06-MAR-2002; 2002US-0362699P.
 XX
 XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX

WPI; 2003-029926/02.
 DR N-FSDB; ACA45280.

XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX

PS Claim 25; SEQ ID NO 69334; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

XX SQ Sequence 409 AA;

Query Match 66.7%; Score 6; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7

Db 189 VDDTFY 194
|||||

RESULT 26

ADY24554
ID ADY24554 standard; protein; 479 AA.

AC ADY24554;

XX 21-APR-2005 (first entry)

XX Plant full length insert polypeptide seqid 72338.

XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.

XX Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 05-NOV-2001; 2001US-00985678.

XX (LIU//) LIU J.

XX (ZHOU//) ZHOU Y.

XX (KOVA//) KOVALIC D K.

XX (SCRE//) SCREEN S E.

XX (TAB//) TABASKA J E.

XX (CAO//) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX

DR WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.

PS Claim 1; SEQ ID NO 72338; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the invention.

XX SQ Sequence 479 AA;

Query Match 66.7%; Score 6; DB 8; Length 479;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9

Db 321 DTFYV 326
|||||

RESULT 27

AAG04697

ID AAG04697 standard; protein; 485 AA.

XX AAG04697;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 823.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

XX 29-MAR-1999; 99US-0126785P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 08-APR-1999; 99US-0128714P.

XX 16-APR-1999; 99US-0129845P.

XX 19-APR-1999; 99US-0130077P.

XX 21-APR-1999; 99US-0130449P.


```

PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161406P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 66.7%; Score 6; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
Db 327 DTFYV 332

RESULT 28
ADN72665
ID ADN72665 standard; protein; 485 AA.
XX
AC ADN72665;
XX
DT 15-JUL-2004 (first entry)
XX
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 560.
XX
KW plant; transgenic; E2Fa/Dpa transcription factor; growth regulator;
KW animal feed product; thale cress; cell wall biosynthesis;
KW nitrogen metabolism; carbon metabolism.
XX
OS Arabidopsis thaliana.
XX
PN WO2004035798-A2.
XX
PD 29-APR-2004.
XX
XX
XX 20-OCT-2003; 2003WO-EP011658.
XX
XX 18-OCT-2002; 2002EP-00079408.
XX
PA (CROP-) CROPDESIGN NV.
XX
PI Inze D, De Veylder L, Vlieghe K;
XX
XX WPI; 2004-348466/32.
XX
XX N-PSDB; ADN72664.
XX
XX Altering plant characteristics, useful for producing plants for enzyme or
PT pharmaceutical production comprises modifying in a plant, expression of
PT one or more nucleic acids and/or modifying level or activity of one or
PT more proteins.
XX
XX Claim 1; SEQ ID NO 560; 134pp; English.
XX
XX This invention relates to a novel method for altering one or more plant
CC characteristics. Specifically, it refers to identifying genes that are up
CC - or down-regulated in transgenic plants overexpressing the heterodimeric

```

```

CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
CC alter plant characteristics accordingly. The present invention describes
CC generating transgenic plants for the production of growth regulators,
CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
CC the altered plant characteristics are selected from increased yield or
CC biomass, enhanced survival capacity, stress tolerance, plant architecture
CC or physiology, altered endoreplication, biochemistry, signal
CC transduction, storage lipid mobilization and/or altered photosynthesis,
CC each relative to the corresponding wild type plants. Accordingly, these
CC sequences can also be useful as positive or negative selectable markers
CC during transformation of cells or tissues. The identified genes play a
CC role in a variety of biological processes such as DNA replication, cell
CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
CC transcription factors. This polypeptide sequence is thale cress protein
CC expressed by a gene upregulated 1.3 fold or more in plants overexpressing
CC the E2Fa/Dpa transcription factor, given in an exemplification of the
CC invention.
XX
SQ Sequence 485 AA;

Query Match 66.7%; Score 6; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
Db 327 DTFYV 332

RESULT 29
AAG04696
ID AAG04696 standard; protein; 496 AA.
XX
AC AAG04696;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 822.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX
XX 05-MAR-1999; 99US-0123180P.
XX
XX 09-MAR-1999; 99US-0123548P.
XX
XX 23-MAR-1999; 99US-0125788P.
XX
XX 25-MAR-1999; 99US-0126264P.
XX
XX 29-MAR-1999; 99US-0126785P.
XX
XX 01-APR-1999; 99US-0127462P.
XX
XX 06-APR-1999; 99US-0128234P.
XX
XX 08-APR-1999; 99US-0128714P.
XX
XX 16-APR-1999; 99US-0129845P.
XX
XX 19-APR-1999; 99US-0130077P.
XX
XX 21-APR-1999; 99US-0130449P.
XX
XX 23-APR-1999; 99US-0130510P.
XX
XX 28-APR-1999; 99US-0130891P.
XX
XX 30-APR-1999; 99US-0131449P.
XX
XX 30-APR-1999; 99US-0132048P.
XX
XX 04-MAY-1999; 99US-0132407P.
XX
XX 05-MAY-1999; 99US-0132484P.
XX
XX 06-MAY-1999; 99US-0132486P.
XX
XX 06-MAY-1999; 99US-0132487P.
XX
XX 07-MAY-1999; 99US-0132863P.

```

PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139452P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144633P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.

PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148315P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149428P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158365P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.


```
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 23-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 66.7%; Score 6; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
    |||||
Db 338 DTFYV 343

RESULT 30
AAG42270
ID AAG42270 standard; protein; 500 AA.
AC AAG42270;
XX
XX
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52696.
XX
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
XX
PN EP1033405-A2.
XX
XX
PD 06-SEP-2000.
XX
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.

PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139452P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
```

```
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147202P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149802P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.

PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 66.7%; Score 6; DB 3; Length 500;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYYV 9
Db 342 DTFYYV 347

RESULT 31
ABB92358
ID ABB92358 standard; protein; 500 AA.
XX
AC ABB92358;
XX
DT 31-MAY-2002 (first entry)
XX
DE Herbicidally active polypeptide SEQ ID NO 1569.
XX
KW Herbicidal; plant; agriculture; herbicide..
XX
OS Arabidopsis thaliana.
XX
PN WO200210210-A2.
XX
PD 07-FEB-2002.
XX
PF 28-AUG-2001; 2001WO-EP009892.
XX
PR 28-AUG-2001; 2001WO-EP009892.
XX
PA (FARB ) BAYER AG.
XX
PI Tietjen K, Weidler M;
XX
WPI; 2002-269010/31.
PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms.
XX
PS Claim 5; SEQ ID NO 1569; 261pp + Sequence Listing; English.
XX
CC The invention relates to identifying target proteins (ABB90790-ABB94016)
CC for herbicidally active compounds, comprising aligning and comparing
CC nucleic acid or amino acid sequences from plant with nucleic acid or
CC amino acid sequences from non-plant organisms using suitable search
CC parameters, where plant sequences having an E-value greater by a factor
CC of 3 than the E-value of most similar non-plant sequences are selected.
CC The polypeptides or nucleic acids encoding them are useful for
CC identifying modulators. The identified modulators are useful as
CC herbicides
XX
SQ Sequence 500 AA;

Query Match 66.7%; Score 6; DB 5; Length 500;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYYV 9
Db 342 DTFYYV 347

RESULT 32
AAG42269
```

ID	AAG42269	standard; protein; 510 AA.
XX	AC	AAG42269;
XX	XX	
DT	18-OCT-2000	(first entry)
XX	XX	
DE	Arabidopsis thaliana	protein fragment SEQ ID NO: 52695.
XX	XX	
KW	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
KW	termination sequence.	
XX	XX	
OS	Arabidopsis thaliana.	
XX	XX	
FN	EPI033405-A2.	
XX	XX	
PD	06-SEP-2000.	
XX	XX	
PF	25-FEB-2000; 2000EP-00301439.	
XX	XX	
PR	25-FEB-1999;	99US-0121825P.
PR	05-MAR-1999;	99US-0123180P.
PR	09-MAR-1999;	99US-0123548P.
PR	23-MAR-1999;	99US-0125788P.
PR	25-MAR-1999;	99US-0126264P.
PR	29-MAR-1999;	99US-0126785P.
PR	01-APR-1999;	99US-0127462P.
PR	06-APR-1999;	99US-0128234P.
PR	08-APR-1999;	99US-0128714P.
PR	16-APR-1999;	99US-0129845P.
PR	19-APR-1999;	99US-0130077P.
PR	21-APR-1999;	99US-0130449P.
PR	23-APR-1999;	99US-0130510P.
PR	23-APR-1999;	99US-0130891P.
PR	28-APR-1999;	99US-0131449P.
PR	30-APR-1999;	99US-0132048P.
PR	30-APR-1999;	99US-0132407P.
PR	04-MAY-1999;	99US-0132484P.
PR	05-MAY-1999;	99US-0132485P.
PR	06-MAY-1999;	99US-0132486P.
PR	06-MAY-1999;	99US-0132487P.
PR	07-MAY-1999;	99US-0132863P.
PR	11-MAY-1999;	99US-0134256P.
PR	14-MAY-1999;	99US-0134218P.
PR	14-MAY-1999;	99US-0134219P.
PR	14-MAY-1999;	99US-0134321P.
PR	14-MAY-1999;	99US-0134370P.
PR	18-MAY-1999;	99US-0134768P.
PR	18-MAY-1999;	99US-0134941P.
PR	20-MAY-1999;	99US-0135124P.
PR	21-MAY-1999;	99US-0135353P.
PR	24-MAY-1999;	99US-0135629P.
PR	25-MAY-1999;	99US-0136021P.
PR	27-MAY-1999;	99US-0136392P.
PR	28-MAY-1999;	99US-0136782P.
PR	01-JUN-1999;	99US-0137222P.
PR	03-JUN-1999;	99US-0137528P.
PR	04-JUN-1999;	99US-0137502P.
PR	07-JUN-1999;	99US-0137724P.
PR	08-JUN-1999;	99US-0138094P.
PR	10-JUN-1999;	99US-0138540P.
PR	10-JUN-1999;	99US-0138847P.
PR	14-JUN-1999;	99US-0139119P.
PR	16-JUN-1999;	99US-0139452P.
PR	16-JUN-1999;	99US-0139453P.
PR	17-JUN-1999;	99US-0139492P.
PR	18-JUN-1999;	99US-0139545P.
PR	18-JUN-1999;	99US-0139455P.
PR	18-JUN-1999;	99US-0139456P.
PR	18-JUN-1999;	99US-0139457P.
PR	18-JUN-1999;	99US-0139458P.
PR	18-JUN-1999;	99US-0139459P.
PR	18-JUN-1999;	99US-0139460P.
PR	18-JUN-1999;	99US-0139461P.
PR	18-JUN-1999;	99US-0139462P.
PR	18-JUN-1999;	99US-0139463P.
PR	18-JUN-1999;	99US-0139750P.
PR	18-JUN-1999;	99US-0139763P.
PR	21-JUN-1999;	99US-0139817P.
PR	22-JUN-1999;	99US-0139899P.
PR	23-JUN-1999;	99US-0140353P.
PR	23-JUN-1999;	99US-0140354P.
PR	24-JUN-1999;	99US-0140695P.
PR	28-JUN-1999;	99US-0140823P.
PR	29-JUN-1999;	99US-0140991P.
PR	30-JUN-1999;	99US-0141287P.
PR	01-JUL-1999;	99US-0141842P.
PR	01-JUL-1999;	99US-0142154P.
PR	02-JUL-1999;	99US-0142055P.
PR	06-JUL-1999;	99US-0142390P.
PR	08-JUL-1999;	99US-0142803P.
PR	09-JUL-1999;	99US-0142920P.
PR	12-JUL-1999;	99US-0142977P.
PR	13-JUL-1999;	99US-0143542P.
PR	14-JUL-1999;	99US-0143624P.
PR	15-JUL-1999;	99US-0144005P.
PR	16-JUL-1999;	99US-0144085P.
PR	16-JUL-1999;	99US-0144086P.
PR	19-JUL-1999;	99US-0144325P.
PR	19-JUL-1999;	99US-0144331P.
PR	19-JUL-1999;	99US-0144332P.
PR	19-JUL-1999;	99US-0144333P.
PR	19-JUL-1999;	99US-0144334P.
PR	19-JUL-1999;	99US-0144335P.
PR	20-JUL-1999;	99US-014435

```
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 66.7%; Score 6; DB 3; Length 510;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFYIV 9
Db 352 DTFYIV 357

RESULT 33
ADM48028
ID ADM48028 standard; protein; 510 AA.
XX AC
XX ADM48028;
XX AC
DT 03-JUN-2004 (first entry)
XX AC
XX Polypeptide sequence #78 useful in producing transgenic plants.

XX Plant; maize; rice; sorghum; thale cress; soybean; wheat; transgenic;
KW osmotic stress; sugar transport; cell cycle pathway; plant height;
KW carbohydrate transport; crop productivity; plant growth;
KW stress resistance; disease resistance; insect resistance; heat tolerance;
KW nitrogen assimilation; water stress tolerance;
KW photosynthetic carbon fixation; virus resistance; gene therapy.
XX
OS Zea mays.
XX
XX US2003233670-A1.
XX 18-DEC-2003.
XX
XX 04-DEC-2002; 2002US-00310154.
XX
XX 04-DEC-2001; 2001US-0337358P.
XX (EDGE/) EDGERTON M D.
XX (CHOM/) CHOMET P S.
XX (LACC/) LACCETTI L B.
XX Edgerton MD, Chomet PS, Laccetti LB;
XX
XX WPI; 2004-061374/06.
XX N-PSDB; ADM47660.
XX
XX New polynucleotide, useful for manipulating plant protein quality,
PT improving plant growth, yield and crop productivity or grain composition
PT or producing plants with improved properties.
XX
XX Claim 8; SEQ ID NO 446; 144pp; English.
XX
XX The present invention relates to polynucleotide sequences, and the
CC proteins they encode. The sequences are isolated from a variety of
CC organisms such as plants (e.g. maize, rice, sorghum, thale cress,
CC soybean, and wheat), cyanobacteria, bacteria, yeast and other fungi. The
CC polynucleotide and polypeptide sequences of the invention are useful in
CC the production of transgenic plants that have improved properties. Also
CC disclosed are methods of producing fertile transgenic plants, preferably
CC maize, with desired phenotypes. The polynucleotide and polypeptide
CC sequences are useful for improving plants by providing protection against
CC osmotic stress, improving altering sugar transport and/or metabolism,
CC modifying the cell cycle pathway, reducing plant height, modifying
CC carbohydrate transport, improving crop productivity, improving plant
CC growth and stress resistance, improving disease resistance, improving
CC insect resistance, improving cold or heat tolerance, improving nitrogen
CC assimilation, improving stalk strength, improving water stress tolerance,
CC improving photosynthetic carbon fixation, improving biotic and abiotic
CC stress resistance, improving resistance to oxidative stress, providing
CC increased vigour, reducing senescence, and conferring virus resistance.
CC The present sequence represents a polypeptide sequence of the invention.
CC Note: The sequence data for this patent is not provided in the printed
CC specification but is obtained in electronic format from the USPTO website
CC at seqdata.uspto.gov.
XX
SQ Sequence 510 AA;

Query Match 66.7%; Score 6; DB 8; Length 510;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFYIV 9
Db 348 DTFYIV 353

RESULT 34
ABB59871
ID ABB59871 standard; protein; 800 AA.
XX AC
XX ABB59871;
XX
```

DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster polypeptide SEQ ID NO 6405.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 XX 27-SEP-2001.
 XX
 XX 23-MAR-2001; 2001WO-US009231.
 PF
 XX 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 XX N-PSDB; ABL03974.
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 6405; 2lpp + Sequence Listing; English.
 XX
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL01840-ABL0175), expressed DNA
 CC sequences (ABL01840-ABL0175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 800 AA;
 SQ
 Query Match 66.7%; Score 6; DB 4; Length 800;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 DDTFFY 8
 DB 755 DDTFFY 760
 RESULT 35
 ABB71398
 ID ABB71398 standard; protein; 900 AA.
 XX
 AC ABB71398;
 XX
 XX 26-MAR-2002 (first entry)
 DT
 XX Drosophila melanogaster polypeptide SEQ ID NO 40986.
 DE
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 XX 27-SEP-2001.
 XX
 XX 23-MAR-2001; 2001WO-US009231.
 PF

XX 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 XX N-PSDB; ABL15501.
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 40986; 2lpp + Sequence Listing; English.
 XX
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL01840-ABL0175), expressed DNA
 CC sequences (ABL01840-ABL0175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 900 AA;
 SQ
 Query Match 66.7%; Score 6; DB 4; Length 900;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 DTFYV 9
 DB 304 DTFYV 309
 RESULT 36
 ADN21456
 ID ADN21456 standard; protein; 1136 AA.
 XX
 AC ADN21456;
 XX
 XX 02-DEC-2004 (first entry)
 DT
 XX Bacterial polypeptide #4109.
 DE
 XX
 KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX
 OS Bacteria.
 XX
 XX US2003233675-A1.
 PN
 PD 18-DEC-2003.
 XX
 XX 20-FEB-2003; 2003US-00369493.
 PF
 XX 21-FEB-2002; 2002US-0360039P.
 PR
 XX (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX Claim 1; SEQ ID NO 4109; 122pp; English.
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1136 AA;
Query Match 66.7%; Score 6; DB 8; Length 1136;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;
QY 4 DTFYYV 9
Db 338 DTFYYV 343
|||||
RESULT 37
AAU89238
ID AAU89238 standard; peptide; 21 AA.
AC AAU89238;
XX
XX 18-JUN-2002 (first entry)
DE Insulin/insulin-like growth factor receptor-binding peptide #1194.
XX
XX Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
KW ophthalmological; insulin; receptor; gene therapy; diabetes;
KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
KW diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.
XX
XX Synthetic.
XX WO200172771-A2.
PN
XX 04-OCT-2001.
PD
XX 29-MAR-2000; 2000WO-US008528.
PF
XX 29-MAR-2000; 2000WO-US008528.
PR
XX (DGIB-) DGI BIOTECHNOLOGIES LLC.
PA (NOVO) NOVO NORDISK AS.

XX Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
PI Hansen PH, Ravera M, Hsiao K;
XX WPI; 2002-025774/03.
XX Modulating insulin activity in mammalian cells, for treating e.g.
PT diabetes and tumors, comprises using peptides that bind to insulin or
PT insulin-like growth factor receptors.
XX Disclosure; Fig 10-2; 390pp; English.
XX The invention relates to a method of modulating insulin activity in
CC mammalian cells by administering a peptide that binds the insulin
CC receptor (IR). A composition containing a peptide, optionally expressed
CC from gene therapy vectors, that binds to Site 1 of IR and an insulin
CC agonist are useful for treating diabetes. Also, peptides that are
CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC useful for treating insulin-like growth factor (IGF)-sensitive tumours
CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC receptor agonists are useful for treating neurological diseases,
CC including stroke and diabetic neuropathy. The peptides are also useful in
CC screening for compounds that bind to IR or IGF-1 receptor, potential
CC therapeutics and research reagents. AAU8034-AAU90957 represent IR and/or
CC IGF-1 receptor-binding peptides and related amino acid sequences of the
CC invention
XX
SQ Sequence 21 AA;
Query Match 55.6%; Score 5; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 DDTFY 7
Db 4 DDTFY 8
|||||
RESULT 38
ADA04060
ID ADA04060 standard; peptide; 21 AA.
XX
XX AC ADA04060;
XX
XX 06-NOV-2003 (first entry)
DE Insulin receptor (IR) related Formula 1 motif peptide SEQ ID NO:691.
XX
XX insulin-like growth factor receptor; IGF; modulate; insulin receptor;
KW IR; insulin; cytostatic; IGF agonist; IGF antagonist; cancer;
KW leukaemia; sarcoma; lymphoma; carcinoma.
XX
XX Synthetic.
XX Homo sapiens.
XX WO2003027246-A2.
XX
XX 03-APR-2003.
PD
XX 24-SEP-2002; 2002WO-US030412.
PF
XX 24-SEP-2001; 2001US-00962756.
PR
XX (NOVO) NOVO NORDISK AS.
PA (DGIB-) DGI BIOTECHNOLOGIES.
XX
XX Pillutla R, Dedova O, Blume AJ, Goldstein NI, Brissette R;
PI Wang P, Liu H, Hsiao K, Lennick M, Fletcher P;
XX WPI; 2003-363211/34.
DR
XX Modulating insulin-like growth factor receptor (IGFR) activity in IGF-

PT responsive mammalian cells, useful for treating cancer comprises
 PT contacting the cells with an amino acid sequence to modulate the activity
 of IGFR.
 XX
 XX Disclosure; Fig 10; 372pp; English.
 XX
 XX The present invention describes a method for modulating insulin-like
 CC growth factor receptor (IGFR) activity in insulin-like growth factor-
 CC responsive mammalian cells comprising contacting the cells with an amino
 CC acid sequence to modulate the activity of IGFR. In modulating IGFR
 CC activity, the amino acid sequence comprises X1X2X3X4X5 (I), where X1, X2
 CC and X5 = phenylalanine or tyrosine; X3 = aspartic acid, glutamic acid,
 CC glycine or serine; and X4 = tryptophan, tyrosine or phenylalanine. The
 CC amino acid sequence is not insulin, insulin-like growth factor, an anti-
 CC insulin receptor antibody, an anti-insulin-like growth receptor antibody,
 CC or its fragment. Also described: (1) decreasing or increasing IGFR
 CC activity in IGF-responsive mammalian cells by contacting the cells with
 CC an amino acid sequence to decrease or increase the activity of IGFR; (2)
 CC an IGFR modulator, agonist or antagonist; (3) identifying IGFR modulator;
 CC and (4) enhancing survival of an IGF-responsive mammalian cell by
 CC contacting the cell with (I) to enhance the survival of the cell. IGFR
 CC modulators have cytostatic activity, and can be used as IGF agonists or
 CC IGFR antagonists. The methods, modulators, agonists and antagonists are
 CC useful for treating cancer, e.g. leukemia, sarcoma, lymphoma or
 CC carcinoma. The methods are useful for identifying molecular structures
 CC that are capable of acting as an IGFR agonist or antagonist. The present
 CC sequence represents a peptide given in the exemplification of the present
 XX invention.
 XX
 SQ Sequence 21 AA;

Query Match 55.6%; Score 5; DB 6; Length 21;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 |||||
 DB 4 DDTFY 8

RESULT 39

ADH95273
 ID ADH95273 standard; protein; 21 AA.
 AC ADH95273;
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX
 DE Insulin receptor motif polypeptide, SEQ ID No 691.
 XX
 XX insulin receptor; insulin; insulin-like growth factor receptor; agonist;
 KW antagonist; antidiabetic; diabetes; insulin shock.
 KW
 XX Unidentified.
 OS
 XX WO2003070747-A2.
 PN
 XX 28-AUG-2003.
 PD
 XX 24-SEP-2002; 2002WO-US030312.
 PF
 XX 24-SEP-2001; 2001US-00962756.
 PR
 XX (NOVO) NOVO NORDISK AS.
 PA (DGI-B-) DGI BIOTECHNOLOGIES.
 PA
 XX Pillutla R, Brissette R, Blume AJ, Schaeffer L, Brandt J;
 PI Goldstein NI, Spetzler J, Ostergaard S;
 XX WPI; 2003-833235/77.
 DR
 XX Modulating insulin-like growth factor receptor (IGFR) activity in IGF-
 PT responsive mammalian cells, useful for treating diabetes comprises

PT contacting the cells with an amino acid sequence to modulate the activity
 of IGFR.
 XX
 XX Claim 7; SEQ ID NO 691; 328pp; English.
 XX
 XX The invention relates to a novel method for decreasing or increasing
 CC insulin receptor activity in mammalian cells. The invention further
 CC relates to peptide sequences capable of binding to insulin and/or insulin
 CC -like growth factor receptors with either agonist or antagonist activity.
 CC The peptide sequences are identified from various peptide libraries. The
 CC novel method comprises administering to the mammalian cells an amino acid
 CC having subsequences that binds to site 1 and site 2 of an insulin
 CC receptor. The subsequences are joined C-terminus to N-terminus and
 CC oriented site 1 to site 2. The sequence is not insulin or insulin-like
 CC growth factor. The peptide sequences of the invention have antidiabetic
 CC activity. The peptides are useful for treating diabetes or insulin shock.
 CC This sequence represents an insulin receptor/insulin growth factor
 CC receptor binding polypeptide relating to the invention.
 XX
 SQ Sequence 21 AA;

Query Match 55.6%; Score 5; DB 7; Length 21;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 |||||
 DB 4 DDTFY 8

RESULT 40

ADL67964
 ID ADL67964 standard; peptide; 21 AA.
 XX
 AC ADL67964;
 XX
 XX 20-MAY-2004 (first entry)
 DT
 XX
 DE IGF-1R/IR binding peptide seq id 691.
 XX
 KW cytostatic; insulin-like growth factor receptor activity;
 KW insulin-like growth factor-responsive mammalian cell;
 KW insulin-like growth factor receptor modulator;
 KW insulin-like growth factor receptor antagonist;
 KW insulin-like growth factor receptor agonist; insulin receptor;
 KW cancer; breast cancer; prostate cancer; therapeutic; peptide hormone;
 KW ovarian cancer; peptide library; IGF-IR; IR.
 XX
 OS Unidentified.
 XX
 XX US2004023887-A1.
 PN
 XX 05-FEB-2004.
 PD
 XX 24-SEP-2002; 2002US-00253493.
 PF
 XX 02-SEP-1998; 98US-00146127.
 PR 29-MAR-2000; 2000US-00538038.
 PR 24-SEP-2001; 2001US-00962756.
 XX
 XX (PILL/) PILLUTLA R.
 PA (DEDO/) DEDOVA O.
 PA (BLUM/) BLUME A J.
 PA (GOLD/) GOLDSTEIN N I.
 PA (BRIS/) BRISSETTE R.
 PA (WANG/) WANG P.
 PA (LIUH/) LIU H.
 PA (HSIA/) HSIAO K.
 PA (LENN/) LENNICK M.
 PA (FLET/) FLETCHER P.
 XX
 XX Pillutla R, Dedova O, Blume AJ, Goldstein NI, Brissette R;

PI Wang P, Liu H, Hsiao K, Lennick M, Fletcher P;
 XX WPI; 2004-132606/13.
 XX Disclosure; SEQ ID NO 691; 242pp; English.
 XX The invention describes the use of molecular structures, preferably
 CC peptides for modulating, increasing or decreasing insulin-like growth
 CC factor receptor activity in insulin-like growth factor-responsive
 CC mammalian cells. Also described are: modulating, decreasing or increasing
 CC insulin-like growth factor receptor activity in insulin-like growth
 CC factor-responsive mammalian cells; an insulin-like growth factor
 CC modulator; an insulin-like growth factor receptor antagonist; an insulin-
 CC like growth factor receptor agonist; identifying an insulin-like growth
 CC factor receptor modulator; and enhancing survival of an insulin-like
 CC growth factor-responsive mammalian cell. The molecular structures of the
 CC peptides are useful for modulating, increasing or decreasing insulin-like
 CC growth factor receptor activity in insulin-like growth factor-responsive
 CC mammalian cells. The peptide sequences are useful for binding to insulin
 CC and/or insulin-like growth factor receptors with either agonist or
 CC antagonist activity. As agonists, the peptides are useful for development
 CC of therapeutics to supplement or replace endogenous peptide hormones. The
 CC antagonist peptides can also be developed as therapeutics. The IR and IGF
 CC -IR agonist and antagonist peptides are useful as lead compounds for
 CC identifying other more potent or selective therapeutics, assay reagents
 CC for identifying other useful ligands, as research tools for further
 CC analysis of IR and IGF-IR. The IGF-IR antagonists are useful as treatment
 CC for cancer, e.g. breast, prostate, colorectal or ovarian cancer. This is
 CC the amino acid sequence of a IGF-IR/IR binding peptide obtained by
 CC panning a peptide library against the insulin-like growth factor 1
 CC receptor (IGF-IR) and insulin receptor (IR). Note: This sequence is also
 CC available in electronic format from the US patent office at
 CC ftp.seqdata.uspto.gov/sequence.html?docID=20040023887.
 XX Sequence 21 AA;
 SQ

Query Match 55.6%; Score 5; DB 8; Length 21;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 Db |||||
 4 DDTFY 8

RESULT 41
 ADM37809
 ID ADM37809 standard; peptide; 21 AA.
 XX AC
 XX ADM37809;
 DT 03-JUN-2004 (first entry)
 DE Anti-IR formula 1 motif peptide #427.
 XX insulin receptor activity; insulin-related disease;
 KW insulin-like growth factor-related disease; diabetes; insulin shock.
 XX Synthetic.
 OS
 XX US2003236190-A1.
 PN
 XX 25-DEC-2003.
 PD
 XX 24-SEP-2002; 2002US-00253471.
 PF
 XX 02-SEP-1998; 98US-00146127.
 PR 29-MAR-2000; 2000US-00538038.
 PR 24-SEP-2001; 2001US-00962756.
 XX (PILL/) PILLUTLA R.
 PA (BRIS/) BRISSETTE R.
 PA (BLUM/) BLUME A J.

PA (SCHA/) SCHAPPER L.
 PA (BRAN/) BRANDT J.
 PA (GOLD/) GOLDSTEIN N I.
 PA (SPET/) SPETZLER J.
 PA (OSTE/) OSTERGAARD S.
 PA (HANS/) HANSEN P H.
 XX Pillutla R, Brissette R, Blume AJ, Schaffer L, Brandt J;
 PI Goldstein NI, Spetzler J, Ostergaard S, Hansen PH;
 XX WPI; 2004-081583/08.
 XX Decreasing or increasing insulin receptor activity in mammalian cells
 PT using peptide sequences that bind insulin and/or insulin-like growth
 PT factor receptors, useful for treating diabetes and insulin shock.
 XX Claim 7; SEQ ID NO 691; 203pp; English.
 XX The invention relates to a method of decreasing insulin receptor activity
 CC in mammalian cells which comprises administering an amino acid sequence
 CC having a subsequence comprising a sequence that binds to Site 1 and Site
 CC 2 of insulin receptor, where the subsequences are linked C-terminus to N-
 CC terminus and oriented Site 1 to Site 2, where the amino acid sequence is
 CC not insulin, insulin-like growth factor or their fragments. The methods
 CC and compositions of the present invention are useful for treating insulin
 CC - or insulin-like growth factor-related diseases or conditions, such as
 CC diabetes and insulin shock. The present sequence is used in the
 CC exemplification of the present invention.
 XX Sequence 21 AA;
 SQ

Query Match 55.6%; Score 5; DB 8; Length 21;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 Db |||||
 4 DDTFY 8

RESULT 42
 ADA04794
 ID ADA04794 standard; peptide; 27 AA.
 XX AC
 XX ADA04794;
 DT 06-NOV-2003 (first entry)
 XX IGF-1R binding peptide SEQ ID NO:1425.
 DE
 XX insulin-like growth factor receptor; IGF; modulate; insulin receptor;
 KW IR; insulin; cytostatic; IGF agonist; IGF antagonist; cancer;
 KW leukaemia; sarcoma; lymphoma; carcinoma.
 XX Synthetic.
 OS
 XX Homo sapiens.
 XX WO2003027246-A2.
 PN
 XX 03-APR-2003.
 PD
 XX 24-SEP-2002; 2002WO-US030412.
 PF
 XX 24-SEP-2001; 2001US-00962756.
 PR (NOVO) NOVO NORDISK AS.
 PA (DGI-) DGI BIOTECHNOLOGIES.
 XX Pillutla R, Dedova O, Blume AJ, Goldstein NI, Brissette R;
 PI Wang P, Liu H, Hsiao K, Lennick M, Fletcher P;
 XX WPI; 2003-363211/34.
 DR
 XX

PT Modulating insulin-like growth factor receptor (IGFR) activity in IGF-
 PT responsive mammalian cells, useful for treating cancer comprises
 PT contacting the cells with an amino acid sequence to modulate the activity
 of IGFR.

XX Example 11; Fig 43; 372pp; English.

XX
 XX The present invention describes a method for modulating insulin-like
 CC growth factor receptor (IGFR) activity in insulin-like growth factor-
 CC responsive mammalian cells comprising contacting the cells with an amino
 CC acid sequence to modulate the activity of IGFR. In modulating IGFR
 CC activity, the amino acid sequence comprises XIX2K3X4X5 (I), where X1, X2
 CC and X5 = phenylalanine or tyrosine; X3 = aspartic acid, glutamic acid,
 CC glycine or serine; and X4 = tryptophan, tyrosine or phenylalanine. The
 CC amino acid sequence is not insulin, insulin-like growth factor, an anti-
 CC insulin receptor antibody, an anti-insulin-like growth receptor antibody,
 CC or its fragment. Also described: (1) decreasing or increasing IGFR
 CC activity in IGF-responsive mammalian cells by contacting the cells with
 CC an amino acid sequence to decrease or increase the activity of IGFR; (2)
 CC an IGFR modulator, agonist or antagonist; (3) identifying IGFR modulator;
 CC and (4) enhancing survival of an IGF-responsive mammalian cell by
 CC contacting the cell with (1) to enhance the survival of the cell. IGFR
 CC modulators have cytostatic activity, and can be used as IGFR agonists or
 CC IGFR antagonists. The methods, modulators, agonists and antagonists are
 CC useful for treating cancer, e.g. leukaemia, sarcoma, lymphoma or
 CC carcinoma. The methods are useful for identifying molecular structures
 CC that are capable of acting as an IGFR agonist or antagonist. The present
 CC invention represents a peptide given in the exemplification of the present
 XX sequence 27 AA;

SQ Sequence 27 AA;

Query Match 55.6%; Score 5; DB 6; Length 27;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 Db |||||
 1 DDTFY 5

RESULT 43

ID ADH96007
 AC ADH96007 standard; protein; 27 AA.

XX ADH96007;

XX 22-APR-2004 (first entry)

XX Insulin growth factor receptor peptide, SEQ ID No 1425.

XX insulin receptor; insulin; insulin-like growth factor receptor; agonist;
 KW antagonist; antidiabetic; diabetes; insulin shock.

XX Unidentified.

XX WO2003070747-A2.

XX 28-AUG-2003.

XX 24-SEP-2002; 2002WO-US030312.

XX 24-SEP-2001; 2001US-00962756.

XX (NOVO) NOVO NORDISK AS.

XX (DGIB-) DGI BIOTECHNOLOGIES.

XX Pillutla R, Brissette R, Blume AJ, Schaeffer L, Brandt J;

PI Goldstein NI, Spetzler J, Ostergaard S;

XX WPI; 2003-833235/77.

XX Modulating insulin-like growth factor receptor (IGFR) activity in IGF-

PT responsive mammalian cells, useful for treating diabetes comprises
 PT contacting the cells with an amino acid sequence to modulate the activity
 of IGFR.

XX Example 14; SEQ ID NO 1425; 328pp; English.

XX
 CC The invention relates to a novel method for decreasing or increasing
 CC insulin receptor activity in mammalian cells. The invention further
 CC relates to peptide sequences capable of binding to insulin and/or insulin
 CC -like growth factor receptors with either agonist or antagonist activity.
 CC The peptide sequences are identified from various peptide libraries. The
 CC novel method comprises administering to the mammalian cells an amino acid
 CC having subsequences that binds to site 1 and site 2 of an insulin
 CC receptor. The subsequences are joined C-terminus to N-terminus and
 CC oriented site 1 to site 2. The sequence is not insulin or insulin-like
 CC growth factor. The peptide sequences of the invention have antidiabetic
 CC activity. The peptides are useful for treating diabetes or insulin shock.
 CC This sequence represents an insulin receptor/ insulin growth factor
 CC receptor binding polypeptide relating to the invention.

XX Sequence 27 AA;

Query Match 55.6%; Score 5; DB 7; Length 27;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 Db |||||
 1 DDTFY 5

RESULT 44

ID ADL68698

XX ADL68698 standard; peptide; 27 AA.

XX ADL68698;

XX 20-MAY-2004 (first entry)

XX IGF-1R/IR binding peptide seq id 1425.

XX cytostatic; insulin-like growth factor receptor activity;

KW insulin-like growth factor-responsive mammalian cell;

KW insulin-like growth factor receptor modulator;

KW insulin-like growth factor receptor antagonist;

KW insulin-like growth factor receptor agonist; insulin receptor;

KW insulin-like growth factor receptor; therapeutic; peptide hormone;

KW cancer; breast cancer; prostate cancer; colorectal cancer;

KW ovarian cancer; peptide library; IGF-1R; IR.

XX Unidentified.

XX US2004023887-A1.

XX 05-FEB-2004.

XX 24-SEP-2002; 2002US-00253493.

XX 02-SEP-1998; 98US-00146127.

XX 29-MAR-2000; 2000US-00538038.

XX 24-SEP-2001; 2001US-00962756.

XX (PILL/) PILLUTLA R.

XX (DEDO/) DEDOVA O.

XX (BLUM/) BLUME A J.

XX (GOLD/) GOLDSTEIN N I.

XX (BRIS/) BRISSETTE R.

XX (WANG/) WANG P.

XX (LIUH/) LIU H.

XX (HSIA/) HSIAO K.

XX (LENN/) LENNICK M.

XX (FLET/) FLETCHER P.

XX

PI Pillutla R, Dedova O, Blume AJ, Goldstein NI, Brissette R;
 PI Wang P, Liu H, Hsiao K, Lennick M, Fletcher P;
 XX WPI; 2004-132606/13.
 PS Disclosure; SEQ ID NO 1425; 242pp; English.
 XX
 CC The invention describes the use of molecular structures, preferably
 CC peptides for modulating, increasing or decreasing insulin-like growth
 CC factor receptor activity in insulin-like growth factor-responsive
 CC mammalian cells. Also described are: modulating, decreasing or increasing
 CC insulin-like growth factor receptor activity in insulin-like growth
 CC factor-responsive mammalian cells; an insulin-like growth factor
 CC modulator; an insulin-like growth factor receptor antagonist; an insulin-
 CC like growth factor receptor agonist; identifying an insulin-like growth
 CC factor receptor modulator; and enhancing survival of an insulin-like
 CC growth factor-responsive mammalian cell. The molecular structures of the
 CC peptides are useful for modulating, increasing or decreasing insulin-like
 CC growth factor receptor activity in insulin-like growth factor-responsive
 CC mammalian cells. The peptide sequences are useful for binding to insulin
 CC and/or insulin-like growth factor receptors with either agonist or
 CC antagonist activity. As agonists, the peptides are useful for development
 CC of therapeutics to supplement or replace endogenous peptide hormones. The
 CC antagonist peptides can also be developed as therapeutics. The IR and IGF
 CC -1R agonist and antagonist peptides are useful as lead compounds for
 CC identifying other more potent or selective therapeutics, assay reagents
 CC for identifying other useful ligands, as research tools for further
 CC analysis of IR and IGF-1R. The IGF-1R antagonists are useful as treatment
 CC for cancer, e.g. breast, prostate, colorectal or ovarian cancer. This is
 CC the amino acid sequence of a IGF-1R/IR binding peptide obtained by
 CC panning a peptide library against the insulin-like growth factor 1
 CC receptor (IGF-1R) and insulin receptor (IR). Note: This sequence is also
 CC available in electronic format from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docID=20040023887.
 XX
 SQ Sequence 27 AA;

Query Match 55.6%; Score 5; DB 8; Length 27;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 Db |||||
 1 DDTFY 5

RESULT 45
 ADM38543
 ID ADM38543 standard; peptide; 27 AA.
 XX
 AC ADM38543;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Insulin and IGF-1 receptor associated peptide #164.
 XX
 KW insulin receptor activity; insulin-related disease;
 KW insulin-like growth factor-related disease; diabetes; insulin shock.
 XX
 OS Synthetic.
 XX
 OS US2003236190-A1.
 XX
 XX 25-DEC-2003.
 XX
 PF 24-SEP-2002; 2002US-00253471.
 XX
 PR 02-SEP-1998; 98US-00146127.
 XX
 PR 29-MAR-2000; 2000US-00538038.
 PR
 PR 24-SEP-2001; 2001US-00962756.
 XX
 XX (PILL/) PILLUTLA R.
 PA (BRIS/) BRISSETTE R.

PA (BLUM/) BLUME A J.
 PA (SCHA/) SCHAFER L.
 PA (BRAN/) BRANDT J.
 PA (GOLD/) GOLDSTEIN N I.
 PA (SPET/) SPETZLER J.
 PA (OSTE/) OSTERGAARD S.
 PA (HANS/) HANSEN P H.
 XX
 PI Pillutla R, Brissette R, Blume AJ, Schaffer L, Brandt J;
 PI Goldstein NI, Spetzler J, Ostergaard S, Hansen PH;
 XX WPI; 2004-081583/08.
 DR Decreasing or increasing insulin receptor activity in mammalian cells
 CC using peptide sequences that bind insulin and/or insulin-like growth
 CC factor receptors, useful for treating diabetes and insulin shock.
 PT
 FT
 XX Disclosure; SEQ ID NO 1425; 203pp; English.
 XX
 CC The invention relates to a method of decreasing insulin receptor activity
 CC in mammalian cells which comprises administering an amino acid sequence
 CC having a subsequence comprising a sequence that binds to Site 1 and Site
 CC 2 of insulin receptor, where the subsequences are linked C-terminus to N-
 CC terminus and oriented Site 1 to Site 2, where the amino acid sequence is
 CC not insulin, insulin-like growth factor or their fragments. The methods
 CC and compositions of the present invention are useful for treating insulin
 CC or insulin-like growth factor-related diseases or conditions, such as
 CC diabetes and insulin shock. The present sequence is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 27 AA;

Query Match 55.6%; Score 5; DB 8; Length 27;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 Db |||||
 1 DDTFY 5

RESULT 46
 ABO57827
 ID ABO57827 standard; protein; 59 AA.
 XX
 AC ABO57827;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human genome derived single exon protein #4061.
 XX
 KW Human; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.
 XX
 OS Homo sapiens.
 XX
 OS US2003194704-A1.
 XX
 XX 16-OCT-2003.
 XX
 PF 03-APR-2002; 2002US-00029386.
 XX
 PR 03-APR-2002; 2002US-00029386.
 XX
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 XX
 XX Penn SG, Rank DR, Hanzel DK;
 PI
 XX WPI; 2004-119264/12.
 XX
 XX New human genome-derived single exon nucleic acid probes useful for human

PT Gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.

XX Claim 45; SEQ ID NO 31461; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 688 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridises under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe protein of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704

XX Sequence 59 AA;

Query Match 55.6%; Score 5; DB 8; Length 59;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 Db 48 DDTFY 52

RESULT 47
 AAU44424
 ID AAU44424 standard; protein; 62 AA.
 XX
 AC AAU44424;

XX 27-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #5320.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181581-A2.

XX 01-NOV-2001.

PD 11-OCT-2002; 2002WO-US032727.

XX 20-APR-2001; 2001WO-US012865.
 PF

XX 21-APR-2000; 2000US-0199047P.
 PR

PR 02-JUN-2000; 2000US-0208841P.
 PR

XX 07-JUL-2000; 2000US-0216747P.
 XX

PA (CORI-) CORIXA CORP.

XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.
 DR

DR N-PSDB; AAS59522.

XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.

XX Example 1; SEQ ID NO 5619; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 62 AA;

Query Match 55.6%; Score 5; DB 4; Length 62;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 Db 8 VDDTF 12

RESULT 48
 ABM40943
 ID ABM40943 standard; protein; 62 AA.
 XX
 AC ABM40943;

XX 20-OCT-2003 (first entry)

XX Propionibacterium acnes predicted ORF-encoded polypeptide #5619.

XX Acne vulgaris; anti-seborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.

XX Propionibacterium acnes.

XX WO2003033515-A1.

XX 24-APR-2003.

XX 11-OCT-2002; 2002WO-US032727.

```

XX PR 15-OCT-2001; 2001US-00978825.
XX PA (CORI-) CORIXA CORP.
XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
PI Zhang Y, Wang S, Jen S, Lodes WJ, Benson DR, Jones R, Carter D;
XX Barth B, Vallieue-Douglas J;
XX WPI; 2003-381789/36.
DR N-PSDB; ACF64451.
XX
XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PT or for stimulating an immune response specific for a P. acnes protein.
XX
PS Example 1; SEQ ID NO 5619; 1481pp; English.
XX
XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention; antibodies against polypeptides of the
CC polynucleotide of the invention; fusion proteins comprising a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising T cells prepared
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 62 AA;
Query Match 55.6%; Score 5; DB 6; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTF 6
Db 8 VDDTF 12
|||||
|||||

RESULT 49
ADM97962
ID ADM97962 standard; peptide; 74 AA.
XX ADM97962;
AC Vetispiradiene.
DT 01-JUL-2004 (first entry)
XX
XX sesquiterpene synthase; cubebol synthase; GFTbSC; transformed plant cell;
KW farnesyl-pyrophosphate; valencene; bicyclo-germacrene; cubebol;
KW delta-cadinene; perfumery; GFTpsA; GFTpsB; GFTpsDL; GFTpsD2; GFTpsE.
XX
OS Solanum tuberosum.
XX

```

```

FH Key Location/Qualifiers
FT Misc-difference 5 /note= "Conserved residue"
FT Misc-difference 11. .13 /note= "Conserved residues"
FT Misc-difference 26 /note= "Conserved residue"
FT Misc-difference 28 /note= "Conserved residue"
FT Misc-difference 30. .31 /note= "Conserved residue"
FT Misc-difference 33 /note= "Conserved residues"
FT Misc-difference 35 /note= "Conserved residue"
FT Misc-difference 42. .43 /note= "Conserved residue"
FT Misc-difference 49 /note= "Conserved residues"
FT Misc-difference 54 /note= "Conserved residue"
FT Misc-difference 63. .64 /note= "Conserved residues"
FT Misc-difference 67 /note= "Conserved residue"
FT Misc-difference 74 /note= "Conserved residue"
XX WO2004031376-A2.
XX 15-APR-2004.
XX 02-OCT-2003; 2003WO-IB005072.
XX 04-OCT-2002; 2002US-0415765P.
XX 02-DEC-2002; 2002WO-IB005070.
XX (FIRM ) FIRMENICH SA.
XX Schalk M, Clark A;
XX WPI; 2004-330180/30.
XX
XX New sesquiterpene synthase, useful for converting farnesyl-pyrophosphate
PT to various oxygenated and aliphatic sesquiterpenes including valencene,
PT bicyclogermacrene, cubebol, and delta-cadinene.
XX
XX Disclosure; Fig 4; 66pp; English.
XX
XX This sequence represents a peptide fragment from a sesquiterpene
CC synthase, around residues 280-355. This peptide fragment was used in the
CC production of degenerate primers for the isolation of sesquiterpene
CC synthase coding sequences from grapefruit. The isolated sequences may be
CC used in the production of sesquiterpene synthases by culturing a
CC transformed plant cell in conditions conducive to the production of a
CC sesquiterpene synthase. The sesquiterpene synthases of the invention are
CC useful for converting farnesyl-pyrophosphate to various oxygenated and
CC aliphatic sesquiterpenes, including valencene, bicyclo-germacrene,
CC cubebol, delta-cadinene. Sesquiterpene compounds are used in perfumery. A
CC plant-independent system of production of sesquiterpene compounds would
CC be of interest, to remove the price link to plant availability.
XX
XX Sequence 74 AA;
Query Match 55.6%; Score 5; DB 8; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTF 6
Db 62 VDDTF 66
|||||
|||||

```

RESULT 50
ADM97960
ID ADM97960 standard; peptide; 74 AA.
XX AC ADM97960;
XX 01-JUL-2004 (first entry)
XX DE 5-epi-Aristolochene.
XX KW sesquiterpene synthase; cubebol synthase; GFTpsC; transformed plant cell;
KW farnesyl-pyrophosphate; valencene; bicyclo-germacrene; cubebol;
KW delta-cadinene; perfumery; GFTpsA; GFTpsB; GFTpsD1; GFTpsD2; GFTpsE.
XX OS Nicotiana tabacum.
XX XX

Key Location/Qualifiers
FH Misc-difference 5 /note= "Conserved residue"
FT FT
FT Misc-difference 11..13
FT FT
FT Misc-difference 26 /note= "Conserved residues"
FT FT
FT Misc-difference 28 /note= "Conserved residue"
FT FT
FT Misc-difference 30..31 /note= "Conserved residue"
FT FT
FT Misc-difference 33 /note= "Conserved residues"
FT FT
FT Misc-difference 35 /note= "Conserved residue"
FT FT
FT Misc-difference 42..43 /note= "Conserved residue"
FT FT
FT Misc-difference 49 /note= "Conserved residues"
FT FT
FT Misc-difference 54 /note= "Conserved residue"
FT FT
FT Misc-difference 63..64 /note= "Conserved residue"
FT FT
FT Misc-difference 67 /note= "Conserved residues"
FT FT
FT Misc-difference 74 /note= "Conserved residue"
FT FT
XX WO2004031376-A2.
XX PN
XX PD 15-APR-2004.
XX PP 02-OCT-2003; 2003WO-IB005072.
XX XX
PR 04-OCT-2002; 2002US-0415765P.
PR 02-DEC-2002; 2002WO-IB005070.
XX XX
PA (FIRM) FIRMENICH SA.
XX XX
PI Schalk M, Clark A;
XX XX
DR WPI; 2004-330180/30.
XX XX
PT New sesquiterpene synthase, useful for converting farnesyl-pyrophosphate
PT to various oxygenated and aliphatic sesquiterpenes including valencene,
PT bicyclogermacrene, cubebol, and delta-cadinene.
XX XX
XX Disclosure; Fig 4; 66pp; English.
XX XX
CC This sequence represents a peptide fragment from a sesquiterpene
CC synthase, around residues 280-355. This peptide fragment was used in the
CC production of degenerate primers for the isolation of sesquiterpene
CC synthase coding sequences from grapefruit. The isolated sequences may be
CC used in the production of sesquiterpene synthases by culturing a
CC transformed plant cell in conditions conducive to the production of a
CC sesquiterpene synthase. The sesquiterpene synthases of the invention are
CC useful for converting farnesyl-pyrophosphate to various oxygenated and

CC aliphatic sesquiterpenes, including valencene, bicyclo-germacrene,
CC cubebol, delta-cadinene. Sesquiterpene compounds are used in perfumery. A
CC plant-independent system of production of sesquiterpene compounds would
CC be of interest, to remove the price link to plant availability.
XX XX
SQ Sequence 74 AA;
Query Match 55.6%; Score 5; DB 8; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTF 6
DB 62 VDDTF 66

RESULT 51
ADM97963
ID ADM97963 standard; peptide; 74 AA.
XX AC ADM97963;
XX 01-JUL-2004 (first entry)
XX DE Vetispiradiene.
XX KW sesquiterpene synthase; cubebol synthase; GFTpsC; transformed plant cell;
KW farnesyl-pyrophosphate; valencene; bicyclo-germacrene; cubebol;
KW delta-cadinene; perfumery; GFTpsA; GFTpsB; GFTpsD1; GFTpsD2; GFTpsE.
XX OS Hyoscyamus muticus.
XX XX

Key Location/Qualifiers
FH Misc-difference 5 /note= "Conserved residue"
FT FT
FT Misc-difference 11..13 /note= "Conserved residues"
FT FT
FT Misc-difference 26 /note= "Conserved residue"
FT FT
FT Misc-difference 28 /note= "Conserved residue"
FT FT
FT Misc-difference 30..31 /note= "Conserved residue"
FT FT
FT Misc-difference 33 /note= "Conserved residues"
FT FT
FT Misc-difference 35 /note= "Conserved residue"
FT FT
FT Misc-difference 42..43 /note= "Conserved residue"
FT FT
FT Misc-difference 49 /note= "Conserved residues"
FT FT
FT Misc-difference 54 /note= "Conserved residue"
FT FT
FT Misc-difference 63..64 /note= "Conserved residues"
FT FT
FT Misc-difference 67 /note= "Conserved residues"
FT FT
FT Misc-difference 74 /note= "Conserved residue"
FT FT
XX WO2004031376-A2.
XX PN
XX PD 15-APR-2004.
XX PP 02-OCT-2003; 2003WO-IB005072.
XX XX
PR 04-OCT-2002; 2002US-0415765P.
PR 02-DEC-2002; 2002WO-IB005070.
XX XX
PA (FIRM) FIRMENICH SA.
XX XX
PI Schalk M, Clark A;
XX XX

DR WPI; 2004-330180/30.

XX New sesquiterpene synthase, useful for converting farnesyl-pyrophosphate

PT to various oxygenated and aliphatic sesquiterpenes including valencene,

PT bicyclogermacrene, cubebol, and delta-cadinene.

XX Disclosure; Fig 4; 66pp; English.

XX This sequence represents a peptide fragment from a sesquiterpene

CC synthase, around residues 280-355. This peptide fragment was used in the

CC production of degenerate primers for the isolation of sesquiterpene

CC synthase coding sequences from grapefruit. The isolated sequences may be

CC used in the production of sesquiterpene synthases by culturing a

CC transformed plant cell in conditions conducive to the production of a

CC sesquiterpene synthase. The sesquiterpene synthases of the invention are

CC useful for converting farnesyl-pyrophosphate to various oxygenated and

CC aliphatic sesquiterpenes, including valencene, bicyclo-germacrene,

CC cubebol, delta-cadinene. Sesquiterpene compounds are used in perfumery. A

CC plant-independent system of production of sesquiterpene compounds would

CC be of interest, to remove the price link to plant availability.

XX Sequence 74 AA;

Query Match 55.6%; Score 5; DB 8; Length 74;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6

Db 62 VDDTF 66

|||||

RESULT 52

AEA51017

ID AEA51017 standard; protein; 74 AA.

XX AC AEA51017;

XX 11-AUG-2005 (first entry)

DT Tobacco 5-epi-aristolochene synthase protein.

DE Plant; enzyme; 5-epi-aristolochene synthase.

XX Nicotiana tabacum.

XX Key Location/Qualifiers

FH Region 9..13

FT /note= "Region used to design primer TpsVF1"

FT Region 30..36

FT /note= "Region used to design primer TpsVF2"

FT Region 63..69

FT /note= "Region used to design primer TpsVR3"

XX WO2005052163-A2.

PN 09-JUN-2005.

XX 19-NOV-2004; 2004WO-IB003836.

PF 26-NOV-2003; 2003US-0525512P.

PR 09-DEC-2003; 2003WO-IB006459.

XX (FIRM) FIRMENICH SA.

XX Schalk M;

PI WPI; 2005-418005/42.

XX New nucleic acid encoding a patchoulol synthase or gamma-curcumene

PT synthase or a polypeptide having sesquiterpene synthase activity, useful

PT for making terpenoids used in perfumery, cosmetics and medicine.

XX Example 7; SEQ ID NO 19; 75pp; English.

XX The present invention relates to patchoulol synthase, gamma-curcumene

CC synthase and sesquiterpene synthase polypeptides and their encoding

CC polynucleotides. The invention is useful for making terpenoids used in

CC perfumery, cosmetics and medicine. The present sequence is the tobacco 5-

XX epi-aristolochene synthase protein.

SQ Sequence 74 AA;

Query Match 55.6%; Score 5; DB 9; Length 74;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6

Db 62 VDDTF 66

|||||

RESULT 53

AEA51019

ID AEA51019 standard; protein; 74 AA.

XX AC AEA51019;

XX 11-AUG-2005 (first entry)

DT Potato vetispiradiene synthase protein.

DE Plant; enzyme; vetispiradiene synthase.

XX Solanum tuberosum.

XX Key Location/Qualifiers

FH Region 9..13

FT /note= "Region used to design primer TpsVF1"

FT Region 30..36

FT /note= "Region used to design primer TpsVF2"

FT Region 63..69

FT /note= "Region used to design primer TpsVR3"

XX WO2005052163-A2.

PN 09-JUN-2005.

XX 19-NOV-2004; 2004WO-IB003836.

PF 26-NOV-2003; 2003US-0525512P.

PR 09-DEC-2003; 2003WO-IB006459.

XX (FIRM) FIRMENICH SA.

XX Schalk M;

PI WPI; 2005-418005/42.

XX New nucleic acid encoding a patchoulol synthase or gamma-curcumene

PT synthase or a polypeptide having sesquiterpene synthase activity, useful

PT for making terpenoids used in perfumery, cosmetics and medicine.

XX Example 7; SEQ ID NO 19; 75pp; English.

XX The present invention relates to patchoulol synthase, gamma-curcumene

CC synthase and sesquiterpene synthase polypeptides and their encoding

CC polynucleotides. The invention is useful for making terpenoids used in

CC perfumery, cosmetics and medicine. The present sequence is the potato

CC vetispiradiene synthase protein.

SQ Sequence 74 AA;

Query Match 55.6%; Score 5; DB 9; Length 74;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PS Example 7; SEQ ID NO 17; 75pp; English.

XX The present invention relates to patchoulol synthase, gamma-curcumene

CC synthase and sesquiterpene synthase polypeptides and their encoding

CC polynucleotides. The invention is useful for making terpenoids used in

CC perfumery, cosmetics and medicine. The present sequence is the tobacco 5-

XX epi-aristolochene synthase protein.

SQ Sequence 74 AA;

Query Match 55.6%; Score 5; DB 9; Length 74;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6

Db 62 VDDTF 66

|||||

RESULT 53

AEA51019

ID AEA51019 standard; protein; 74 AA.

XX AC AEA51019;

XX 11-AUG-2005 (first entry)

DT Potato vetispiradiene synthase protein.

DE Plant; enzyme; vetispiradiene synthase.

XX Solanum tuberosum.

XX Key Location/Qualifiers

FH Region 9..13

FT /note= "Region used to design primer TpsVF1"

FT Region 30..36

FT /note= "Region used to design primer TpsVF2"

FT Region 63..69

FT /note= "Region used to design primer TpsVR3"

XX WO2005052163-A2.

PN 09-JUN-2005.

XX 19-NOV-2004; 2004WO-IB003836.

PF 26-NOV-2003; 2003US-0525512P.

PR 09-DEC-2003; 2003WO-IB006459.

XX (FIRM) FIRMENICH SA.

XX Schalk M;

PI WPI; 2005-418005/42.

XX New nucleic acid encoding a patchoulol synthase or gamma-curcumene

PT synthase or a polypeptide having sesquiterpene synthase activity, useful

PT for making terpenoids used in perfumery, cosmetics and medicine.

XX Example 7; SEQ ID NO 19; 75pp; English.

XX The present invention relates to patchoulol synthase, gamma-curcumene

CC synthase and sesquiterpene synthase polypeptides and their encoding

CC polynucleotides. The invention is useful for making terpenoids used in

CC perfumery, cosmetics and medicine. The present sequence is the potato

CC vetispiradiene synthase protein.

SQ Sequence 74 AA;

Query Match 55.6%; Score 5; DB 9; Length 74;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 Db 62 VDDTF 66

RESULT 54
 AEA51020
 ID AEA51020 standard; protein; 74 AA.
 XX AC AEA51020;
 XX XX
 XX 11-AUG-2005 (first entry)
 XX DE Hyoscyamus muticus vetispiradiene synthase protein.
 XX XX
 XX KW Plant; enzyme; vetispiradiene synthase.
 XX OS Hyoscyamus muticus.
 XX XX
 FH Key Location/Qualifiers
 FT Region 9..13
 FT /note= "Region used to design primer TpsVF1"
 FT Region 30..36
 FT /note= "Region used to design primer TpsVF2"
 FT Region 63..69
 FT /note= "Region used to design primer TpsVR3"
 FT XX
 XX WO2005052163-A2.
 XX PN
 XX 09-JUN-2005.
 XX XX
 XX 19-NOV-2004; 2004WO-IB0003836.
 XX XX
 XX 26-NOV-2003; 2003US-0525512P.
 XX PR 09-DEC-2003; 2003WO-IB0006459.
 XX PA (FIRM) FIRMENICH SA.
 XX XX
 XX Schalk M;
 XX PI
 XX WPI; 2005-418005/42.
 XX DR
 XX New nucleic acid encoding a patchoulol synthase or gamma-curcumene
 XX PT synthase or a polypeptide having sesquiterpene synthase activity, useful
 XX FT for making terpenoids used in perfumery, cosmetics and medicine.
 XX PT
 XX XX
 XX Example 7; SEQ ID NO 20; 75pp; English.
 XX PS
 XX The present invention relates to patchoulol synthase, gamma-curcumene
 XX CC synthase and sesquiterpene synthase polypeptides and their encoding
 XX CC polynucleotides. The invention is useful for making terpenoids used in
 XX CC perfumery, cosmetics and medicine. The present sequence is the Hyoscyamus
 XX CC muticus vetispiradiene synthase protein.
 XX CC
 SQ Sequence 74 AA;
 Query Match 55.6%; Score 5; DB 9; Length 74;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 Db 62 VDDTF 66

RESULT 55
 ADC88085
 ID ADC88085 standard; protein; 78 AA.
 XX AC ADC88085;
 XX XX
 XX 01-JAN-2004 (first entry)
 XX DT

XX Ribosomal protein similar to FCWP1 #301.
 DE
 XX
 KW Antifungal protein; ribosomal protein; FCWP1; AlyAPP;
 KW Plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;
 KW Colletotrichum; Diplodia; Fusarium; Gaeumannomyces; Helminthosporium;
 KW Macrophomina; Mycosphaerella; Nectria; Peronospora; Phoma;
 KW Phymatotrichum; Phytophthora; Plasmodiopsis; Podosphaera; Puccinia; Puthium;
 KW Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Sclerotium; Sclerotinia;
 KW Septoria; Thielaviopsis; Venturia; Verticillium.
 XX
 OS Unidentified.
 XX
 XX US6573361-B1.
 PN
 XX
 XX 03-JUN-2003.
 PD
 XX
 XX 07-DEC-2000; 2000US-00732210.
 PF
 XX
 XX 07-DEC-1999; 99US-0169340P.
 PR
 XX 07-DEC-1999; 99US-0169513P.
 PR
 XX (MONS) MONSANTO TECHNOLOGY LLC.
 PA
 XX
 XX Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;
 PI
 XX WPI; 2003-754558/71.
 XX DR
 XX Novel antifungal protein FCWP1, isolated from Fusarium culmorum, useful
 XX PT for controlling fungal infections in plants.
 XX FT
 XX
 XX Example 21; SEQ ID NO 338; 27pp; English.
 XX PS
 XX The invention relates to an isolated antifungal ribosomal protein from
 XX CC fusarium culmorum, FCWP1. Also included is a fusion protein between the
 XX CC signal peptide of the antifungal protein AlyAPP from Alyssum and FCWP1,
 XX CC encoded by the nucleic acid appearing as ADC87758. The FCWP1 proteins are
 XX CC useful for controlling fungal infections in plants, such as those caused
 XX CC by Alternaria (e.g. Alternaria brassicola, Alternaria solani),
 XX CC Aecochyta (e.g. Aecochyta pisi); Botrytis (e.g. Botrytis cinerea),
 XX CC Cercospora (e.g. Cercospora kikuchii, Cercospora zea-maydis),
 XX CC Colletotrichum (e.g. Colletotrichum lindemuthianum), Diplodia (e.g.
 XX CC Diplodia maydis), Fusarium (e.g. Fusarium nivale, Fusarium oxysporum,
 XX CC Fusarium graminearum, Fusarium culmorum, Fusarium solani, Fusarium
 XX CC moniliforme, Fusarium roseum), Gaeumannomyces (e.g. Gaeumannomyces
 XX CC graminis f.sp. tritici), Helminthosporium (e.g. Helminthosporium turcicum
 XX CC, Helminthosporium carbonum, Helminthosporium maydis), Macrophomina
 XX CC (e.g. Macrophomina phaseolina, Maganaporthe grisea), Mycosphaerella
 XX CC (e.g. Mycosphaerella figiensis), Nectria (Nectria haematococca),
 XX CC Peronospora (e.g. Peronospora manshurica, Peronospora tabacina), Phoma
 XX CC (e.g. Phoma betae), Phymatotrichum (e.g. Phymatotrichum omnivorum),
 XX CC Phytophthora (e.g. Phytophthora cinnamomi, Phytophthora cactorum,
 XX CC Phytophthora phaseoli, Phytophthora parasitica, Phytophthora
 XX CC citrophthora), Plasmodiopsis (e.g. Plasmodiopsis viticola), Puccinia
 XX CC (e.g. Puccinia leucotricha), Puccinia (e.g. Puccinia sorghi, Puccinia
 XX CC striiformis, Puccinia graminis f.sp. tritici, Puccinia asparagi,
 XX CC Puccinia recondita, Puccinia arachidis), Puthium (e.g. Puthium
 XX CC aphanidermatum), Pyrenophora (e.g. Pyrenophora tritici-repentens),
 XX CC Pyricularia (e.g. Pyricularia oryzae), Pythium (e.g. Pythium ultimum),
 XX CC Rhizoctonia (e.g. Rhizoctonia solani, Rhizoctonia cerealis), Sclerotium
 XX CC (e.g. Sclerotium rolfsii), Sclerotinia (e.g. Sclerotinia sclerotiorum),
 XX CC Septoria (e.g. Septoria lycopersici, Septoria glycoses, Stagonospora
 XX CC nodorum / Phaeosphaeria nodorum, Septoria tritici), Thielaviopsis (e.g.
 XX CC Thielaviopsis basicola), Uncinula (e.g. Uncinula necator), Venturia
 XX CC (e.g. Venturia inaequalis) or Verticillium (e.g. Verticillium dahliae,
 XX CC Verticillium albo-atrum). Mutations in the proteolytic consensus
 XX CC sequences contained within FCWP1 provides improved stability of its
 XX CC antifungal activity. Also disclosed are ribosomal proteins with similar
 XX CC PI (>7) and molecular weight (<20kDa) to FCWP1, which may act as
 XX CC antifungal proteins. The present sequence represents one of the ribosomal
 XX CC proteins similar to FCWP1. Note: The sequence data for this patent did
 XX CC not form part of the printed specification, but was obtained in

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 109 AA;

Query Match 55.6%; Score 5; DB 4; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFF 6
 |||||
 Db 85 VDDTFF 89

RESULT 58

ADX92114
 ID ADX92114 standard; protein; 110 AA.

AC ADX92114;

DT 21-APR-2005 (first entry)

DE Plant full length insert polypeptide seqid 54778.

XX plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.

XX Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 05-NOV-2001; 2001US-00985678.

XX (LIU//) LIU Y.
 PA (ZHOU//) ZHOU Y.
 PA (KOVA//) KOVALIC D K.
 PA (SCRE//) SCREEN S E.
 PA (TAB//) TABASKA J E.
 PA (CAOY//) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.

XX Claim 1; SEQ ID NO 54778; 15pp; English.

PS The invention describes a recombinant DNA construct comprising a
 XX polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.secdta.uspco.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.

SQ Sequence 110 AA;

Query Match 55.6%; Score 5; DB 8; Length 110;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 |||||
 Db 89 KVDDT 93

RESULT 59

ADM05832

ID ADM05832 standard; protein; 118 AA.

AC ADM05832;

XX 20-MAY-2004 (first entry)

DT Human protein of the invention SEQ ID NO:4517.

DE human; gene therapy; diagnostic marker; pharmaceutical.

XX Homo sapiens.

XX EP1347046-A1.

XX 24-SEP-2003.

XX 12-APR-2002; 2002EP-00008400.

XX 22-MAR-2002; 2002JP-00137785.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

PI Seki N, Yoshikawa T, Otsuka M, Naganari K, Masuho Y;

XX WPI; 2003-723558/69.

DR N-PSDB; ADM03389.

XX New polynucleotides and polypeptides are useful in gene therapy, for
 PT developing a diagnostic marker or medicines for regulating their
 PT expression and activity, or as a target of gene therapy.

XX

```

PS Claim 1; SEQ ID NO 4517; 305pp; English.
XX
CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.
XX
SQ Sequence 118 AA;

Query Match          55.6%; Score 5; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
Db      |||||
        26 DTFYY 30

RESULT 60
AEC88762
ID AEC88762 standard; protein; 118 AA.
XX
AC AEC88762;
XX
DT 01-DEC-2005 (first entry)
XX
DE Human cDNA clone protein TESTI20335200, SEQ ID 4517.
XX
KW Osteopathic; Cytostatic; Antiinflammatory; Gastrointestinal-Gen.;
KW Antulcer; Gene Therapy; Osteoporosis; cancer; inflammation; gastritis;
KW stomach ulcer; gastrointestinal ulcer.
XX
OS Homo sapiens.
XX
FN EP1580263-A1.
XX
PD 28-SEP-2005.
XX
PF 12-APR-2002; 2004EP-00027348.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PR 12-APR-2002; 2002EP-00008400.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2005-567421/69.
DR N-PSDB; AEC86319.
XX
XX New full-length cDNA sequences, useful for treating diseases, e.g.
PT osteoporosis, cancer, inflammation, gastritis, or gastroduodenal ulcer.
XX
PS Example 3; SEQ ID NO 4517; 296pp; English.
XX
CC The present invention relates to novel human cDNAs (AEC84246-AEC86688)
CC encoding proteins AEC86689-AEC89131. The cDNAs are useful for analyzing
CC the functions of the proteins, and for developing medicines for diseases
CC e.g. osteoporosis, cancer, inflammation, gastritis, or gastroduodenal
CC ulcer. Note: The sequence data for this patent did not form part of the
CC printed specification but was obtained in electronic format directly from
CC EPO.
XX
SQ Sequence 118 AA;

Query Match          55.6%; Score 5; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
Db      |||||
        26 DTFYY 30

RESULT 60
AEC88762
ID AEC88762 standard; protein; 118 AA.
XX
AC AEC88762;
XX
DT 01-DEC-2005 (first entry)
XX
DE Human cDNA clone protein TESTI20335200, SEQ ID 4517.
XX
KW Osteopathic; Cytostatic; Antiinflammatory; Gastrointestinal-Gen.;
KW Antulcer; Gene Therapy; Osteoporosis; cancer; inflammation; gastritis;
KW stomach ulcer; gastrointestinal ulcer.
XX
OS Homo sapiens.
XX
FN EP1580263-A1.
XX
PD 28-SEP-2005.
XX
PF 12-APR-2002; 2004EP-00027348.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PR 12-APR-2002; 2002EP-00008400.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2005-567421/69.
DR N-PSDB; AEC86319.
XX
XX New full-length cDNA sequences, useful for treating diseases, e.g.
PT osteoporosis, cancer, inflammation, gastritis, or gastroduodenal ulcer.
XX
PS Example 3; SEQ ID NO 4517; 296pp; English.
XX
CC The present invention relates to novel human cDNAs (AEC84246-AEC86688)
CC encoding proteins AEC86689-AEC89131. The cDNAs are useful for analyzing
CC the functions of the proteins, and for developing medicines for diseases
CC e.g. osteoporosis, cancer, inflammation, gastritis, or gastroduodenal
CC ulcer. Note: The sequence data for this patent did not form part of the
CC printed specification but was obtained in electronic format directly from
CC EPO.
XX
SQ Sequence 118 AA;

Query Match          55.6%; Score 5; DB 9; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
Db      |||||
        26 DTFYY 30

RESULT 61
AAW13923
ID AAW13923 standard; protein; 119 AA.
XX
AC AAW13923;
XX
DT 15-MAY-1997 (first entry)
XX
DE Heavy chain #2 for anti-HB virus antibody.
XX
KW Antibody; heavy chain; light chain; variable region; human; monoclonal;
KW complementarity determining region; human; adr type hepatitis B virus;
KW HB virus; CDR; virus antigen; anti-HB antibody; vaccine.
XX
OS Homo sapiens.
XX
FN JP09020798-A.
XX
PD 21-JAN-1997.
XX
PF 11-JUL-1995; 95JP-00174752.
XX
PR 11-JUL-1995; 95JP-00174752.
XX
PA (ASAH ) ASAH KASEI KOGYO KK.
XX
DR WPI; 1997-140911/13.
DR N-PSDB; AAT60118.
XX
PT Human anti-Hepatitis B antibody - used in a adr type HB virus vaccine.
XX
PS Claim 8; Page 11-12; 20pp; Japanese.
XX
CC AAW13921-W13928 represent the sequences for the heavy and light chains of
CC the human monoclonal antibodies of the invention. The antibody of the
CC invention preferably contains the sequence represented by AAW13912 in the
CC complementarity determining region-1 (CDR-1) of the heavy chain variable
CC region. The antibody of the invention also contains the sequence
CC represented by AAW13913 in the CDR-3 of the light chain variable region.
CC The antibody is capable of binding to adr type hepatitis B (HB) virus
CC antigen. A human anti-HB virus monoclonal antibody preparation which is
CC highly safe and is effective to adr type HB virus can be provided, using
CC the monoclonal antibody. It can also be used as a vaccine against HB
CC infection.
XX
SQ Sequence 119 AA;

Query Match          55.6%; Score 5; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db      |||||
        86 KVDDT 90

RESULT 62
AAW11635
ID AAW11635 standard; protein; 126 AA.
XX
AC AAW11635;
XX
DT 13-MAY-1997 (first entry)
XX

```

DE Human anti-RSV monoclonal antibody RP-2 VH domain.
 XX Monoclonal antibody; MAbs; RP-1; RP-2; respiratory syncytial virus; RSV;
 KW fusion protein; F-protein; vaccine; immunotherapy; therapy;
 KW Epstein Barr virus; immortalisation; recombinant antibody.
 XX Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Region 1. .30
 FT /label= FR1
 FT /note= "framework region 1"
 FT Region 31. .37
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 38. .51
 FT /label= FR2
 FT /note= "framework region 2"
 FT Region 52. .67
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 68. .99
 FT /label= FR3
 FT /note= "framework region 3"
 FT Region 100. .115
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 FT Region 116. .126
 FT /label= FR4
 FT /note= "framework region 4"
 XX
 PN W09640252-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96WO-US010070.
 XX
 PR 07-JUN-1995; 95US-00488376.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Brams P, Chamat SS, Pan L, Walsh EE, Heard CJ, Newman RA;
 XX
 DR WPI; 1997-099892/09.
 DR N-PSDB; AAT61237.
 XX
 PT Human monoclonal antibody specific for respiratory syncytial virus fusion
 PT protein - used for the prevention and treatment of RSV infection.
 XX
 PS Example 6; Fig 7b; 85pp; English.
 XX
 CC Amino acid sequences were deduced for the RP-1 VL, RP-2 VH, RP-2 VL and
 CC RP-1 VH domains (AAW11634-37) of human monoclonal antibodies (hMAbs) RP-1
 CC and RP-2, which show high affinity for respiratory syncytial virus (RSV)
 CC fusion protein. The hMAbs were obtained by antigen priming of naive human
 CC splenocytes in vitro; transfer of primed splenocytes to a SCID mouse;
 CC boosting with antigen; isolating human antibody-producing B-cells from
 CC the SCID mice; and immortalisation of the B-cells using Epstein Barr
 CC virus. DNA (see also AAT61236-39) encoding the RP-1 and RP-2 heavy and
 CC light variable domains can be incorporated into vectors (e.g. NEOSPLA)
 CC and used to transfect eukaryotic (e.g. CHO) cells (see also AAW11638-41)
 CC to provide a constant, stable supply of anti-RSV F-protein hMAbs for use
 CC in the treatment or prevention of RSV infection. (N.B. Fig 7b is referred
 CC to as the RP-1 VH domain in the specification, but is identical to the RP
 CC -2 VH domain of Fig 11b)
 XX
 SQ Sequence 126 AA;
 Query Match 55.6%; Score 5; DB 2; Length 126;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 DDTFY 7

Db 57 DDTFY 61
 RESULT 63
 ABU07100
 ID ABU07100 standard; protein; 127 AA.
 XX
 AC ABU07100;
 XX
 DT 17-FEB-2003 (first entry)
 XX
 DE Maize Starch synthase III (SSIII) LINKR domain related protein #24.
 XX
 KW Starch; starch synthase; glucan association domain; GLASS; linker domain;
 KW LINKR; glucosyl transferase domain; GLYTR; C-terminal end; CTEND;
 KW granule bound starch synthase; GBSS; morphology; retrogradation;
 KW waterbinding; swelling potential.
 XX
 OS Unidentified.
 XX
 PN W0200279410-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 29-MAR-2002; 2002WO-US009574.
 XX
 PR 30-MAR-2001; 2001US-0279720P.
 XX
 PA (BADI) BASF PLANT SCI GMBH.
 XX
 PI Commuri P, Keeling PL, Ramirez N, McKean A, Gao Z, Guan H;
 XX
 DR WPI; 2003-040678/03.
 XX
 PT New DNA encoding fusion protein consisting of 4 different functional
 PT domains selected from glucan association domain, linker domain, glucosyl
 PT transferase domain, and C-terminal end, useful for producing modified
 PT starches.
 XX
 PS Claim 19; Page 203-210; 265pp; English.
 XX
 CC The invention describes an isolated DNA molecule encoding a fusion
 CC protein consisting of 4 different functional domains selected from glucan
 CC association domain (GLASS), linker domain (LINKR), glucosyl transferase
 CC domain (GLYTR), and C-terminal end (CTEND) which are operably linked to
 CC one another. The DNA molecule is useful for expressing in plants
 CC polypeptides including starch synthase enzymes as fusion proteins with
 CC improved affinity to starch and modified catalytic capabilities and to
 CC the in vivo and in vitro synthesis of glucan chains of modified lengths
 CC as compared to plants producing native starch or starch produced with
 CC native starch synthases. Expression of the starch synthase fusion
 CC proteins along with granule bound starch synthase (GBSS) will lead to a
 CC modified starch having an altered or improved morphology, retrogradation,
 CC waterbinding, or swelling potential of the granules, gel strength,
 CC adhesiveness, cohesiveness, hardness, elasticity, increased or decreased
 CC granule size, degree of branching, crystallinity, degree of cross-
 CC linking, and increased or decreased glucan chain lengths. This is the
 CC amino acid sequence of a starch synthase functional domain associated
 CC protein
 XX
 SQ Sequence 127 AA;
 Query Match 55.6%; Score 5; DB 6; Length 127;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 DDTFY 7
 Db 84 DDTFY 88
 RESULT 64

```

AEA24151
ID AEA24151 standard; protein; 128 AA.
XX
AC AEA24151;
XX
DT 11-AUG-2005 (first entry)
XX
DE Anti-HAAH antibody heavy chain variable region #6.
XX
KW Antibody therapy; aspartyl (asparaginyl) beta-hydroxylase; AAH; HAAH;
KW cancer; neoplasm; lung tumor; liver tumor; colon tumor; pancreas tumor;
KW prostate tumor; ovary tumor; brain tumor; breast tumor; cytostatic;
KW antibody; heavy chain variable region.
XX
OS Homo sapiens.
XX
PN WO2005049802-A2.
XX
PD 02-JUN-2005.
XX
PF 15-NOV-2004; 2004WO-US038197.
XX
PR 14-NOV-2003; 2003US-0520114P.
XX
PS 19-APR-2004; 2004US-0563514P.
XX
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Wittrup DK, Yeung YA;
XX
DR WPI; 2005-417728/42.
XX
PT New composition comprising anti-hydroxylase antibodies, useful for
PT diagnosing or treating cancer, e.g. lung, liver, colon, pancreas,
PT prostate, ovary, bile duct, brain, or breast cancer.
XX
PS Disclosure; SEQ ID NO 11; 107pp; English.
XX
CC The invention relates to a composition comprising an isolated human
CC antibody or its fragment or other variant, where the antibody, the
CC fragment or the other variant specifically binds to an aspartyl
CC (asparaginyl) beta-hydroxylase (AAH). The invention also relates to an
CC isolated nucleic acid molecule comprising a sequence encoding a human
CC antibody or its fragment or other variant, where the antibody, the
CC fragment or the other variant specifically binds to human AAH (HAAH), an
CC expression vector comprising the nucleic acid molecule, a host cell
CC comprising the expression vector, a method of modulating an AAH activity
CC in a cell, a method of treating a patient who has a cancer associated
CC with overactive or over expressed AAH, a method for identifying an
CC antibody or its fragment or other variant that specifically binds to an
CC AAH and a method of making a human monoclonal antibody or its fragment or
CC other variant that specifically binds to an AAH. The composition,
CC antibody, nucleic acid, kit and methods are useful for diagnosing or
CC treating cancer, where the cancer cell is a tumor cell of the lung,
CC liver, colon, pancreas, prostate, ovary, bile duct, brain or breast. This
CC sequence represents an anti-HAAH antibody variable region used in the
CC scope of the invention.
XX
SQ Sequence 128 AA;
Query Match 55.6%; Score 5; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDVT 5
DB 87 KVDVT 91
RESULT 65
ABG94245
ID ABG94245 standard; protein; 134 AA.
XX
AC ABG94245;
XX
DT 11-AUG-2005 (first entry)
XX
DE Anti-HAAH antibody heavy chain variable region #6.
XX
KW Antibody therapy; aspartyl (asparaginyl) beta-hydroxylase; AAH; HAAH;
KW cancer; neoplasm; lung tumor; liver tumor; colon tumor; pancreas tumor;
KW prostate tumor; ovary tumor; brain tumor; breast tumor; cytostatic;
KW antibody; heavy chain variable region.
XX
OS Homo sapiens.
XX
PN WO2005049802-A2.
XX
PD 02-JUN-2005.
XX
PF 15-NOV-2004; 2004WO-US038197.
XX
PR 14-NOV-2003; 2003US-0520114P.
XX
PS 19-APR-2004; 2004US-0563514P.
XX
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Wittrup DK, Yeung YA;
XX
DR WPI; 2005-417728/42.
XX
PT New composition comprising anti-hydroxylase antibodies, useful for
PT diagnosing or treating cancer, e.g. lung, liver, colon, pancreas,
PT prostate, ovary, bile duct, brain, or breast cancer.
XX
PS Disclosure; SEQ ID NO 11; 107pp; English.
XX
CC The invention relates to a composition comprising an isolated human
CC antibody or its fragment or other variant, where the antibody, the
CC fragment or the other variant specifically binds to an aspartyl
CC (asparaginyl) beta-hydroxylase (AAH). The invention also relates to an
CC isolated nucleic acid molecule comprising a sequence encoding a human
CC antibody or its fragment or other variant, where the antibody, the
CC fragment or the other variant specifically binds to human AAH (HAAH), an
CC expression vector comprising the nucleic acid molecule, a host cell
CC comprising the expression vector, a method of modulating an AAH activity
CC in a cell, a method of treating a patient who has a cancer associated
CC with overactive or over expressed AAH, a method for identifying an
CC antibody or its fragment or other variant that specifically binds to an
CC AAH and a method of making a human monoclonal antibody or its fragment or
CC other variant that specifically binds to an AAH. The composition,
CC antibody, nucleic acid, kit and methods are useful for diagnosing or
CC treating cancer, where the cancer cell is a tumor cell of the lung,
CC liver, colon, pancreas, prostate, ovary, bile duct, brain or breast. This
CC sequence represents an anti-HAAH antibody variable region used in the
CC scope of the invention.
XX
SQ Sequence 128 AA;
Query Match 55.6%; Score 5; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDVT 5
DB 87 KVDVT 91
RESULT 65
ABG94245
ID ABG94245 standard; protein; 134 AA.
XX
AC ABG94245;
XX
DT 10-DEC-2002 (first entry)
XX
DE Apis cerana phospholipase A2 protein.
XX
KW Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
KW cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
KW vaccine; infectious disease; honeybee.
XX
OS Apis cerana.
OS Synthetic.
XX
PN WO200256905-A2.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002WO-IB000166.
XX
PR 19-JAN-2001; 2001US-0262379P.
XX
PR 04-MAY-2001; 2001US-0288549P.
XX
PR 05-OCT-2001; 2001US-0326998P.
XX
PR 07-NOV-2001; 2001US-0331045P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
PI Piossek C;
XX
DR WPI; 2002-627351/67.
XX
PT Molecular antigen array used in the production of vaccines for infectious
PT diseases.
XX
PS Claim 161; Page 386; 441pp; English.
XX
CC This invention relates to a novel ordered and repetitive antigen array
CC used in the production of vaccines for infectious diseases. The invention
CC also discloses a composition comprising a non-natural molecular scaffold
CC comprising a core particle selected from a core particle of a non-natural
CC origin and a core particle of natural origin and an organiser comprising
CC at least one first attachment site, where the organiser is connected to
CC the core particle by at least one covalent bond. Also disclosed is an
CC antigen or antigenic determinant with at least one second attachment
CC site, where the antigen or antigenic determinant is amyloid beta peptide
CC (Abeta1-42) or its fragment and where the second attachment site is
CC selected from an attachment site not naturally occurring with the antigen
CC or antigenic determinant and an attachment site naturally occurring with
CC the antigen or antigenic determinant, where the second attachment site is
CC capable of association through at least one non-peptide bond to the first
CC attachment site and where the antigen or antigenic determinant and the
CC scaffold interact through the association to form an ordered and
CC repetitive antigen array. The invention also comprises a coat protein
CC capable of forming a capsid which comprises mutant Qbeta coat proteins
CC having an amino acid sequence selected from five amino acid sequences
CC fully defined in the specification. The compounds of the invention may
CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
CC immunisation and as a vaccine. The present sequence represents a protein
CC sequence used to create the compositions of the invention
XX
SQ Sequence 134 AA;
Query Match 55.6%; Score 5; DB 5; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 DDTFY 7
DB 64 DDTFY 68
RESULT 66
ABG80557

```

ID ABG80557 standard; protein; 134 AA.
AC ABG80557;
XX
XX 29-NOV-2002 (first entry)
XX
XX
XX Bee phospholipase A2 #4.
XX
XX Molecular antigen array; vaccine; antigen; antimicrobial;
KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;
KW graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;
KW adult respiratory distress syndrome; ARDS; Crohn's disease;
KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
KW Grave's disease; systemic lupus erythematosus; osteoporosis;
KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
KW angioimmunoproliferative lymphadenopathy; Alzheimer's disease;
KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
KW enterokinase; cysteine-containing linker.
XX
XX Apis cerana.
XX
XX WO200256907-A2.
XX
XX 25-JUL-2002.
XX
XX 21-JAN-2002; 2002WO-IB000168.
XX
XX 19-JAN-2001; 2001US-0262379P.
PR 04-MAY-2001; 2001US-0288549P.
PR 05-OCT-2001; 2001US-0326998P.
PR 07-NOV-2001; 2001US-0331045P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (NOVS) NOVARTIS PHARMA AG.
PA (MAUR/) MAURER P.
PA (LECH/) LECHNER P.
PA (ORTM/) ORTMANN R.
PA (LUEO/) LUEOEND R.
PA (STAU/) STAUFENBIEL M.
PA (FREY/) FREY P.
XX
XX Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
PI Renner WA, Bachmann M, Tissot A, Sebbel P, Flossek C;
XX
XX WPI; 2002-636514/68.
XX
XX Molecular antigen array used in the production of vaccines for infectious
XX diseases.
XX
XX Disclosure; Page 363-364; 418pp; English.
XX
XX The invention relates to a composition comprising: (a) a non-natural
CC molecular scaffold comprising: (i) a core particle selected from: (i) a
CC core particle of a non-natural origin; and (ii) a core particle of natural
CC origin; and (ii) an organiser comprising at least one first attachment
CC site, where the organiser is connected to the core particle by at least
CC one covalent bond; (b) an antigen or antigenic determinant with at least
CC one second attachment site, where the antigen or antigenic determinant is
CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
CC attachment site is selected from: (i) an attachment site not naturally
CC occurring with the antigen or antigenic determinant; and (ii) an
CC attachment site naturally occurring with the antigen or antigenic
CC determinant, where the second attachment site is capable of association
CC through at least one non-peptide bond to the first attachment site; and
CC where the antigen or antigenic determinant and the scaffold interact
CC through the association to form an ordered and repetitive antigen array.
CC Also included is a process for producing a non-naturally occurring
CC ordered and repetitive antigen array. The composition is used in
CC immunisation and as a vaccine for diseases such as influenza, graft
CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult
CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,

CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
CC gravis, immunoproliferative disease lymphadenopathy,
CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
CC osteoporosis and infectious diseases. The present sequence is an antigen
CC for use in the array of the invention. The antigen is modified to possess
CC a cleavage site (enterokinase or factor Xa) and a Cysteine- containing N-
CC or C-terminal linker peptide which serves as the attachment point to a
XX virus like particle or bacterial protein (the scaffold protein)
XX
XX Sequence 134 AA;
XX
XX Query Match 55.6%; Score 5; DB 5; Length 134;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 DDTFY 7
XX |||||
XX Db 64 DDTFY 68
XX
XX RESULT 67
XX ADE62328
XX ID ADE62328 standard; protein; 138 AA.
XX
XX AC ADE62328;
XX
XX 29-JAN-2004 (first entry)
XX
XX DE Rat Protein P51673, SEQ ID NO 8257.
XX
XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX OS Rattus norvegicus.
XX
XX PN WO2003016475-A2.
XX
XX PD 27-FEB-2003.
XX
XX PF 14-AUG-2002; 2002WO-US025765.
XX
XX PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX GENBANK; P51673.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 138 AA;

Query Match 55.6%; Score 5; DB 7; Length 138;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFF 7
 |||||
 Db 48 DDTFF 52

RESULT 68

AAU19377
 ID AAU19377 standard; protein; 146 AA.

XX AC AAU19377;

XX DT 04-DEC-2001 (first entry)

XX DE Human G protein-coupled receptor nGPCR-2310.

XX KW Human; G protein-coupled receptor; nGPCR-x; antiviral; analgesic;
 KW cytotactic; cardiant; antidiabetic; anorectic; hypotensive; hypertensive;
 KW antiparkinsonian; nootropic; neuroprotective; antidepressant;
 KW viral infection; HIV-1; human immunodeficiency virus; HIV-2; pain;
 KW cancer; metabolic disease; cardiovascular disease; type 2 diabetes;
 KW obesity; anorexia; hypotension; hypertension; myocardial infarction;
 KW atherosclerosis; Parkinson's disease; psychosis; neurological disorder;
 KW schizophrenia; migraine; major depression; anxiety; mental disorder;
 KW manic depression; dyskinesia; Huntington's disease; Tourette's Syndrome.

XX OS Homo sapiens.

XX PN WO200166751-A2.

XX PD 13-SEP-2001.

XX PF 08-MAR-2001; 2001WO-US007370.

XX PR 08-MAR-2000; 2000US-0187583P.

XX PR 08-MAR-2000; 2000US-0187584P.

XX PR 08-MAR-2000; 2000US-0187637P.

XX PR 08-MAR-2000; 2000US-0187639P.

XX PR 08-MAR-2000; 2000US-0187640P.

XX PR 08-MAR-2000; 2000US-0187707P.

XX PR 08-MAR-2000; 2000US-0187708P.

XX PR 08-MAR-2000; 2000US-0187709P.

XX PR 08-MAR-2000; 2000US-0187827P.

XX PR 08-MAR-2000; 2000US-0188290P.

XX PR 08-MAR-2000; 2000US-0188292P.

XX PR 08-MAR-2000; 2000US-0188293P.

XX PA (PHAA) PHARMACIA & UPJOHN CO.

XX PI Vogeli G;

PT Isolated nucleic acid molecules encoding G protein-coupled receptors
 PT termed nGPCR-x, useful in the treatment and diagnosis of viral
 PT infections, cancers and mental disorders (e.g. Parkinson's disease and
 PT schizophrenia).

XX Claim 31; Page 269; 292pp; English.

XX The invention relates to novel isolated nucleic acid molecules encoding G
 CC protein-coupled receptors termed nGPCR-x. nGPCR-x polynucleotides,
 CC polypeptides, and modulators may be used in the treatment of diseases and
 CC conditions such as infections, such as viral infections caused by HIV-1
 CC (human immunodeficiency virus) or HIV-2, pain, cancers, metabolic and
 CC cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity,
 CC anorexia, hypotension, hypertension, myocardial infarction,
 CC atherosclerosis), Parkinson's disease, and psychotic and neurological
 CC disorders, including schizophrenia, migraine, major depression, anxiety,
 CC mental disorder, manic depression, and dyskinesias, such as Huntington's
 CC disease or Tourette's Syndrome and many other diseases and syndromes
 CC listed in the specification. nGPCR-x polynucleotides and polypeptides, as
 CC well as nGPCR-x modulators, may also be used in diagnostic assays for
 CC such diseases or conditions. The present sequence represents a G protein-
 CC coupled receptor of the invention

XX SQ Sequence 146 AA;

Query Match 55.6%; Score 5; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
 |||||
 Db 32 DTFYY 36

RESULT 69

AA853696

ID AA853696 standard; protein; 152 AA.

XX AC AA853696;

XX DT 09-MAR-2001 (first entry)

XX DE Human colon cancer antigen protein sequence SEQ ID NO:1236.

XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW identification; cytostatic; cardioactive; neuroprotective; vulnery;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW nephrotropic; antineoplastic; antibacterial; gene therapy; wound;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder.

XX OS Homo sapiens.

XX PN WO200055351-A1.

XX PD 21-SEP-2000.

XX PF 08-MAR-2000; 2000WO-US005883.

XX PR 12-MAR-1999; 99US-0124270P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;

XX DR WPI; 2000-587534/55.

XX DR N-PSDB; AAC98453.

XX PT Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer.

PS Claim 11; Page 1823-1824; 2104pp; English.

CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal, and
 CC vulnary, nephrotropic, antiinfective and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC proteins and antibodies to the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins may
 CC also be used to prevent diseases such as neural disorders, immune system
 CC disorders, muscular disorders, reproductive disorders, gastrointestinal
 CC disorders, wounds, renal disorders, infectious diseases, and
 CC cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
 CC sequences used in the exemplification of the present invention

XX SQ Sequence 152 AA;

Query Match 55.6%; Score 5; DB 3; Length 152;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 |||||
 Db 55 DDTFY 59

RESULT 70

AAE39932

ID AAE39932 standard; protein; 157 AA.

XX AC AAE39932;

XX 15-JAN-2004 (first entry)

DT Corn phosphoethanolamine cytidyltransferase protein.

DE

XX Phosphatidylethanolamine N-methyltransferase; EC 2.1.1.17; transgenic;
 KW enzyme; transgenic plant; phosphoethanolamine cytidyltransferase; corn;
 KW EC 2.7.7.41.

XX Zea mays.

OS

XX US6596926-B1.

PN

XX 22-JUL-2003.

PD

XX 22-SEP-2000; 2000US-00668262.

PF

XX 23-SEP-1999; 99US-0155626P.

PR (DUPO) DU PONT DE NEMOURS & CO E I.

XX

XX Famodu OO, Kinney AJ, Rafalski JA;

PI

XX WPI; 2003-615553/58.

DR

DR N-PSDB; AAD60656.

XX

XX New isolated polynucleotide encoding a phosphatidylethanolamine N-
 PT methyltransferase biosynthetic enzyme, useful for creating transgenic
 PT plants, as probes for genetic mapping or as a genetic marker.

FT

XX Example 3; Col 29-30; 28pp; English.

PS

XX The present invention relates to an isolated polynucleotide encoding a
 CC phosphatidylethanolamine N-methyltransferase (EC 2.1.1.17) biosynthetic
 CC enzyme. The invention is useful in creating transgenic plants in which
 CC the polypeptides are present at higher or lower levels than normal cell
 CC types. The invention is also useful as probes for genetically and
 CC physically mapping the genes. The present sequence is corn phospho-
 CC ethanolamine cytidyltransferase (EC 2.7.7.41) protein from clone cc71se-

CC b.pk0008.g2

XX SQ Sequence 157 AA;

Query Match 55.6%; Score 5; DB 7; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 |||||
 Db 128 KVDDT 132

RESULT 71

ADJ26813

ID ADJ26813 standard; protein; 157 AA.

XX AC ADJ26813;

XX 20-MAY-2004 (first entry)

DT Corn phosphoethanolamine cytidyl transferase protein #1.

DE

XX Phosphatidylcholine biosynthesis; PC; protein synthesis; gene expression;
 KW herbicide; phosphoethanolamine cytidyl transferase; corn; enzyme.

XX Zea mays.

OS

XX US2003177523-A1.

PN

XX 18-SEP-2003.

PD

XX 01-MAY-2003; 2003US-00427442.

PF

XX 23-SEP-1999; 99US-0155626P.

PR 22-SEP-2000; 2000US-00668262.

XX

XX (FAMO/) FAMODU O O.
 PA (KINN/) KINNEY A J.
 PA (RAPA/) RAFALSKI J A.

PI Famodu OO, Kinney AJ, Rafalski JA;

XX

XX WPI; 2003-898656/82.

DR

DR N-PSDB; ADJ26812.

XX

XX New phosphatidylcholine biosynthetic enzyme polypeptide, useful for
 PT studying protein synthesis in plants, for manipulating gene expression or
 PT for providing possible target for herbicides.

FT

XX Claim 10; SEQ ID NO 2; 30pp; English.

PS

XX The present invention relates to novel phosphatidylcholine (PC)
 CC biosynthetic enzymes and polynucleotides encoding such proteins. The
 CC nucleic acid sequences of the invention are useful for studying protein
 CC synthesis in plants, for manipulating gene expression or for providing
 CC possible target for herbicides. The present sequence is corn
 CC phosphoethanolamine cytidyl transferase, a phosphatidylcholine
 CC biosynthetic enzyme of the invention.

XX SQ Sequence 157 AA;

Query Match 55.6%; Score 5; DB 7; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 |||||
 Db 128 KVDDT 132

RESULT 72

ABE70518

ID ABB70518 standard; protein; 159 AA.
XX
AC ABB70518;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 38346.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI: 2001-656860/75.
DR N-PSDB; ABL14621.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 38346; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 159 AA;

Query Match 55.6%; Score 5; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 53 KVDDT 57

RESULT 73
AAW31742
ID AAW31742 standard; protein; 166 AA.
XX
AC AAW31742;
XX
DT 26-MAR-1998 (first entry)
XX
DE Canine obese protein (OB protein) variant lacking Gln28.
XX
KW Canine obese protein; OB protein; body fat reduction; dog; obesity;
KW type II diabetes; elevated blood lipid level; lean body mass;
KW insulin sensitivity; osteoporosis.
XX
OS Synthetic.
OS Canis sp.

XX Key Location/Qualifiers
FH Protein 1..21
FT Protein /label= leader_sequence
FT Protein 22..166
FT Protein /label= mature_peptide
XX
PN WO9732022-A2.
XX
PD 04-SEP-1997.
XX
PF 28-FEB-1997; 97WO-US003209.
XX
PR 01-MAR-1996; 96US-00609408.
XX
PA (AMGE-) AMGEN INC.
XX
PI Hernday N;
XX
DR WPI: 1997-448690/41.
DR N-PSDB; AAT98868.
XX
PT New isolated canine obese (OB) protein and related DNA - used to develop
PT products for treating dogs for e.g. obesity, type II diabetes, elevated
PT blood lipid levels or for increasing lean body mass.
XX
PS Claim 1; Page; 44pp; English.
XX
CC The present sequence represents a canine obese (OB) protein variant which
CC lacks Gln28, with respect to the full length sequence (AAW31741). A
CC variant which possesses a N-terminal Met residue in place of the leader
CC sequence (AAW37096) also exists. The OB protein activity results in a
CC decrease in body fat. The canine OB protein can be used for treating dogs
CC who suffer from, e.g. obesity, type II diabetes, elevated blood lipid
CC levels, or to increase lean body mass. They can also be used for e.g.
CC increasing insulin sensitivity, increasing red blood cells (and
CC oxygenation in the blood) and decreasing bone resorption or osteoporosis.
CC The products can also be used for diagnostic purposes, e.g. for
CC characterising or detecting defects in canine OB genes or gene products.
CC note:- this sequence does not appear in the specification; it was created
CC using information provided
XX
SQ Sequence 166 AA;

Query Match 55.6%; Score 5; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 26 KVDDT 30

RESULT 74
ABB70366
ID ABB70366 standard; protein; 170 AA.
XX
AC ABB70366;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 37890.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.

XX Nucleic acids encoding polypeptides from *Staphylococcus epidermidis*,
PT useful for vaccinating against infections, e.g. endocarditis.
PS Claim 18; Page 665; 2189pp; English.
XX
CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAG81454 to AAG83120, from *Staphylococcus epidermidis*, (I)
CC and (II) can have antibacterial activity and therefore can be used in
CC vaccination. The nucleic acids (I) may be used to produce the S.
CC *epidermidis* polypeptides (II) via the production of vectors containing
CC them which are used to produce host cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. *epidermidis* infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. *epidermidis* genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to AAH55098
CC represent oligonucleotide sequences and primers which are used in the
CC exemplification of the present invention. N.B. The present invention
CC specifically claims all the polynucleotide sequences given in the
CC sequence listing of the present specification, however the sequence
CC listing only goes up to SEQ ID NO:4454 so even though sequences are given
CC in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present
CC for SEQ ID NO:4455 to 4464
XX
SQ Sequence 177 AA;

Query Match 55.6%; Score 5; DB 4; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||
DB 18 KVDDT 22

RESULT 77
ADY11020
ID ADY11020 standard; protein; 182 AA.
XX
AC ADY11020;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polypeptide seqid 66835.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
XX protein content.
XX
OS Unidentified.
XX
XX US2004034888-A1.
FN
PD 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
PR
XX 05-NOV-2001; 2001US-00985678.
XX
XX (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TAB/) TABASKA J E.

PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
XX WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 66835; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 182 AA;

Query Match 55.6%; Score 5; DB 8; Length 182;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||
DB 134 KVDDT 138

RESULT 78
ADY11256
ID ADY11256 standard; protein; 182 AA.
XX
AC ADY11256;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polypeptide seqid 67071.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
XX protein content.
XX
OS Unidentified.
XX
XX US2004034888-A1.
FN
PD 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
PR
XX 05-NOV-2001; 2001US-00985678.
XX

PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAS/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 67071; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034889. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 182 AA;

Query Match 55.6%; Score 5; DB 8; Length 182;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 134 KVDDT 138
|||||

RESULT 79
ABU30050
ID ABU30050 standard; protein; 189 AA.
XX
AC ABU30050;
XX
DT 19-JUN-2003 (first entry)
XX
XX Protein encoded by Prokaryotic essential gene #15577.
XX
DE Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Enterococcus faecium.
XX
PN WO200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
DR N-PSDB; ACA33920.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 57974; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 189 AA;

Query Match 55.6%; Score 5; DB 6; Length 189;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 59 KVDDT 63
|||||

RESULT 80
ADY10671
ID ADY10671 standard; protein; 189 AA.
XX
AC ADY10671;
XX
XX 21-APR-2005 (first entry)
XX
XX Plant full length insert polypeptide seqid 66486.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;

KW Galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 XX protein content.
 XX Unidentified.
 OS US2004034888-A1.
 PN 19-FEB-2004.
 PD 28-APR-2003; 2003US-00425114.
 PF 06-MAY-1999; 99US-00304517.
 XX 05-NOV-2001; 2001US-00985678.
 XX (LIU/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAO/) CAO Y.
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 PI WPI; 2004-180133/17.
 DR New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX Claim 1; SEQ ID NO 66486; 15pp; English.
 XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 XX Sequence 189 AA;
 SQ Query Match 55.6%; Score 5; DB 8; Length 189;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVDDT 5
 DB 141 KVDDT 145
 RESULT 81
 ABG21277
 ID ABG21277 standard; protein; 201 AA.
 XX AC ABG21277;
 XX 18-FEB-2602 (first entry)
 DT Novel human diagnostic protein #21268.
 XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX Homo sapiens.
 OS WO200175067-A2.
 PN 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-US008631.
 PF 31-MAR-2000; 2000US-00540217.
 XX 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 PI WPI; 2001-639362/73.
 DR N-PSDB; AAS85464.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX Claim 20; SEQ ID NO 51636; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: the sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 201 AA;
 SQ Query Match 55.6%; Score 5; DB 4; Length 201;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTF 6
 DB 159 VDDTF 163
 RESULT 82
 ADC94805
 ID ADC94805 standard; protein; 202 AA.
 XX AC ADC94805;
 XX 01-JAN-2004 (first entry)
 DT E. faecium protein sequence SEQ ID 4432.
 DE Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
 KW abdominal-pelvic infection.

XX OS Enterococcus faecium.
 XX PN US6583275-B1.
 XX XX
 XX PD 24-JUN-2003.
 XX PP 30-JUN-1998; 98US-00107532.
 XX PR 02-JUL-1997; 97US-0051571P.
 XX PR 14-MAY-1998; 98US-0085598P.
 XX XX
 XX PA (GENO-) GENOME THERAPEUTICS CORP.
 XX XX
 XX PI Doucette-Stamm LA, Bush D;
 XX XX
 XX DR WPI; 2003-799836/75.
 XX DR N-PSDB; ADC91151.
 XX XX
 XX PT New isolated nucleic acid derived from Enterococcus faecium encoding an
 XX PT Enterococcus faecium polypeptide useful for detection, prevention and
 XX PT treatment of a pathological condition resulting from a bacterial
 XX PT infection.
 XX XX
 XX PS Example 1; SEQ ID NO 4432; 243pp; English.
 XX XX
 XX CC The invention relates to an isolated nucleic acid derived from
 XX CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having
 XX CC one of 10 fully defined sequences given in the (or comprising 40
 XX CC sequential nucleotides chosen from any of the nucleic acids, its
 XX CC complement or sequences hybridising to it). Also included are a
 XX CC recombinant vector comprising the nucleic acid operably linked to
 XX CC transcription regulatory element, a cell comprising the vector and a
 XX CC single-stranded probe comprising the nucleic acid. The nucleic acids are
 XX CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
 XX CC The nucleic acids is useful for diagnosing pathological conditions
 XX CC resulting from E. faecium bacterial infection (e.g. urinary tract
 XX CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
 XX CC infection) and for screening drugs such as agonists and antagonists. The
 XX CC nucleic acid is useful for recombinant production of Candida albicans -
 XX CC derived peptides or antisense polypeptides. Pharmaceutical compositions
 XX CC and vaccines containing the nucleic acid are useful for preventing or
 XX CC treating Enterococcus faecium infections. The present sequence represents
 XX CC one if the disclosed E. faecium proteins.
 XX XX
 XX SQ Sequence 202 AA;
 Query Match 55.6%; Score 5; DB 7; Length 202;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVDVT 5
 Db 72 KVDVT 76
 RESULT 83
 AAB96683
 ID AAB96683 standard; protein; 211 AA.
 XX AC AAB96683;
 XX XX
 XX DT 29-OCT-2001 (first entry)
 XX XX
 XX DE Putative P. abyssi dolichol phosphate mannose synthase related protein.
 XX XX
 XX KW Hyperthermophilic archaeon; hyperthermophilic protein.
 XX XX
 XX OS Pyrococcus abyssi.
 XX XX
 XX PN PR2792651-A1.
 XX XX
 XX PD 27-OCT-2000.

XX XX 21-APR-1999; 99FR-00005034.
 XX XX
 XX PR 21-APR-1999; 99FR-00005034.
 XX XX
 XX PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PA (IFRE-) IFREMER INST FR RECH EXPL MER.
 XX XX
 XX PI Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;
 XX PI Querrellou J, Weissenbach J, Saurin W, Heilig R;
 XX XX
 XX DR WPI; 2001-126236/14.
 XX XX
 XX XX New nucleotide sequences isolated from Pyrococcus abyssi encode proteins
 XX PT useful in industry.
 XX XX
 XX PS Claim 7; Page 1441; 1657pp; French.
 XX XX
 XX CC The present invention relates to the genomic sequence of Pyrococcus
 XX CC abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is
 XX CC a hyperthermophilic archaeon, which is isolated from deep-sea
 XX CC hydrothermal vents. The present sequence is one such P. abyssi protein.
 XX CC The proteins of the present invention have various potential industrial
 XX CC uses, since the proteins are stable at very high temperatures, some up to
 XX CC 110 degrees centigrade. Note: This patent is in the same patent family as
 XX CC WO200065062, which contains additional sequences as shown in AAB99132-
 XX CC AAB99143, AAH75903-AAH75920 and AAG66436
 XX XX
 XX SQ Sequence 211 AA;
 Query Match 55.6%; Score 5; DB 4; Length 211;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVDVT 5
 Db 139 KVDVT 143
 RESULT 84
 AAY29015
 ID AAY29015 standard; protein; 230 AA.
 XX AC AAY29015;
 XX XX
 XX DT 24-SEP-1999 (first entry)
 XX XX
 XX DE T. gondii immunogenic protein.
 XX XX
 XX KW Immunogenic protein; Toxoplasma gondii protein; oocyst shedding; cat;
 XX KW T. gondii infection; enteric apicomplexa oocyst; Cryptosporidium oocyst;
 XX KW Toxoplasma oocyst.
 XX XX
 XX OS Toxoplasma gondii.
 XX XX
 XX PN WO9932633-A1.
 XX XX
 XX PD 01-JUL-1999.
 XX XX
 XX PF 18-DEC-1998; 98WO-US027137.
 XX XX
 XX PR 19-DEC-1997; 97US-00994825.
 XX XX
 XX PA (HESK-) HESKA CORP.
 XX XX
 XX PI Milhausen MJ, Lutz SB, Ng RK;
 XX XX
 XX DR WPI; 1999-418930/35.
 XX DR N-PSDB; AAX91216.
 XX XX
 XX PT New isolated Toxoplasma gondii nucleic acids used, e.g. to treat
 XX PT infection caused by this microorganism.
 XX XX

PS Claim 29; Page 188-189; 381pp; English.

XX The invention provides isolated Toxoplasma gondii nucleic acids that

CC encode immunogenic polypeptides. The T. gondii nucleic acid molecules,

CC immunogenic proteins and antibodies to the proteins can be used to

CC inhibit T. gondii oocyst shedding in a cat due to infection with T.

CC gondii. They can be used for preventing T. gondii infection and for

CC preventing the spread of T. gondii infection. They can also be used for

CC detecting T. gondii infection. The detection method can be used to detect

CC parasite cysts or oocysts in feces, e.g. from enteric apicomplexa oocysts

XX such as Cryptosporidium oocysts and Toxoplasma oocysts

SQ Sequence 230 AA;

Query Match 55.6%; Score 5; DB 2; Length 230;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5

Db 168 KVDDT 172

RESULT 85

AAU25486

ID AAU25486 standard; protein; 230 AA.

XX AAU25486;

XX 17-DEC-2001 (first entry)

XX T. gondii immunogenic protein P4604-54.

XX Immunogenic protein; oocyst; faeces; enteric apicomplexa oocyst;

KW Cryptosporidium oocyst; Toxoplasma oocyst; Giardia cyst; vaccine;

KW oocyte shedding.

XX Toxoplasma gondii.

XX US2001014447-A1.

XX 16-AUG-2001.

XX 18-DEC-1998; 98US-00216393.

XX 19-DEC-1997; 97US-00994825.

XX (MILH/) MILHAUSEN M J.

XX Milhausen MJ;

XX WPI; 2001-529100/58.

DR N-PSDB; AAS42539.

XX Detecting parasite oocysts or cysts in feces, comprises eluting DNA from

PT sample into aqueous solution by heating, amplifying DNA with primers

PT specific for oocysts or cysts being detected, and detecting amplification

PT product.

XX Example 2; Page 67; 188pp; English.

XX The invention relates to detection of parasite oocysts or cysts in a

CC faeces sample comprising contacting the sample with a solid support,

CC drying and then washing the sample with an aqueous wash solution, adding

CC an aqueous elution solution and eluting DNA from the sample by heating

CC and amplifying by PCR oocyst/cyst-specific DNA and detecting the

CC amplification products. The method is useful for detecting parasite

CC oocysts e.g., enteric apicomplexa oocysts such as Cryptosporidium oocysts

CC or Toxoplasma oocysts, or for detecting parasite cysts e.g. Giardia

CC cysts. The method is also useful for developing vaccines to prevent

CC oocyte shedding in cats. The present sequence represents an immunogenic

XX protein from Toxoplasma gondii

SQ Sequence 230 AA;

Query Match 55.6%; Score 5; DB 4; Length 230;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5

Db 168 KVDDT 172

RESULT 86

ADG17081

ID ADG17081 standard; protein; 230 AA.

XX ADG17081;

XX 26-FEB-2004 (first entry)

XX T. gondii protein #15.

XX Toxoplasma gondii; oocyst shedding; genetic vaccine; vaccine.

KW Toxoplasma gondii.

XX US2003194393-A1.

XX 16-OCT-2003.

XX 17-DEC-2002; 2002US-00321856.

XX 19-DEC-1997; 97US-00994825.

PR 18-DEC-1998; 98US-00216393.

XX (MILH/) MILHAUSEN M J.

XX Milhausen MJ;

XX WPI; 2003-899768/82.

DR N-PSDB; ADG17080.

XX Novel immunogenic Toxoplasma gondii proteins useful for inhibiting oocyst

PT shedding by cats infected with Toxoplasma gondii.

XX Claim 6; SEQ ID NO 31; 198pp; English.

XX The invention relates to an isolated Toxoplasma gondii protein. The

CC protein is useful for inhibit oocyst shedding by cats infected with

CC Toxoplasma gondii. The protein is useful for preventing or ameliorating

CC diseases caused by infection with T. gondii. The nucleic acid can be used

CC as genetic vaccine which encodes the protein. The protein and the nucleic

CC acid are used as diagnostic reagents for detection of T. gondii

CC infection. The present sequence is used in the exemplification of the

CC invention.

XX Sequence 230 AA;

Query Match 55.6%; Score 5; DB 7; Length 230;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5

Db 168 KVDDT 172

RESULT 87

AAB25468

ID AAB25468 standard; protein; 235 AA.

XX AAB25468;

XX 27-NOV-2000 (first entry)

XX Pinus radiata cell signalling involved protein SEQ ID NO:787.
 DE
 XX
 KW Bucalyptus grandis; Pinus radiata; Monterey pine; plant; modification;
 KW plant;cell signalling; modulation; transgenic plant; pathogen; growth;
 KW environmental change; development; cell proliferation; differentiation;
 KW elongation; survival; disease resistance; nutrient metabolism.
 XX
 OS Pinus radiata.
 XX
 PN WO200042171-A1.
 XX
 PD 20-JUL-2000.
 XX
 PP 11-JAN-2000; 2000WO-US000724.
 XX
 PR 12-JAN-1999; 99US-00228986.
 PR 01-NOV-1999; 99US-0162866P.
 XX
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 XX
 PI Strabala TJ, Nieuwenhuizen NJ;
 XX
 DR WPI; 2000-476052/41.
 XX
 PT Isolated polynucleotide encoding a polypeptide involved in cell signaling
 PT used for generating transgenic plants with modified responses to external
 PT signals.
 XX
 PS Claim 3; Page 364; 527pp; English.
 XX
 CC AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide
 CC and protein sequences isolated from eucalyptus (Eucalyptus grandis) or
 CC pine (Pinus radiata also known as Monterey pine). The protein sequences
 CC are involved in cell signalling. The polynucleotide and protein sequences
 CC can be used to modify the response of plant cells to external signals
 CC e.g. environmental changes or pathogens during the growth and development
 CC of a plant. They can be used to modify cell proliferation,
 CC differentiation, elongation and survival, resistance to disease and
 CC nutrient metabolism. Examples of modifications which can be produced are
 CC altered fruit ripening and senescence of leaves and flowers e.g. to delay
 CC senescence and prolong the life of cut flowers or enhance senescence of
 CC reproductive organs to engineer sterile plants. Other modifications can
 CC be used to delay senescence in selected cell types or organs providing
 CC fruit and vegetables which have a longer shelf life between harvest and
 CC consumption, or to decrease branching frequency in forest tree species
 CC giving long stretches of valuable knot-free clear wood which can be used
 CC in solid timber furniture and veneers
 XX
 SQ Sequence 235 AA;
 Query Match 55.6%; Score 5; DB 3; Length 235;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 DDTFFY 7
 DB 117 DDTFFY 121
 RESULT 88
 ADQ66091
 ID ADQ66091 standard; protein; 238 AA.
 AC
 XX
 AC ADQ66091;
 XX
 XX 07-OCT-2004 (first entry)
 DT
 XX
 DE Novel human protein sequence #1064.
 KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
 KW gene therapy; diagnostic marker; morbid state; osteoporosis;
 KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;

KW cancer.
 XX
 OS Homo sapiens.
 XX
 PN EP1440981-A2.
 XX
 PD 28-JUL-2004.
 XX
 PP 21-JAN-2004; 2004EP-00001196.
 XX
 PR 21-JAN-2003; 2003JP-00102206.
 PR 03-MAY-2003; 2003JP-00131392.
 XX
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Nagai K, Irie R;
 XX
 DR WPI; 2004-535376/52.
 DR N-PSDB; ADQ63903.
 XX
 PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 XX
 PS Claim 1; SEQ ID NO 3252; 2449pp; English.
 XX
 CC The invention relates to 2495 novel polynucleotides (I) and their encoded
 CC polypeptides, sequences hybridizing to these nucleotides, sequences
 CC encoding partial polypeptides and sequences having 70% or 90% identity to
 CC the nucleotide and protein sequences. The nucleotides and polypeptides
 CC are useful as diagnostic markers or therapeutic target for the diseases
 CC or morbid states. They are also useful for treating osteoporosis,
 CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
 CC dementia and various cancers. This sequence corresponds to a protein
 CC sequence of the invention.
 XX
 SQ Sequence 238 AA;
 Query Match 55.6%; Score 5; DB 8; Length 238;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTF 6
 DB 43 VDDTF 47
 RESULT 89
 ADY64614
 ID ADY64614 standard; protein; 238 AA.
 XX
 AC ADY64614;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE S. mansoni protein SEQ ID 32.
 XX
 KW Schistosomacide; schistosomiasis; psychiatric disorder; vaccine;
 KW diagnosis.
 XX
 OS Schistosoma mansoni.
 XX
 PN WO2005023979-A2.
 XX
 PD 17-MAR-2005.
 XX
 PP 10-SEP-2004; 2004WO-BR000170.
 XX
 PR 11-SEP-2003; 2003US-0502277P.
 XX
 PA (AMPA-) FUNDACAO AMPARO A PESQUISA DO ESTADO.
 XX
 PI Verjovski-Almeida S, Leite LCC, Farias LP, Miyasato PA, Kawano T;

PI Demarco R, Garcia JCL, Martins EAL, Ho PL, Nascimento ALTO;
 PI Dias-Neto E, Setubal JC, Menck CFM, Madeira AMEN, Rodrigues V;
 PI Gargioni C;
 XX WPI; 2005-223357/23.
 XX
 XX New isolated nucleic acid molecule encoding a Schistosoma mansoni
 PT protein, useful for as a vaccine or for preventing, diagnosing, or
 PT treating Schistosoma mansoni infection.
 PT
 PS Disclosure; SEQ ID NO 32; 52pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule encoding a
 CC Schistosoma mansoni protein, or its portion which is at least 20 amino
 CC acids in length. Also included are an expression vector comprising the
 CC nucleic acid operably linked to a promoter, a recombinant cell
 CC transformed/transfected with the nucleic acid (or expression vector), an
 CC immunogenic composition comprising the nucleic acid in combination with a
 CC pharmaceutical adjuvant or carrier, an isolated S. mansoni protein
 CC comprising an amino acid sequence encoded by the nucleic acid, an
 CC immunogenic composition comprising the isolated S. mansoni protein, an
 CC isolated antibody which specifically binds to the isolated S. mansoni
 CC protein, a hybridoma cell line which produces the isolated antibody, a
 CC method for determining a S. mansoni infection in a subject and a computer
 CC readable medium having recorded in it a nucleic acid molecule from S.
 CC mansoni genome. The nucleic acid molecule is useful for preventing,
 CC diagnosing, or treating S. mansoni infection (schistosomiasis). It can
 CC also be used as vaccine against S. mansoni. The present sequence is a
 CC Schistosoma mansoni protein of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences. Also, SEQ ID 2141-2152 are
 CC mentioned in the specification but are not included in the sequence
 CC listing.
 XX
 SQ Sequence 238 AA;
 Query Match 55.6%; Score 5; DB 9; Length 238;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVDDT 5
 Db 3 KVDDT 7
 RESULT 90
 ADX70680
 ID ADX70680 standard; protein; 240 AA.
 XX
 AC ADX70680;
 XX
 XX 21-APR-2005 (first entry)
 DT
 DE Plant full length insert polypeptide seqid 40046.
 XX
 KW plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 XX
 OS Unidentified.
 XX
 XX US2004034888-A1.
 PN
 XX 19-FEB-2004.
 PD
 XX 28-APR-2003; 2003US-00425114.
 PF
 XX

PR 06-MAY-1999; 99US-00304517.
 PR 05-NOV-2001; 2001US-00985678.
 XX
 PA (LIUU/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX WPI; 2004-180133/17.
 DR
 XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 PS Claim 1; SEQ ID NO 40046; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 XX
 SQ Sequence 240 AA;
 Query Match 55.6%; Score 5; DB 8; Length 240;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTF 6
 Db 130 VDDTF 194
 RESULT 91
 AAG28321
 ID AAG28321 standard; protein; 244 AA.
 XX
 AC AAG28321;
 XX
 XX 17-OCT-2000 (first entry)
 DT
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 33494.
 DE
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW protein identification; signal transduction pathway; gene expression control; promoter;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.
 XX
 XX EP1033405-A2.
 PN
 XX 06-SEP-2000.
 PD
 XX 25-FEB-2000; 2000EP-00301439.
 PF
 XX

PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 18-MAY-1999; 99US-0134370P.
PR 19-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140823P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142820P.
PR 12-JUL-1999; 99US-0142877P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 21-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 22-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.

```

PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 26-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 55.6%; Score 5; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
DB 202 DTFYY 206

RESULT 92
ADS22321
ID ADS22321 standard; protein; 245 AA.
AC ADS22321;
XX
DT
XX
XX 02-DEC-2004 (first entry)
DE Bacterial polypeptide #11354.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.

(PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 11354; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plant properties.
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition, improved lignin production or improved galactomannan
XX production. This sequence represents a bacterial polypeptide used in the
XX scope of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 245 AA;
Query Match 55.6%; Score 5; DB 8; Length 245;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
DB 158 DDTFY 162

RESULT 93
ADM20093
ID ADM20093 standard; protein; 254 AA.
XX
XX ADM20093;
XX
XX 20-MAY-2004 (first entry)
XX
XX Protein encoded by novel human channel/transporter gene #165 clone 2.
XX
XX immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
XX cyostatic; cardiant; vasotropic; cerebroprotective; neurotropic;
XX neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
XX gene therapy; channel/transporter protein; rheumatoid arthritis;
XX neoplasm; cardiac arrest; cerebrovascular disorder; cerebral ischemia;
XX angiogenesis; nervous system disorder; Alzheimer's disease;
XX ocular disorder; corneal infection; wound healing;
XX epithelial cell proliferation; skin aging; sunburn; transplantation;
XX chemotaxis; food additive.
XX
OS Homo sapiens.
XX

```

PN WO200154472-A2.
XX 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US001307.
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.

PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239355P.
PR 13-OCT-2000; 2000US-0239377P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-02559678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI

XX WPI; 2001-476159/51.
 DR N-PSDB; ADM19614.
 PT Isolated nucleic acid molecule encoding a channel/transporter protein is
 XX used in preventing, treating or ameliorating a medical condition.
 PS Claim 11; SEQ ID NO 900; 809pp; English.
 CC The invention relates to an isolated nucleic acid molecule encoding a
 CC channel/transporter protein or sequences at least 95% identical to a
 CC these. The nucleic acids and proteins encoded by them are used to
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
 CC in diagnosing a pathological condition or susceptibility to a
 CC pathological condition. The antibodies to the proteins can also be used
 CC in alleviating symptoms associated with the disorders and in diagnostic
 CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays
 CC (ELISA). Disorders which are diagnosed or treated include autoimmune
 CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
 CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
 CC arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis,
 CC nervous system disorders e.g. Alzheimer's disease, infections caused by
 CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection.
 CC The polypeptides can also be used to aid wound healing and epithelial
 CC cell proliferation, to prevent skin aging due to sunburn, to maintain
 CC organs before transplantation, for supporting cell culture of primary
 CC tissues, to regenerate tissues and in chemotaxis. The polypeptides can
 CC also be used as a food additive or preservative to increase or decrease
 CC storage capabilities. This sequence corresponds to a protein of the
 CC invention.
 XX Sequence 254 AA;
 SQ

Query Match 55.6%; Score 5; DB 4; Length 254;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 Db 117 VDDTF 121
 |||||

RESULT 94
 AAE37328
 ID AAE37328 standard; protein; 254 AA.
 XX AAE37328;
 AC
 XX
 XX 27-AUG-2003 (first entry)
 DT Human VLCFABE MOOSE00006 protein from ctg12729.
 DE
 XX Human; very long chain fatty acid biosynthesis enzyme; VLCFA; VLCFABE;
 KW non-insulin dependent diabetes mellitus; NIDDM; adrenoleukodystrophy;
 KW ALD; autosomal dominant macular dystrophy; adMD; Alzheimer's disease;
 KW coronary heart disease; stroke; myocardial infarction; gene therapy.
 XX Homo sapiens.
 OS
 XX WO2003040392-A2.
 PN
 XX 15-MAY-2003.
 PD
 XX 04-NOV-2002; 2002WO-IB004610.
 PF
 XX 06-NOV-2001; 2001US-0332864P.
 PR
 XX (DECO-) DECODE GENETICS EHF.
 PA
 XX Betts M, Sigurdsson GT;
 PI
 XX WPI; 2003-430674/40.
 DR

DR N-PSDB; AAD56495.
 XX
 PT New isolated nucleic acid molecule comprising a very long chain fatty
 PT acid biosynthesis enzyme nucleic acid, useful for treating a disease
 PT associated with the biosynthesis enzyme nucleic acid.
 XX
 PS Claim 10; Page 87; 90pp; English.
 XX
 CC The invention relates to very long chain fatty acid (VLCFA) biosynthesis
 CC enzymes (VLCFABE) and polynucleotides encoding such proteins. Sequences
 CC of the invention are useful for treating VLCFABE diseases such as non-
 CC insulin dependent diabetes mellitus (NIDDM), adrenoleukodystrophy (ALD),
 CC autosomal dominant macular dystrophy (adMD), Alzheimer's disease and
 CC coronary heart diseases such as stroke and myocardial infarction. They
 CC are also used in gene therapy. The present sequence is human VLCFABE
 CC protein
 XX Sequence 254 AA;
 SQ

Query Match 55.6%; Score 5; DB 6; Length 254;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
 Db 201 DTFYY 205
 |||||

RESULT 95
 ADX74695
 ID ADX74695 standard; protein; 254 AA.
 XX ADX74695;
 AC
 XX 21-APR-2005 (first entry)
 DT Plant full length insert polypeptide seqid 44061.
 DE
 XX plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 XX Unidentified.
 OS
 XX US2004034888-A1.
 PN
 XX 19-FEB-2004.
 PD
 XX 28-APR-2003; 2003US-00425114.
 PF
 XX 06-MAY-1999; 99US-00304517.
 PR
 XX 05-NOV-2001; 2001US-00985678.
 XX (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABAS/) TABASKA J E.
 PA (CAOY/) CAO Y.
 XX
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 PI WPI; 2004-180133/17.
 DR
 XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.

XX Claim 1; SEQ ID NO 44061; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a

CC polynucleotide consisting of a sequence encoding an amino acid sequence

CC available in electronic form from the US patent office at

CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide

CC of the invention are also useful in physical arrays of molecules and as

CC plant breeding markers. The recombinant DNA construct is useful for

CC improving plant tolerance to cold, heat, drought, herbicides, extreme

CC osmotic conditions, pathogens or pests, for manipulating growth rate in

CC plant cells by modification of the cell cycle pathway, for conferring

CC increased resistance to plant disease, for producing galactomannan,

CC lignin or plant growth regulators, for increasing the rate of homologous

CC recombination in plants, for improving yield by modification of

CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

CC or by providing improved plant growth and development under at least one

CC stress condition or for modifying seed oil or protein yield and/or

CC content. This is the amino acid sequence of a plant full length insert

CC polypeptide that can be used in the recombinant DNA construct of the

CC invention.

XX SQ Sequence 254 AA;

Query Match 55.6%; Score 5; DB 8; Length 254;

Best Local Similarity 100.0%; Pred. No. 4.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVDDT 5

Db 99 KVVDDT 103

RESULT 96

AEA24176

ID AEA24176 standard; protein; 259 AA.

XX AEA24176;

XX 11-AUG-2005 (first entry)

XX Anti-HAAH single-chain Fv antibody fragment #6.

XX Antibody therapy; aspartyl (asparaginy) beta-hydroxylase; AAH; HAAH;

KW cancer; neoplasm; lung tumor; liver tumor; colon tumor; pancreas tumor;

KW prostate tumor; ovary tumor; brain tumor; breast tumor; cytostatic;

KW antibody; Fv.

XX Homo sapiens.

OS

XX WO2005049802-A2.

FN

XX 02-JUN-2005.

XX 15-NOV-2004; 2004WO-US038197.

XX 14-NOV-2003; 2003US-0520114P.

PR 19-APR-2004; 2004US-0563514P.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX Wittrup DK, Yeung YA;

PI WPI; 2005-417728/42.

XX New composition comprising anti-hydroxylase antibodies, useful for

PT diagnosing or treating cancer, e.g. lung, liver, colon, pancreas,

PT prostate, ovary, bile duct, brain, or breast cancer.

XX Claim 10; SEQ ID NO 36; 107pp; English.

XX The invention relates to a composition comprising an isolated human

CC antibody or its fragment or other variant, where the antibody, the

CC fragment or the other variant specifically binds to an aspartyl

CC (asparaginy) beta-hydroxylase (AAH). The invention also relates to an

CC isolated nucleic acid molecule comprising a sequence encoding a human

CC antibody or its fragment or other variant, where the antibody, the

CC fragment or the other variant specifically binds to human AAH (HAAH), an

CC expression vector comprising the nucleic acid molecule, a host cell

CC comprising the expression vector, a method of modulating an AAH activity

CC in a cell, a method of treating a patient who has a cancer associated

CC with overactive or over expressed AAH, a method for identifying an

CC antibody or its fragment or other variant that specifically binds to an

CC AAH and a method of making a human monoclonal antibody or its fragment or

CC other variant that specifically binds to an AAH. The composition,

CC antibody, nucleic acid, kit and methods are useful for diagnosing or

CC treating cancer, where the cancer cell is a tumor cell of the lung,

CC liver, colon, pancreas, prostate, ovary, bile duct, brain or breast. This

CC sequence represents an anti-HAAH single-chain Fv antibody fragment used

CC in the scope of the invention.

XX SQ Sequence 259 AA;

Query Match 55.6%; Score 5; DB 9; Length 259;

Best Local Similarity 100.0%; Pred. No. 4.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVDDT 5

Db 87 KVVDDT 91

RESULT 97

ADJ11794

ID ADJ11794 standard; protein; 266 AA.

XX ADJ11794;

XX 20-MAY-2004 (first entry)

XX Rice protein modulated by post-transcriptional gene silencing SeqID 430.

DE rice; post-transcriptional gene silencing; PTGS; plant; trans-activation;

KW cereal; plant-viral interaction.

KW

XX Oryza sp.

OS

XX US2003135888-A1.

PN

XX 17-JUL-2003.

PD

XX 26-SEP-2002; 2002US-00259165.

PF

XX 26-SEP-2001; 2001US-0325277P.

PR 27-NAR-2002; 2002US-0368327P.

PR 04-APR-2002; 2002US-0370620P.

XX (ZHUT/) ZHU T.

PA (WANG/) WANG X.

PA (CHAN/) CHANG H.

PA (BRIG/) BRIGGS S P.

PA (COOP/) COOPER B.

PA (GLAZ/) GLAZEBROOK J.

PA (GOFF/) GOFF S A.

PA (KATA/) KATAGIRI F.

PA (KREP/) KREPS J.

PA (MOUG/) MOUGHAMER T.

PA (PROV/) PROVART N.

PA (RICK/) RICHE D.

XX Zhu T, Wang X, Chang H, Briggs SP, Cooper B, Glazebrook J;

PI Goff SA, Katagiri F, Kreps J, Moughamer T, Provart N, Ricke D;

PI WPI; 2003-829655/77.

DR N-PSDB; ADJ11793.

XX

PT New polynucleotide, useful for modulating gene expression within a cell
 PT by posttranscriptional gene silencing.
 XX
 PS Disclosure; SEQ ID NO 430; 79pp; English.
 XX
 CC This invention relates to a novel method for identifying isolated
 CC polynucleotides that are modulated by post-transcriptional gene silencing
 CC (PTGS). Specifically, it refers to the regulation of gene expression in
 CC plants via PTGS and the trans-activation of homologous genes due to
 CC increased RNA degradation. The present invention describes clusters of
 CC polynucleotides from cereals, in particular rice, as well as homologues
 CC and the polypeptide sequences derived thereof, where gene expression is
 CC altered in response to PTGS. As such, the elucidation of gene silencing
 CC mechanisms can lead to more efficiently expressed transgenes, and can
 CC also improve the understanding of plant-viral interactions and targeting
 CC the suppression of specific plant genes. This polypeptide sequence is a
 CC rice protein sequence that is modulated by gene silencing, given in an
 CC exemplification of the invention. NOTE: This sequence does not appear in
 CC the printed specification but has been obtained in electronic format from
 CC the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID=20030135888.
 XX
 SQ Sequence 266 AA;

Query Match 55.6%; Score 5; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 89 KVDDT 93
 |||||

RESULT 98
 ADJ11440
 ID ADJ11440 standard; protein; 266 AA.
 XX
 AC ADJ11440;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Rice protein modulated by post-transcriptional gene silencing SeqID 76.
 KW rice; post-transcriptional gene silencing; PTGS; plant; trans-activation;
 KW cereal; plant-viral interaction.
 XX
 OS Oryza sp.
 XX
 PN US2003135888-A1.
 XX
 XX 17-JUL-2003.
 PD
 XX
 PF 26-SEP-2002; 2002US-00259165.
 XX
 PR 26-SEP-2001; 2001US-0325277P.
 PR 27-MAR-2002; 2002US-0368327P.
 PR 04-APR-2002; 2002US-0370620P.
 XX
 XX (ZHUT/) ZHU T.
 PA (WANG/) WANG X.
 PA (CHAN/) CHANG H.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZEBROOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (MOUG/) MOUGHAMER T.
 PA (PROV/) PROVART N.
 PA (RICK/) RICKE D.
 XX
 XX Zhu T, Wang X, Chang H, Briggs SP, Cooper B, Glazebrook J;
 PI Goff SA, Katagiri F, Kreps J, Moughamer T, Provart N, Ricke D;

XX
 DR WPI; 2003-829655/77.
 DR N-PSDB; ADJ11439.
 XX
 PT New polynucleotide, useful for modulating gene expression within a cell
 PT by posttranscriptional gene silencing.
 XX
 PS Claim 7; SEQ ID NO 76; 79pp; English.
 XX
 CC This invention relates to a novel method for identifying isolated
 CC polynucleotides that are modulated by post-transcriptional gene silencing
 CC (PTGS). Specifically, it refers to the regulation of gene expression in
 CC plants via PTGS and the trans-activation of homologous genes due to
 CC increased RNA degradation. The present invention describes clusters of
 CC polynucleotides from cereals, in particular rice, as well as homologues
 CC and the polypeptide sequences derived thereof, where gene expression is
 CC altered in response to PTGS. As such, the elucidation of gene silencing
 CC mechanisms can lead to more efficiently expressed transgenes, and can
 CC also improve the understanding of plant-viral interactions and targeting
 CC the suppression of specific plant genes. This polypeptide sequence is a
 CC rice protein sequence that is modulated by gene silencing, given in an
 CC exemplification of the invention. NOTE: This sequence does not appear in
 CC the printed specification but has been obtained in electronic format from
 CC the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID=20030135888.
 XX
 SQ Sequence 266 AA;

Query Match 55.6%; Score 5; DB 7; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 89 KVDDT 93
 |||||

RESULT 99
 ABM88716
 ID ABM88716 standard; protein; 278 AA.
 XX
 AC ABM88716;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Rice abiotic stress responsive polypeptide SEQ ID NO:6962.
 XX
 KW Rice abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
 XX
 OS Oryza sativa.
 XX
 PN WO2003008540-A2.
 XX
 XX 30-JAN-2003.
 PD
 XX
 PF 21-JUN-2002; 2002WO-US019668.
 XX
 PR 22-JUN-2001; 2001US-0300112P.
 PR 24-AUG-2001; 2001US-0314662P.
 PR 26-SEP-2001; 2001US-0325277P.
 PR 21-NOV-2001; 2001US-0332132P.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 XX Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
 PI Moughamer T, Provart N, Ricke D, Zhu T;
 XX
 DR WPI; 2003-248011/24.
 XX
 XX New stress-responsive nucleic acid, useful for altering the
 PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
 PT stress, salt stress or osmotic stress.
 XX

PS Claim 1; SEQ ID NO 6962; 89pp; English.

CC The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, osmotic stress or any of their combinations. The present sequence is used in the exemplification of the invention

CC Sequence 278 AA;

Query Match 55.6%; Score 5; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
|||||

Db 239 VDDTF 243

RESULT 100

ABU43599

ID ABU43599 standard; protein; 280 AA.

XX AC ABU43599;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #29126.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Staphylococcus haemolyticus.

XX PN W0200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362659P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX PR WPI; 2003-029926/02.

XX DR N-PSDB; ACA47465.

XX ST New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 71523; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway; (8) required for proliferation, or that inhibits cellular proliferation; (9) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

CC Sequence 280 AA;

Query Match 55.6%; Score 5; DB 6; Length 280;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
|||||

Db 174 KVDDT 178

RESULT 101

ABO82245

ID ABO82245 standard; protein; 285 AA.

XX AC ABO82245;

XX DT 29-JUL-2004 (first entry)

XX DE Pseudomonas aeruginosa polypeptide #14420.

XX KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX OS Pseudomonas aeruginosa.

XX PN US6551795-B1.

XX PD 22-APR-2003.

XX PF 18-FEB-1999; 99US-00252991.

XX PR 18-FEB-1998; 98US-0074788P.

XX PR 27-JUL-1998; 98US-0094190P.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX DR WPI; 2003-615309/58.

XX DR N-PSDB; ABD15816.

XX ST Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.

PS Disclosure; SEQ ID NO 30991; 455pp; English.

XX The invention relates to *Pseudomonas aeruginosa* polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-*P. aeruginosa* drugs, as templates for recombinant
 CC production of *P. aeruginosa*-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of *P. aeruginosa*-caused
 CC infection, and in detection of *P. aeruginosa* sequences or other sequences
 CC of *Pseudomonas* species using biochip technology. Sequences ABO67826-
 CC ABO84396 represent *P. aeruginosa* polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 XX Sequence 285 AA;

Query Match 55.6%; Score 5; DB 7; Length 285;
 Best Local Similarity 100.0%; Pred. No. 5e+02; 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

QY 1 KVVDDT 5
 |||||
 Db 196 KVVDDT 200

RESULT 102
 ADR46377
 ID ADR46377 standard; protein; 297 AA.

XX ADR46377;

DT 04-NOV-2004 (first entry)

DE Human EndoG protein.

KW cytototoxic; immunotoxin; cancer; mitochondrial malate dehydrogenase;
 KW enzyme; human; MDH; EndoG.

OS Homo sapiens.

PN WO2004070012-A2.

PD 19-AUG-2004.

PF 02-FEB-2004; 2004WO-US002974.

PR 02-FEB-2003; 2003US-00444191.

PR 03-FEB-2003; 2003US-0444191P.

PR 08-APR-2003; 2003US-0460855P.

XX (PALO-) PALO ALTO INST MOLECULAR MEDICINE.

XX Wright SC, Larrick JW, Nock SR, Wilson DS;

XX WPI; 2004-604434/58.

DR N-PSDB; ADR46378.

XX New compositions comprising proteins and encoding nucleic acids having a
 PT DNA nuclease or cell killing activity and are operably linked to cancer
 PT cell binding antibodies or growth factors, useful for treating cancer.

PS Claim 6; SEQ ID NO 24; 225pp; English.

XX The present invention relates to a composition comprising an isolated
 CC amino acid sequence that comprises a portion of human mitochondrial
 CC malate dehydrogenase protein (MDH), particularly the minimum activator of
 CC DNA fragmentation and activator of DNA fragmentation sequences. The
 CC composition is useful for treating cancer chosen from liver cancer,
 CC gastric cancer, head cancer, neck cancer, lung cancer, breast cancer,

CC prostate cancer, cervical cancer, pancreatic cancer, colon cancer,
 CC ovarian cancer, stomach cancer, oesophagus cancer, mouth cancer, tongue
 CC cancer, gum cancer, skin cancer, muscle cancer, heart cancer, bronchial
 CC cancer, cartilage cancer, bone cancer, testis cancer, kidney cancer,
 CC endometrium cancer, uterus cancer, bladder cancer, bone marrow cancer,
 CC lymphoma cancer, spleen cancer, thymus cancer, thyroid cancer, brain
 CC cancer, neuron cancer, gall bladder cancer, ocular cancer, joint cancer,
 CC glioblastoma, mesothelioma, lymphoma, leukaemia, melanoma, squamous cell
 CC carcinoma, osteosarcoma, and Kaposi's sarcoma. The present sequence is a
 CC protein shown in the exemplification of the invention.

XX Sequence 297 AA;

Query Match 55.6%; Score 5; DB 8; Length 297;

Best Local Similarity 100.0%; Pred. No. 5.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 |||||
 Db 156 DDTFY 160

RESULT 103
 ABM81069
 ID ABM81069 standard; protein; 297 AA.

XX ABM81069;

DT 18-NOV-2004 (first entry)

DE Tumour-associated antigenic target (TAT) polypeptide PRO70290, SEQ:2762.

KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 KW gene therapy; cytostatic.

XX Homo sapiens.

PN WO2004030615-A2.

PD 15-APR-2004.

PF 29-SEP-2003; 2003WO-US028547.

PR 02-OCT-2002; 2002US-0414971P.

PA (GETH) GENENTECH INC.

XX Wu TD, Zhang Z, Zhou Y;

XX WPI; 2004-347921/32.

DR N-PSDB; ACN38936.

XX New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.

XX Claim 12; SEQ ID NO 2762; 7273pp; English.

XX The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a

CC flow, increasing plant tolerance to cold or heat, improving plant
CC tolerance to extreme osmotic and drought conditions, and improving plant
CC tolerance to plant pests or pathogens. They can also be used in physical
CC arrays of molecules, plant breeding markers, computer-based storage and
CC analysis systems. The present sequence is one of the 5544 plant protein
CC sequences of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20040216190.
XX
XX SQ Sequence 300 AA;

Query Match 55.6%; Score 5; DB 8; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 142 KVDDT 146

RESULT 106
ADA35398
ID ADA35398 standard; protein; 301 AA.
XX
AC ADA35398;
XX
DT 20-NOV-2003 (first entry)
XX
DE Acinetobacter baumannii protein #2559.
XX
KW Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
KW plant biocontrol agent.
XX
OS Acinetobacter baumannii.
XX
PN US6562958-B1.
XX
PD 13-MAY-2003.
XX
PF 04-JUN-1999; 99US-00328352.
XX
PR 09-JUN-1998; 98US-0088701P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton G, Bush D;
XX
DR WPI; 2003-576092/54.
DR N-PSDB; ADA31272.
XX
PT New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
PT for diagnosing a bacterial disease, as components of antibacterial
PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for
PT plants.
XX
PS Example; SEQ ID NO 6685; 328pp; English.
XX
CC The invention relates to isolated Acinetobacter baumannii nucleic acids.
CC The A. baumannii nucleic acids and polypeptides are useful as reagents
CC for diagnosing a bacterial disease, as components of antibacterial
CC vaccines, as targets for antibacterial drugs, to detect the presence of
CC A. baumannii and other Acinetobacter species in a sample, in screening
CC compounds for the ability to interfere with the A. baumannii life cycle
CC or to inhibit A. baumannii infection, and as biocontrol agents for
CC plants. The present sequence represents the amino acid sequence of an A.
CC baumannii protein.
XX
XX SQ Sequence 301 AA;

Query Match 55.6%; Score 5; DB 6; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 215 KVDDT 219

RESULT 107
AAG20740
ID AAG20740 standard; protein; 302 AA.
XX
AC AAG20740;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23044.

Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.

PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142300P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 20-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145132P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0146389P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.

PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151085P.
PR 27-AUG-1999; 99US-0151066P.
PR 30-AUG-1999; 99US-0151080P.
PR 31-AUG-1999; 99US-0151303P.
PR 01-SEP-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154019P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 13-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 55.6%; Score 5; DB 3; Length 302;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDOT 5
Db 151 KVDOT 155

RESULT 108

ADN21573
ID ADN21573 standard; protein; 306 AA.
AC ADN21573;
XX
XX 02-DEC-2004 (first entry)
XX Bacterial polypeptide #4226.
DE
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
XX Bacteria.
OS
XX US2003233675-A1.
PN
XX 18-DEC-2003.
PD
XX 20-FEB-2003; 2003US-00369493.
PF
XX 21-FEB-2002; 2002US-0360039P.
PR
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 4226; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 306 AA;

Query Match 55.6%; Score 5; DB 8; Length 306;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
Db 153 DDTFY 157

RESULT 109
AAG51074
ID AAG51074 standard; protein; 307 AA.
XX
AC AAG51074;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64786.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 18-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135533P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.

PR 17-JUN-1999; 99US-01139492P.
PR 18-JUN-1999; 99US-01139454P.
PR 18-JUN-1999; 99US-01139455P.
PR 18-JUN-1999; 99US-01139456P.
PR 18-JUN-1999; 99US-01139457P.
PR 18-JUN-1999; 99US-01139458P.
PR 18-JUN-1999; 99US-01139459P.
PR 18-JUN-1999; 99US-01139460P.
PR 18-JUN-1999; 99US-01139461P.
PR 18-JUN-1999; 99US-01139462P.
PR 18-JUN-1999; 99US-01139463P.
PR 18-JUN-1999; 99US-01139750P.
PR 18-JUN-1999; 99US-01139763P.
PR 21-JUN-1999; 99US-01139817P.
PR 22-JUN-1999; 99US-01139899P.
PR 23-JUN-1999; 99US-01140353P.
PR 23-JUN-1999; 99US-01140354P.
PR 24-JUN-1999; 99US-01140695P.
PR 28-JUN-1999; 99US-01140823P.
PR 29-JUN-1999; 99US-01140911P.
PR 30-JUN-1999; 99US-01141287P.
PR 01-JUL-1999; 99US-01141842P.
PR 01-JUL-1999; 99US-01142154P.
PR 02-JUL-1999; 99US-01142055P.
PR 06-JUL-1999; 99US-01142330P.
PR 08-JUL-1999; 99US-01142803P.
PR 09-JUL-1999; 99US-01142920P.
PR 12-JUL-1999; 99US-01142977P.
PR 13-JUL-1999; 99US-01143542P.
PR 14-JUL-1999; 99US-01143624P.
PR 15-JUL-1999; 99US-01144005P.
PR 16-JUL-1999; 99US-01144085P.
PR 16-JUL-1999; 99US-01144086P.
PR 19-JUL-1999; 99US-01144325P.
PR 19-JUL-1999; 99US-01144331P.
PR 19-JUL-1999; 99US-01144332P.
PR 19-JUL-1999; 99US-01144333P.
PR 19-JUL-1999; 99US-01144334P.
PR 19-JUL-1999; 99US-01144335P.
PR 20-JUL-1999; 99US-01144332P.
PR 20-JUL-1999; 99US-01144632P.
PR 20-JUL-1999; 99US-01144884P.
PR 21-JUL-1999; 99US-01144814P.
PR 21-JUL-1999; 99US-01145086P.
PR 21-JUL-1999; 99US-01145088P.
PR 22-JUL-1999; 99US-01145085P.
PR 22-JUL-1999; 99US-01145087P.
PR 22-JUL-1999; 99US-01145089P.
PR 22-JUL-1999; 99US-01145192P.
PR 23-JUL-1999; 99US-01145145P.
PR 23-JUL-1999; 99US-01145218P.
PR 23-JUL-1999; 99US-01145224P.
PR 26-JUL-1999; 99US-01145276P.
PR 27-JUL-1999; 99US-01145913P.
PR 27-JUL-1999; 99US-01145918P.
PR 27-JUL-1999; 99US-01145919P.
PR 28-JUL-1999; 99US-01145951P.
PR 02-AUG-1999; 99US-01146386P.
PR 02-AUG-1999; 99US-01146388P.
PR 02-AUG-1999; 99US-01146389P.
PR 03-AUG-1999; 99US-01147038P.
PR 04-AUG-1999; 99US-01147204P.
PR 04-AUG-1999; 99US-01147302P.
PR 05-AUG-1999; 99US-01147192P.
PR 05-AUG-1999; 99US-01147260P.
PR 06-AUG-1999; 99US-01147103P.
PR 06-AUG-1999; 99US-01147416P.
PR 09-AUG-1999; 99US-01147493P.
PR 09-AUG-1999; 99US-01147935P.
PR 10-AUG-1999; 99US-01148171P.
PR 11-AUG-1999; 99US-01148319P.
PR 12-AUG-1999; 99US-01148341P.
PR 13-AUG-1999; 99US-01148565P.

PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-01511080P.
PR 30-AUG-1999; 99US-01511303P.
PR 31-AUG-1999; 99US-01511438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 55.6%; Score 5; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 KVVDDT 5

Db 155 KVVDDT 159

RESULT 110

AAG14587
ID AAG14587 standard; protein; 307 AA.
XX
AC AAG14587;
XX
DT 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 14507.
DE
XX Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-01233548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130810P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-01320408P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-01343221P.
PR 14-MAY-1999; 99US-01343221P.
PR 18-MAY-1999; 99US-0134370P.
PR 19-MAY-1999; 99US-0134768P.
PR 20-MAY-1999; 99US-0134941P.
PR 21-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.

```

PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 28-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 55.6%; Score 5; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDVT 5
DB 155 KVDVT 159

RESULT 111
AEA20222
ID AEA20222 standard; protein; 308 AA.
XX
AC AEA20222;
XX
DT 11-AUG-2005 (first entry)
XX

```

```

DE Novel human polypeptide SEQ ID NO 916.
XX
XX
XX vulnery; CNS-gen.; gene therapy; diagnostic; forensic; mapping;
XX DNA purification; protein purification; osteoarthritis; antiarthritic;
XX osteopathic; musculoskeletal disease; osteoporosis; endocrine disease;
XX periodontal disease; antiinflammatory; mouth disease; burns; injury;
XX peripheral neuropathy; Alzheimers disease; neuroprotective; neurologic;
XX degeneration; parkinsons disease; antiparkinsonian; neurologic disease;
XX cerebrovascular ischemia; cerebroprotective; vasotropic;
XX cardiovascular disease; autoimmune disease; immunosuppressive;
XX immune disorder; viral infection; virucide; infection; cancer;
XX cytostatic; neoplasm.
XX
XX Homo sapiens.
XX
XX WC2005049806-A2.
XX
XX 02-JUN-2005.
XX
XX 11-MAR-2004; 2004WO-US007412.
XX
XX 14-MAR-2003; 2003US-00389559.
XX
XX (NUVE-) NUVELO INC.
XX
XX Tang TY, Wang J, Wang ZW, Zhang J, Ren F, Zhou P, Ma Y;
XX Ghosh M, Xue A, Asundi V, Zhao Q, Wang D, Goodrich R, Chen R;
XX Wehrman T, Weng G, Boyle B;
XX
XX WPI; 2005-417730/42.
XX
XX N-PSDB; AEA19655.
XX
XX New polynucleotide encoding a polypeptide with biological activity,
XX useful for treating a disease or disorder, e.g. osteoarthritis, burns,
XX CNS and peripheral disease, stroke, autoimmune disorders, viral
XX infection, or cancer.
XX
XX Claim 20; SEQ ID NO 916; 500pp; English.
XX
XX The invention describes a new isolated polynucleotide (I) encoding a
XX polypeptide with biological activity comprising: a nucleotide sequence of
XX SEQ ID NOS: 1-567 (fully defined); a nucleotide sequence that hybridizes
XX to the sequence of (I) under stringent hybridization conditions; or a
XX nucleotide sequence having greater than 99% sequence identity with the
XX sequence of (I). Also described are: a(n) (expression) vector comprising
XX (I); a host cell genetically engineered to comprise (I) operatively
XX associated with a regulatory sequence that modulates expression of the
XX polynucleotide in the host cell; an isolated polypeptide comprising a
XX sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide
XX is: a polypeptide encoded by (I); or a polypeptide encoded by a
XX polynucleotide hybridizing under stringent conditions with any one of SEQ
XX ID NOS: 1-567; a composition comprising the polypeptide of (3) and a
XX carrier; an antibody directed against the polypeptide of (3); a method
XX for detecting (I) in a sample; a method for detecting the polypeptide of
XX (3) in a sample; a method for identifying a compound that binds to the
XX polypeptide of (3); a method of producing the polypeptide of (3); and a
XX collection of polynucleotides, where the collection comprising of at
XX least one of SEQ ID NOS: 1-567. (I) is a polynucleotide comprising any of
XX the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological
XX activity, which comprises any of the amino acid sequence of SEQ ID NOS:
XX 568-1134. All sequences are fully defined in the specification. The
XX sequences and methods are useful in diagnostics, forensic, and gene
XX mapping, in identifying of mutations responsible for genetic disorders or
XX other traits, in assessing biodiversity, and for producing many other
XX types of data and products dependent on DNA and amino acid sequences. The
XX composition and method are useful for treating a disease or disorder,
XX e.g. osteoporosis, osteoarthritis, periodontal disease, burns, CNS and
XX peripheral disease, Alzheimer's disease, Parkinson's disease, stroke,
XX autoimmune disorders, viral infection, or cancer. This is the amino acid
XX sequence of a novel polypeptide of the invention.
XX
XX Sequence 308 AA;
XX
XX

```

Query Match 55.6%; Score 5; DB 9; Length 308;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTF 6
Db 118 VDDTF 122

RESULT 112

AAG20739

ID AAG20739 standard; protein; 311 AA.

AC AAG20739;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 23043.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 28-APR-1999; 99US-0130891P.

PR 30-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 30-APR-1999; 99US-0132407P.

PR 04-MAY-1999; 99US-0132484P.

PR 05-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

PR 06-MAY-1999; 99US-0132487P.

PR 07-MAY-1999; 99US-0132863P.

PR 11-MAY-1999; 99US-0134256P.

PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.

PR 14-MAY-1999; 99US-0134221P.

PR 14-MAY-1999; 99US-0134370P.

PR 18-MAY-1999; 99US-0134768P.

PR 19-MAY-1999; 99US-0134941P.

PR 20-MAY-1999; 99US-0135124P.

PR 21-MAY-1999; 99US-0135353P.

PR 24-MAY-1999; 99US-0135629P.

PR 25-MAY-1999; 99US-0136021P.

PR 27-MAY-1999; 99US-0136392P.

PR 28-MAY-1999; 99US-0136782P.

PR 01-JUN-1999; 99US-0137222P.

PR 03-JUN-1999; 99US-0137528P.

PR 07-JUN-1999; 99US-0137502P.

PR 08-JUN-1999; 99US-0137724P.

PR 10-JUN-1999; 99US-0138094P.

PR 10-JUN-1999; 99US-0138540P.

PR 10-JUN-1999; 99US-0138847P.

PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 19-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.

PR 11-AUG-1999; 99US-0148319P.
 PR 12-AUG-1999; 99US-0148341P.
 PR 13-AUG-1999; 99US-0148565P.
 PR 16-AUG-1999; 99US-0148684P.
 PR 17-AUG-1999; 99US-01493368P.
 PR 18-AUG-1999; 99US-0149175P.
 PR 20-AUG-1999; 99US-0149426P.
 PR 20-AUG-1999; 99US-0149722P.
 PR 20-AUG-1999; 99US-0149723P.
 PR 20-AUG-1999; 99US-0149929P.
 PR 23-AUG-1999; 99US-0149902P.
 PR 23-AUG-1999; 99US-0149930P.
 PR 26-AUG-1999; 99US-0150566P.
 PR 27-AUG-1999; 99US-0150884P.
 PR 27-AUG-1999; 99US-0151065P.
 PR 27-AUG-1999; 99US-0151066P.
 PR 30-AUG-1999; 99US-0151080P.
 PR 31-AUG-1999; 99US-0151303P.
 PR 31-AUG-1999; 99US-0151438P.
 PR 01-SEP-1999; 99US-0151930P.
 PR 07-SEP-1999; 99US-0152363P.
 PR 10-SEP-1999; 99US-0153070P.
 PR 13-SEP-1999; 99US-0153758P.
 PR 15-SEP-1999; 99US-0154018P.
 PR 16-SEP-1999; 99US-0154039P.
 PR 20-SEP-1999; 99US-0154779P.
 PR 22-SEP-1999; 99US-0155139P.
 PR 23-SEP-1999; 99US-0155486P.
 PR 24-SEP-1999; 99US-0155659P.
 PR 28-SEP-1999; 99US-0156458P.
 PR 29-SEP-1999; 99US-0156596P.
 PR 04-OCT-1999; 99US-0157117P.
 PR 05-OCT-1999; 99US-0157753P.
 PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158029P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.
 PR 14-OCT-1999; 99US-0159330P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 18-OCT-1999; 99US-0159638P.
 PR 21-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 55.6%; Score 5; DB 3; Length 311;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDOT 5

Db 160 KVDOT 164

RESULT 113

ADT55972

ID ADT55972 standard; protein; 311 AA.

XX AC ADT55972;

XX DT 13-JAN-2005 (first entry)

XX DE Plant polypeptide, SEQ ID 6049.

KW Plant; transgenic; cold tolerance; growth rate; drought tolerance;
 KW disease resistance; galactomannan production; plant growth regulator;
 KW heat tolerance; herbicide tolerance; lignin production;
 KW extreme osmotic condition tolerance; pathogens resistance;
 KW pest resistance; yield improvement; seed oil yield; seed protein yield.

XX OS Viridiplantae.

XX PN US2004216190-A1.

XX PD 28-OCT-2004.

XX PF 18-DEC-2003; 2003US-00739930.

XX PR 28-APR-2003; 2003US-00424599.

XX PR 28-APR-2003; 2003US-00425115.

XX PA (KOVA/) KOVALIC D K.

XX PI Kovalic DK;

XX DR WPI; 2004-757369/74.

XX PT New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved biological characteristics.

XX PS Claim 2; SEQ ID NO 6049; 14pp; English.

XX CC The invention relates a recombinant DNA construct comprising a polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO: 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean, Arabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide encoding a polypeptide associated with the property, and growing the transformed plant. The property is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for improving plant drought tolerance, for providing increased resistance to plant disease, for galactomannan production, for production of plant growth regulators, for improving plant heat tolerance, for improving plant tolerance to herbicides, for increasing the rate of homologous recombination in plants, for lignin production, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or pests, for yield improvement by modification of photosynthesis, for modifying seed oil yield and/or content, for modifying seed protein yield and/or content, for yield improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and development under at least one stress condition. The polynucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and genetics, in particular for producing transgenic plants with improved biological characteristics such as increased yield, improved nitrogen flow, increasing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and

CC analysis systems. The present sequence is one of the 5544 plant protein
CC sequences of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20040216190.
XX
SQ Sequence 311 AA;
Query Match 55.6%; Score 5; DB 8; Length 311;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDVT 5
Db 160 KVDVT 164
RESULT 114
ABB49170
ID ABB49170 standard; protein; 313 AA.
XX
AC ABB49170;
XX
DT 05-FEB-2002 (first entry)
XX
DE Listeria monocytogenes protein #1874.
XX
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW vitamin B12; bacterial infection; disease.
XX
OS Listeria monocytogenes.
XX
PN WO200177335-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-FR001118.
XX
PR 11-APR-2000; 2000FR-00004629.
XX
PA (INSP) INST PASTEUR.
XX
PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Psihi H, Dehoux P;
PI Dussurget O, Chetouani F, Nedjari H, Glaeser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Rierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Maduenio E, De Pablos B, Wehlend J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;
XX
DR WPI; 2002-010914/01.
XX
PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT and prevention of Listeria and related bacterial infections, and related
PT polypeptides.
XX
PS Claim 6; SEQ ID NO 1875; 192pp; French.
XX
CC The present invention relates to the genome sequence of Listeria
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of L. monocytogenes and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by L.

CC monocytogenes and related organisms. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 313 AA;
Query Match 55.6%; Score 5; DB 5; Length 313;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 DTFYY 8
Db 24 DTFYY 28
RESULT 115
ADN99771
ID ADN99771 standard; protein; 313 AA.
XX
AC ADN99771;
XX
DT 29-JUL-2004 (first entry)
XX
DE Novel human protein sequence #587.
XX
KW anti-inflammatory; dermatological; neuroprotective; immunomodulator;
KW antibacterial; viricide; antipsoriatic; cytostatic; gene therapy;
KW vaccine; inflammatory; CNS; immune disorder; cancer; psoriasis; diabetes;
KW early aging; hormonal imbalance; ischemic heart disease;
KW ulcerative colitis.
XX
OS Homo sapiens.
XX
PN WO2004038003-A2.
XX
PD 06-MAY-2004.
XX
PF 24-OCT-2003; 2003WO-US033947.
XX
PR 25-OCT-2002; 2002US-0421061P.
PR 25-OCT-2002; 2002US-0421080P.
PR 25-OCT-2002; 2002US-0421552P.
PR 25-OCT-2002; 2002US-0421614P.
PR 30-OCT-2002; 2002US-0422177P.
PR 30-OCT-2002; 2002US-0422178P.
PR 15-NOV-2002; 2002US-0426355P.
PR 15-NOV-2002; 2002US-0426384P.
PR 15-NOV-2002; 2002US-0426394P.
PR 15-NOV-2002; 2002US-0426430P.
PR 15-NOV-2002; 2002US-0426916P.
PR 27-NOV-2002; 2002US-0429224P.
PR 27-NOV-2002; 2002US-0429275P.
PR 27-NOV-2002; 2002US-0429302P.
PR 27-NOV-2002; 2002US-0429326P.
PR 27-NOV-2002; 2002US-0429651P.
PR 04-DEC-2002; 2002US-0430645P.
PR 04-DEC-2002; 2002US-0430651P.
PR 04-DEC-2002; 2002US-0430657P.
PR 04-DEC-2002; 2002US-0430663P.
PR 04-DEC-2002; 2002US-0430668P.
PR 04-DEC-2002; 2002US-0430684P.
PR 05-DEC-2002; 2002US-0430937P.
PR 05-DEC-2002; 2002US-0430965P.
PR 05-DEC-2002; 2002US-0431458P.
PR 12-DEC-2002; 2002US-0433251P.
PR 12-DEC-2002; 2002US-0433500P.
PR 13-DEC-2002; 2002US-0433316P.
PR 13-DEC-2002; 2002US-0433318P.
PR 23-DEC-2002; 2002US-0436236P.
PR 03-JAN-2003; 2003US-0437914P.
PR 17-JAN-2003; 2003US-0440820P.
PR 17-JAN-2003; 2003US-0440821P.

```
PR 18-APR-2003; 2003US-0463700P.
PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463716P.
PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467199P.
PR 02-MAY-2003; 2003US-0467201P.
PR 02-MAY-2003; 2003US-0467203P.
PR 02-MAY-2003; 2003US-0467230P.
PR 19-MAY-2003; 2003US-0471306P.
PR 19-MAY-2003; 2003US-0471336P.
PR 22-MAY-2003; 2003US-0472420P.
PR 22-MAY-2003; 2003US-0472430P.
PR 09-JUN-2003; 2003US-0476609P.
PR 09-JUN-2003; 2003US-0476621P.
PR 09-JUN-2003; 2003US-0476632P.
PR 09-JUN-2003; 2003US-0476641P.
PR 08-JUL-2003; 2003US-0485217P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 08-JUL-2003; 2003US-0485325P.
PR 08-JUL-2003; 2003US-0485359P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
XX
XX
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Kothakota S, Lin H, Linnemann T, Pierce K, Wang Y;
PI Wong JGP, Wu G, Zhang H, Zeng C;
XX
XX WPI; 2004-365511/34.
XX N-PSDB; ADN98987.
XX
XX New nucleic acid molecules, useful in preparing a composition for
PT treating or preventing e.g. inflammatory, CNS, bacterial or viral
PT disorders, cancer, psoriasis, diabetes, ischemic heart disease or
PT ulcerative colitis.
XX
XX Claim 14; SEQ ID NO 1371; 532pp; English.
XX
XX The invention relates to a nucleic acid molecule comprising a
CC polynucleotide sequence or its complement that encodes a polypeptide. The
CC nucleic acid is useful in preparing a composition for treating or
CC preventing inflammatory, CNS, immune, bacterial or viral disorder,
CC cancer, psoriasis, diabetes, early aging, hormonal imbalance, ischemic
CC heart disease or ulcerative colitis. This sequence corresponds to a
CC protein of the invention.
XX
XX Sequence 313 AA;
SQ
Query Match 55.6%; Score 5; DB 8; Length 313;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTF 6
Db 118 VDDTF 122
RESULT 116
AAG14586
ID AAG14586 standard; protein; 316 AA.
XX
XX AAG14586;
XX
XX 17-OCT-2000 (first entry)
PR
```

```
XX
DE
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 14506.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 03-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
XX 01-APR-1999; 99US-0127462P.
XX 08-APR-1999; 99US-0128234P.
XX 16-APR-1999; 99US-0128714P.
XX 16-APR-1999; 99US-0129845P.
XX 19-APR-1999; 99US-0130077P.
XX 21-APR-1999; 99US-0130449P.
XX 23-APR-1999; 99US-0130510P.
XX 23-APR-1999; 99US-0130891P.
XX 28-APR-1999; 99US-0131449P.
XX 30-APR-1999; 99US-0132048P.
XX 30-APR-1999; 99US-0132407P.
XX 04-MAY-1999; 99US-0132484P.
XX 05-MAY-1999; 99US-0132485P.
XX 06-MAY-1999; 99US-0132486P.
XX 06-MAY-1999; 99US-0132487P.
XX 07-MAY-1999; 99US-0132863P.
XX 11-MAY-1999; 99US-0134256P.
XX 14-MAY-1999; 99US-0134218P.
XX 14-MAY-1999; 99US-0134219P.
XX 14-MAY-1999; 99US-0134221P.
XX 14-MAY-1999; 99US-0134370P.
XX 18-MAY-1999; 99US-0134768P.
XX 19-MAY-1999; 99US-0134941P.
XX 20-MAY-1999; 99US-0135124P.
XX 21-MAY-1999; 99US-0135353P.
XX 24-MAY-1999; 99US-0135629P.
XX 25-MAY-1999; 99US-0136021P.
XX 27-MAY-1999; 99US-0136392P.
XX 28-MAY-1999; 99US-0136782P.
XX 01-JUN-1999; 99US-0137222P.
XX 03-JUN-1999; 99US-0137528P.
XX 04-JUN-1999; 99US-0137502P.
XX 07-JUN-1999; 99US-0137724P.
XX 08-JUN-1999; 99US-0138094P.
XX 10-JUN-1999; 99US-0138540P.
XX 10-JUN-1999; 99US-0138847P.
XX 14-JUN-1999; 99US-0139119P.
XX 16-JUN-1999; 99US-0139452P.
XX 16-JUN-1999; 99US-0139453P.
XX 17-JUN-1999; 99US-0139492P.
XX 18-JUN-1999; 99US-0139454P.
XX 18-JUN-1999; 99US-0139455P.
XX 18-JUN-1999; 99US-0139456P.
XX 18-JUN-1999; 99US-0139457P.
XX 18-JUN-1999; 99US-0139458P.
XX 18-JUN-1999; 99US-0139459P.
XX 18-JUN-1999; 99US-0139460P.
XX 18-JUN-1999; 99US-0139461P.
XX 18-JUN-1999; 99US-0139462P.
XX 18-JUN-1999; 99US-0139463P.
XX 18-JUN-1999; 99US-0139750P.
XX 18-JUN-1999; 99US-0139763P.
```

```
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 05-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148313P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149428P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.

PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156598P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157533P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 55.6%; Score 5; DB 3; Length 316;
Best Local Similarity 100.0%; Pred.No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
DB 164 KVDDT 168

RESULT 117
AAGS1073
ID AAGS1073 standard; protein; 316 AA.
XX
AC AAGS1073;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64785.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
```

OS Arabidopsis thaliana.
XX EP1033405-A2.
PD 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134321P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138340P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153707P.
PR 13-SEP-1999; 99US-0153758P.

PR 15-SEP-1999;	99US-0154018P.	XX	WO200154472-A2.
PR 16-SEP-1999;	99US-0154039P.	PN	
PR 20-SEP-1999;	99US-0154779P.	XX	02-AUG-2001.
PR 22-SEP-1999;	99US-0155139P.	PD	
PR 23-SEP-1999;	99US-0155486P.	XX	
PR 24-SEP-1999;	99US-0155659P.	PF	17-JAN-2001; 2001WO-US001307.
PR 28-SEP-1999;	99US-0156458P.	XX	
PR 29-SEP-1999;	99US-0156596P.	PR	31-JAN-2000; 2000US-0179065P.
PR 04-OCT-1999;	99US-0157117P.	PR	04-FEB-2000; 2000US-0180628P.
PR 05-OCT-1999;	99US-0157753P.	PR	24-FEB-2000; 2000US-0184664P.
PR 06-OCT-1999;	99US-0157865P.	PR	02-MAR-2000; 2000US-0186350P.
PR 07-OCT-1999;	99US-0158029P.	PR	16-MAR-2000; 2000US-0189874P.
PR 08-OCT-1999;	99US-0158232P.	PR	17-MAR-2000; 2000US-0190076P.
PR 12-OCT-1999;	99US-0158369P.	PR	18-APR-2000; 2000US-0198123P.
PR 13-OCT-1999;	99US-0159293P.	PR	19-MAY-2000; 2000US-0205515P.
PR 13-OCT-1999;	99US-0159294P.	PR	07-JUN-2000; 2000US-0209467P.
PR 13-OCT-1999;	99US-0159295P.	PR	28-JUN-2000; 2000US-0214886P.
PR 14-OCT-1999;	99US-0159329P.	PR	30-JUN-2000; 2000US-0215135P.
PR 14-OCT-1999;	99US-0159330P.	PR	07-JUL-2000; 2000US-0216647P.
PR 14-OCT-1999;	99US-0159331P.	PR	07-JUL-2000; 2000US-0216880P.
PR 14-OCT-1999;	99US-0159637P.	PR	11-JUL-2000; 2000US-0217487P.
PR 14-OCT-1999;	99US-0159638P.	PR	11-JUL-2000; 2000US-0217496P.
PR 18-OCT-1999;	99US-0159584P.	PR	14-JUL-2000; 2000US-0218290P.
PR 21-OCT-1999;	99US-0160741P.	PR	26-JUL-2000; 2000US-0220963P.
PR 21-OCT-1999;	99US-0160767P.	PR	26-JUL-2000; 2000US-0220964P.
PR 21-OCT-1999;	99US-0160770P.	PR	14-AUG-2000; 2000US-0224518P.
PR 21-OCT-1999;	99US-0160814P.	PR	14-AUG-2000; 2000US-0224519P.
PR 21-OCT-1999;	99US-0160815P.	PR	14-AUG-2000; 2000US-0225213P.
PR 22-OCT-1999;	99US-0160980P.	PR	14-AUG-2000; 2000US-0225214P.
PR 22-OCT-1999;	99US-0160981P.	PR	14-AUG-2000; 2000US-0225266P.
PR 22-OCT-1999;	99US-0160989P.	PR	14-AUG-2000; 2000US-0225267P.
PR 25-OCT-1999;	99US-0161404P.	PR	14-AUG-2000; 2000US-0225268P.
PR 25-OCT-1999;	99US-0161405P.	PR	14-AUG-2000; 2000US-0225270P.
PR 25-OCT-1999;	99US-0161406P.	PR	14-AUG-2000; 2000US-0225447P.
PR 26-OCT-1999;	99US-0161359P.	PR	14-AUG-2000; 2000US-0225757P.
PR 26-OCT-1999;	99US-0161360P.	PR	14-AUG-2000; 2000US-0225758P.
PR 26-OCT-1999;	99US-0161361P.	PR	18-AUG-2000; 2000US-0226279P.
PR 28-OCT-1999;	99US-0161920P.	PR	22-AUG-2000; 2000US-0226681P.
PR 28-OCT-1999;	99US-0161992P.	PR	22-AUG-2000; 2000US-0226688P.
PR 28-OCT-1999;	99US-0161993P.	PR	22-AUG-2000; 2000US-0227182P.
PR 29-OCT-1999;	99US-0162142P.	PR	23-AUG-2000; 2000US-0227009P.
Query Match	55.6%; Score 5; DB 3; Length 316;	PR	30-AUG-2000; 2000US-0228924P.
Best Local Similarity	100.0%; Pred.No. 5.5e+02; Mismatches 0; Indels 0; Gaps 0;	PR	01-SEP-2000; 2000US-0229287P.
Matches 5; Conservative 0;		PR	01-SEP-2000; 2000US-0229343P.
QY 1 KVVDT 5		PR	01-SEP-2000; 2000US-0229344P.
Db 164 KVVDT 168		PR	01-SEP-2000; 2000US-0229345P.
		PR	05-SEP-2000; 2000US-0229509P.
		PR	05-SEP-2000; 2000US-0229513P.
		PR	06-SEP-2000; 2000US-0230437P.
		PR	06-SEP-2000; 2000US-0230438P.
		PR	08-SEP-2000; 2000US-0231242P.
		PR	08-SEP-2000; 2000US-0231243P.
		PR	08-SEP-2000; 2000US-0231244P.
		PR	08-SEP-2000; 2000US-0231413P.
		PR	08-SEP-2000; 2000US-0231414P.
		PR	08-SEP-2000; 2000US-0232080P.
		PR	08-SEP-2000; 2000US-0232081P.
		PR	12-SEP-2000; 2000US-0231968P.
		PR	14-SEP-2000; 2000US-0232397P.
		PR	14-SEP-2000; 2000US-0232398P.
		PR	14-SEP-2000; 2000US-0232399P.
		PR	14-SEP-2000; 2000US-0232400P.
		PR	14-SEP-2000; 2000US-0232401P.
		PR	14-SEP-2000; 2000US-0233063P.
		PR	14-SEP-2000; 2000US-0233064P.
		PR	14-SEP-2000; 2000US-0233065P.
		PR	21-SEP-2000; 2000US-0234223P.
		PR	21-SEP-2000; 2000US-0234274P.
		PR	25-SEP-2000; 2000US-0234997P.
		PR	25-SEP-2000; 2000US-0234998P.
		PR	26-SEP-2000; 2000US-0235484P.
		PR	27-SEP-2000; 2000US-0235834P.
RESULT 118			
ADM19847			
ID ADM19847 standard; protein; 316 AA.			
XX			
AC ADM19847;			
XX			
DT 20-MAY-2004 (first entry)			
XX			
DE Protein encoded by novel human channel/transporter gene #165.			
XX			
KW immunosuppressive; antiarthritic; antirheumatic; antiproliferative;			
KW cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;			
KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;			
KW gene therapy; channel/transporter protein; rheumatoid arthritis;			
KW neoplasm; cardiac arrest; cerebrovascular disorder; cerebral ischemia;			
KW angiogenesis; nervous system disorder; Alzheimer's disease;			
KW ocular disorder; corneal infection; wound healing;			
KW epithelial cell proliferation; skin aging; sunburn; transplantation;			
KW chemotaxis; food additive.			
XX			
OS Homo sapiens.			

PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251388P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0256719P.
 PR 08-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX

PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-476159/51.
 DR N-PSDB; ADM19368.
 XX
 PT Isolated nucleic acid molecule encoding a channel/transporter protein is
 XX used in preventing, treating or ameliorating a medical condition.
 PS Claim 11; SEQ ID NO 654; 809pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule encoding a
 CC channel/transporter protein or sequences at least 95% identical to a
 CC these. The nucleic acids and proteins encoded by them are used to
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
 CC in diagnosing a pathological condition or susceptibility to a
 CC pathological condition. The antibodies to the proteins can also be used
 CC in alleviating symptoms associated with the disorders and in diagnostic
 CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays
 CC (ELISA). Disorders which are diagnosed or treated include autoimmune
 CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
 CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
 CC arrest, cerebrovascular disorders e.g. cerebral ischemia, angiodysplasia,
 CC nervous system disorders e.g. Alzheimer's disease, infections caused by
 CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection.
 CC The polypeptides can also be used to aid wound healing and epithelial
 CC cell proliferation, to prevent skin aging due to sunburn, to maintain
 CC organs before transplantation, for supporting cell culture of primary
 CC tissues, to regenerate tissues and in chemotaxis. The polypeptides can
 CC also be used as a food additive or preservative to increase or decrease
 CC storage capabilities. This sequence corresponds to a protein of the
 CC invention.
 XX
 SQ Sequence 316 AA;
 Query Match 55.8%; Score 5; DB 4; Length 316;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTF 6
 Db 121 VDDTF 125
 RESULT 119
 ABB68103
 ID ABB68103 standard; protein; 317 AA.
 XX
 AC ABB68103;
 XX
 XX 26-MAR-2002 (first entry)
 DT
 DE Drosophila melanogaster polypeptide SEQ ID NO 31101.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmaceutical.
 XX Drosophila melanogaster.
 OS
 XX WO200171042-A2.
 PN
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 XX 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 XX (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 DR

DR N-PSDB; ABL12206.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX
PS Disclosure; SEQ ID NO 31101; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 317 AA;

Query Match 55.6%; Score 5; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
DB 86 KVDDT 90
|||||

RESULT 120
ABB60330
ID ABB60330 standard; protein; 322 AA.
AC ABB60330;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 7782.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
PN
XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US009231.
PF
XX 23-MAR-2000; 2000US-0191637P.
PR
XX 11-JUL-2000; 2000US-00614150.
PR
XX (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
DR
XX N-PSDB; ABL04433.
DR
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
PT
XX
PS Disclosure; SEQ ID NO 7782; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 322 AA;

Query Match 55.6%; Score 5; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
DB 15 VDDTF 19
|||||

RESULT 121
ADY25260
ID ADY25260 standard; protein; 323 AA.
XX
XX AC ADY25260;
XX
XX 21-APR-2005 (first entry)
XX
XX Plant full length insert polypeptide seqid 73044.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.
XX
XX Unidentified.
XX
XX US2004034888-A1.
PN
XX 19-FEB-2004.
PD
XX 28-APR-2003; 2003US-00425114.
PF
XX 06-MAY-1999; 99US-00304517.
PR
XX 05-NOV-2001; 2001US-00985678.
PR
XX (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
PI
XX WPI; 2004-180133/17.
DR
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
PT
XX Claim 1; SEQ ID NO 73044; 15pp; English.
PS
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.seadata.upto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring

CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 XX
 SQ Sequence 323 AA;

Query Match 55.6%; Score 5; DB 8; Length 323;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDVT 5
 |||||
 Db 168 KVDVT 172

RESULT 122
 AAG20738
 ID AAG20738 standard; protein; 326 AA.
 XX
 AC AAG20738;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 23042.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EF1033405-A2.
 XX
 PD 06-SEP-2000.
 PF
 PP 25-FEB-2000; 2000EP-00301439.
 XX
 PP 25-FEB-1999; 99US-0121825P.
 PR 05-MAR-1999; 99US-0123180P.
 PR 09-MAR-1999; 99US-0123548P.
 PR 23-MAR-1999; 99US-0125788P.
 PR 25-MAR-1999; 99US-0126264P.
 PR 29-MAR-1999; 99US-0126785P.
 PR 01-APR-1999; 99US-0127462P.
 PR 06-APR-1999; 99US-0128234P.
 PR 08-APR-1999; 99US-0128714P.
 PR 16-APR-1999; 99US-0129845P.
 PR 19-APR-1999; 99US-0130077P.
 PR 21-APR-1999; 99US-0130449P.
 PR 23-APR-1999; 99US-0130510P.
 PR 23-APR-1999; 99US-0130891P.
 PR 28-APR-1999; 99US-0131449P.
 PR 30-APR-1999; 99US-0132048P.
 PR 10-APR-1999; 99US-0132407P.
 PR 04-MAY-1999; 99US-0132484P.
 PR 05-MAY-1999; 99US-0132485P.
 PR 06-MAY-1999; 99US-0132486P.
 PR 06-MAY-1999; 99US-0132487P.
 PR 07-MAY-1999; 99US-0132863P.
 PR 11-MAY-1999; 99US-0134256P.
 PR 14-MAY-1999; 99US-0134218P.
 PR 14-MAY-1999; 99US-0134219P.
 PR 14-MAY-1999; 99US-0134221P.
 PR 14-MAY-1999; 99US-0134370P.
 PR 18-MAY-1999; 99US-0134768P.
 PR 19-MAY-1999; 99US-0134941P.
 PR 20-MAY-1999; 99US-0135124P.
 PR 21-MAY-1999; 99US-0135353P.
 PR 24-MAY-1999; 99US-0135629P.
 PR 25-MAY-1999; 99US-0136021P.
 PR 27-MAY-1999; 99US-0136392P.
 PR 28-MAY-1999; 99US-0136782P.
 PR 01-JUN-1999; 99US-0137222P.
 PR 03-JUN-1999; 99US-0137528P.
 PR 04-JUN-1999; 99US-0137502P.
 PR 07-JUN-1999; 99US-0137724P.
 PR 08-JUN-1999; 99US-0138094P.
 PR 10-JUN-1999; 99US-0138540P.
 PR 10-JUN-1999; 99US-0138847P.
 PR 14-JUN-1999; 99US-0139119P.
 PR 16-JUN-1999; 99US-0139452P.
 PR 16-JUN-1999; 99US-0139453P.
 PR 17-JUN-1999; 99US-0139492P.
 PR 18-JUN-1999; 99US-0139454P.
 PR 18-JUN-1999; 99US-0139455P.
 PR 18-JUN-1999; 99US-0139456P.
 PR 18-JUN-1999; 99US-0139457P.
 PR 18-JUN-1999; 99US-0139458P.
 PR 18-JUN-1999; 99US-0139459P.
 PR 18-JUN-1999; 99US-0139460P.
 PR 18-JUN-1999; 99US-0139461P.
 PR 18-JUN-1999; 99US-0139462P.
 PR 18-JUN-1999; 99US-0139463P.
 PR 18-JUN-1999; 99US-0139750P.
 PR 18-JUN-1999; 99US-0139763P.
 PR 21-JUN-1999; 99US-0139817P.
 PR 22-JUN-1999; 99US-0139899P.
 PR 23-JUN-1999; 99US-0140353P.
 PR 24-JUN-1999; 99US-0140695P.
 PR 28-JUN-1999; 99US-0140823P.
 PR 28-JUN-1999; 99US-0140991P.
 PR 30-JUN-1999; 99US-0141287P.
 PR 01-JUL-1999; 99US-0141842P.
 PR 01-JUL-1999; 99US-0142154P.
 PR 02-JUL-1999; 99US-0142055P.
 PR 06-JUL-1999; 99US-0142390P.
 PR 09-JUL-1999; 99US-0142803P.
 PR 12-JUL-1999; 99US-0142920P.
 PR 13-JUL-1999; 99US-0142977P.
 PR 14-JUL-1999; 99US-0143542P.
 PR 15-JUL-1999; 99US-0143624P.
 PR 16-JUL-1999; 99US-0144005P.
 PR 16-JUL-1999; 99US-0144085P.
 PR 16-JUL-1999; 99US-0144086P.
 PR 19-JUL-1999; 99US-0144325P.
 PR 19-JUL-1999; 99US-0144331P.
 PR 19-JUL-1999; 99US-0144332P.
 PR 19-JUL-1999; 99US-0144333P.
 PR 19-JUL-1999; 99US-0144334P.
 PR 20-JUL-1999; 99US-0144352P.
 PR 20-JUL-1999; 99US-0144632P.
 PR 20-JUL-1999; 99US-0144884P.
 PR 21-JUL-1999; 99US-0144814P.
 PR 21-JUL-1999; 99US-0145086P.
 PR 21-JUL-1999; 99US-0145088P.
 PR 22-JUL-1999; 99US-0145085P.
 PR 22-JUL-1999; 99US-0145087P.
 PR 22-JUL-1999; 99US-0145089P.
 PR 22-JUL-1999; 99US-0145192P.
 PR 23-JUL-1999; 99US-0145145P.
 PR 23-JUL-1999; 99US-0145218P.
 PR 23-JUL-1999; 99US-0145224P.
 PR 26-JUL-1999; 99US-0145276P.
 PR 27-JUL-1999; 99US-0145913P.
 PR 27-JUL-1999; 99US-0145918P.
 PR 27-JUL-1999; 99US-0145919P.
 PR 28-JUL-1999; 99US-0145951P.
 PR 02-AUG-1999; 99US-0146386P.

```
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 16-SEP-1999; 99US-0154018P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.

PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 55.6%; Score 5; DB 3; Length 326;
Best Local Similarity 100.0%; Pred. No. 5, 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVDDT 5
Db 175 KVVDDT 179

RESULT 123
ABR57463
ID ABR57463 standard; protein; 328 AA.
XX AC ABR57463;
XX DT 15-SEP-2003 (first entry)
XX DE AGC family protein kinase protein p90-Ssk.
XX KW Protein kinase B; PKB/Akt; enzyme; crystal structure; drug discovery;
XX KW protein co-ordinate data; cytostatic; antidiabetic; vasotropic; PKB;
XX KW neotropic; neuroprotective; gene therapy; protein kinase B beta; PKBbeta;
XX KW structural analysis; cancer; diabetes; diabetes; erectile dysfunction;
XX KW neurodegeneration.
XX OS Unidentified.
XX PN WO2003016516-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-GB003735.
XX PR 14-AUG-2001; 2001GB-00019860.
XX PR 01-MAY-2002; 2002GB-00009985.
XX PA (NOVS ) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.
XX PA (CANC-) CANCER RES INST.
XX PI Barford D, Yang J, Hemmings BA, Cron PD;
XX PS WPI; 2003-268328/26.
XX CC New crystal of protein kinase B beta, useful for activating protein
XX CC kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates
XX CC or a tetragonal space group.
XX CC Disclosure; Fig 4; 284pp; English.
XX CC The present invention describes a crystal of protein kinase B beta
XX CC (PKBbeta) comprising (I), where (I) comprises: (a) a tetragonal space
XX CC group P4-1-2-1-2 and unit cell dimensions of: a = 149.33 plus or minus
XX CC 0.5 Angstrom, b = 149.33 plus or minus 0.5 Angstrom, c = 39.77 plus or
XX CC minus 0.5 Angstrom; a = 148.40 plus or minus 0.5 Angstrom, b = 148.40
XX CC plus or minus 0.5 Angstrom, c = 38.55 plus or minus 0.5 Angstrom; a =
XX CC 149.70 plus or minus 0.5 Angstrom, b = 149.70 plus or minus 0.5 Angstrom,
XX CC c = 39.19 plus or minus 0.5 Angstrom; or a = 149.52 plus or minus 0.5
XX CC Angstrom, b = 149.52 plus or minus 0.5 Angstrom, c = 39.06 plus or minus
XX CC 0.5 Angstrom; or (b) the three-dimensional atomic coordinates listed in
XX CC the specification. (I) has cytostatic, antidiabetic, vasotropic,
XX CC neotropic and neuroprotective activities, and can be used in gene
XX CC therapy. The crystal of PKBbeta, and methods from the present invention,
XX CC are useful in activating protein kinases, particularly AGC kinases, for
XX CC identifying modulators of protein kinase activity, and for structural
XX CC analysis of other protein kinases. The crystal may also be used in
XX CC manufacturing a medicament for treating cancer, diabetes, erectile
XX CC dysfunction or neurodegeneration. The present sequence represents an AGC
XX CC family protein kinase which is given in the exemplification of the
```

```
CC present invention
XX Sequence 328 AA;
SQ
Query Match 55.6%; Score 5; DB 6; Length 328;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFY 7
Db 291 DDTFY 295

RESULT 124
AAG51072
ID AAG51072 standard; protein; 329 AA.
AC AAG51072;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64784.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EF1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 23-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135533P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 21-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 28-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
```

PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149802P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 18-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 55.6%; Score 5; DB 3; Length 329;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 177 KVDDT 181

RESULT 125

ABR52858
ID ABR52858 standard; protein; 329 AA.

XX

AC ABR52858;

XX 20-JUN-2003 (first entry)

XX Protein sequence #SEQ ID 581.

XX Multiprotein complex; eukaryote; drug target; diagnosis.

XX Saccharomyces cerevisiae.

XX EP1258494-A1.

XX 20-NOV-2002.

XX 20-DEC-2001; 2001EP-00130253.

XX 15-MAY-2001; 2001EP-00111774.

XX (CELL-) CELLZONE AG.

XX Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;
PI Marzioch M, Schultz JD, Superti-Furga GD;

XX WPI; 2003-250078/25.

XX N-PSDB; ACC60900.

XX New isolated protein complexes useful for diagnosing a disease or
disorder, or as a target for an active agent of a pharmaceutical.
PT Preferably a drug target in the treatment or prevention of disease or
disorder.

XX Disclosure; SEQ ID NO 581; 17pp + Sequence Listing; English.

XX The invention relates to multiprotein complexes from eukaryotes. Proteins
of the invention and DNA sequences encoding them are given in records
CC ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are
CC obtainable by using a protein as a bait and isolating the set of proteins
CC which is attached thereto from cells. Such protein complexes may comprise
CC up to 30 distinct proteins. Protein complexes of the invention are useful
CC for diagnosing a disease or disorder, or as a target for an active agent
CC of a pharmaceutical, preferably a drug target in the treatment or
CC prevention of a disease or disorder. Note: The sequence data for this
CC patent is not represented in the printed specification, but is based on
CC sequence information supplied by the European Patent Office. The complete
CC document is available on CD-ROM

XX SQ Sequence 329 AA;

Query Match 55.6%; Score 5; DB 6; Length 329;

Best Local Similarity 100.0%; Pred. No. 5.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7

Db 153 DDTFY 157

RESULT 126

ADK62318
ID ADK62318 standard; protein; 329 AA.

XX

AC ADK62318;

XX

DT 06-MAY-2004 (first entry)
 DE Disease treating protein complex-derived protein #285.
 XX protein complex; drug target; diagnosis;
 KW Unidentified.
 XX
 OS
 XX
 PN EP1338608-A2.
 XX
 PD 27-AUG-2003.
 XX
 XX 20-DEC-2002; 2002EP-00102902.
 XX
 PF 20-DEC-2001; 2001EP-00130253.
 XX
 PR (CELL-) CELLZOME AG.
 XX
 PA Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;
 PI Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;
 PI Michon A, Leutwein C, Rick J;
 XX
 DR WPI; 2003-638460/61.
 DR N-PSDB; ADK62319.
 XX
 XX New proteins and protein complexes from eukaryotes, useful as targets in
 PT drug screening, or in diagnosing or screening for the presence of a
 PT disease or disorder, or a predisposition for developing a disease or
 PT disorder in a subject.
 XX
 XX Disclosure; SEQ ID NO 569; 13pp; English.
 XX
 CC The invention relates to novel protein complexes comprising a first and a
 CC second protein, or its derivative, fragment, homologue or variant. The
 CC proteins are selected from given protein complexes, which are not defined
 CC in the specification. The variants are encoded by nucleic acids that
 CC hybridize to the nucleic acids encoding the proteins under low stringency
 CC conditions. The protein complexes are useful as targets for an active
 CC agent of a pharmaceutical. These protein complexes are particularly
 CC useful as drug targets for the treatment or preventing of a disease or
 CC disorder. The complexes and methods above are useful in diagnosing or
 CC screening for the presence of a disease or disorder or a predisposition
 CC for developing a disease or disorder in a subject. These are also useful
 CC in screening for a drug for treatment or prevention of a disease or
 CC disorder. The molecule that modulates the amount, activity or protein
 CC components of the complex is useful for the manufacture of a medicament
 CC for the treatment or prevention of a disease or disorder. This sequence
 CC corresponds to a protein of the invention. (Note: the sequence data for
 CC this patent did not form part of the printed specification but was
 CC obtained from the EPO in electronic format).
 XX
 SQ Sequence 329 AA;
 Query Match 55.6%; Score 5; DB 7; Length 329;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 DDTFY 7
 Db 153 DDTFY 157
 RESULT 127
 ADS43699
 ID ADS43699 standard; protein; 329 AA.
 XX
 AC ADS43699;
 XX
 XX 02-DEC-2004 (first entry)
 XX Bacterial polypeptide #22129.
 XX Recombinant DNA construct; transformed plant; improved plant property;

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX
 OS Bacteria.
 XX
 XX US2003233675-A1.
 XX
 PD 18-DEC-2003.
 XX
 XX 20-FEB-2003; 2003US-00369493.
 XX
 PF 21-FEB-2002; 2002US-0360039P.
 XX
 PR (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX
 DR WPI; 2004-061375/06.
 XX
 PT New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 XX Claim 1; SEQ ID NO 22129; 122pp; English.
 XX
 CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 XX Sequence 329 AA;
 Query Match 55.6%; Score 5; DB 8; Length 329;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 DDTFY 7
 Db 153 DDTFY 157
 RESULT 128
 ADT87145
 ID ADT87145 standard; protein; 329 AA.
 XX

AC ADT87145;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Yeast Stress-related protein from gene YUL152W.
 XX
 KW Yeast; Stress-related protein; SRP; environmental stress; abiotic stress;
 XX drought; heat; cold; salt.
 XX
 OS Saccharomyces cerevisiae.
 XX
 FN WO2004092398-A2.
 XX
 PD 28-OCT-2004.
 XX
 PF 15-APR-2004; 2004WO-US011888.
 XX
 PR 15-APR-2003; 2003EP-0008080.
 PR 02-MAY-2003; 2003EP-00039728.
 PR 01-AUG-2003; 2003EP-00016672.
 PR 30-SEP-2003; 2003EP-00022225.
 XX
 PR (BADI) BASF PLANT SCI GMBH.
 PA
 XX Puzio P, Chardonnens A, Shirley A, Wang X, Sarria-Millan R;
 PI McKersie B, Chen R;
 PI
 XX WPI; 2004-766883/75.
 DR N-PSDB; ADT87144.
 XX
 PR New isolated nucleic acid molecule comprises a sequence encoding Stress-
 PT Related Protein (SRP), useful for producing transformed plants with
 PT altered metabolic activity resulting in increased tolerance or resistance
 PT to environmental stress.
 XX
 PS Claim 15; SEQ ID NO 123; 911pp; English.
 XX
 CC The invention relates an isolated nucleic acid molecule comprises a
 CC nucleic acid molecule encoding a Stress-Related Protein (SRP), from Yeast
 CC or E. coli and their homologues from Rice, Soybean and Rape. Also
 CC included are a transformed plant cell with altered metabolic activity
 CC compared to a corresponding non-transformed wild type plant cell (where
 CC the metabolic activity is altered by transformation with a SRP coding
 CC nucleic acid and results in increased tolerance and/or resistance to an
 CC environmental stress as compared to a corresponding non-transformed wild
 CC type plant cell), a transgenic plant generated from the plant cell above
 CC (and which is a monocot or dicot plant, or a gymnosperm plant), a seed
 CC produced by a transgenic plant above (where the seed is genetically
 CC homozygous for a transgene conferring altered metabolic activity
 CC resulting in an increased tolerance to environmental stress as compared
 CC to a corresponding non-transformed wild type plant), a nucleic acid
 CC construct which confers the expression of the nucleic acid molecule above
 CC (comprising one or more regulatory elements, where expression of the SRP
 CC coding nucleic acid in a host cell results in altered metabolic activity
 CC resulting in increased tolerance to environmental stress as compared to a
 CC corresponding non-transformed wild type host cell), a vector comprising
 CC the nucleic acid molecule above or the nucleic acid construct, a host
 CC cell which has been transformed stably or transiently with the vector (or
 CC the nucleic acid molecules above, or the nucleic acid construct), an
 CC isolated Stress Related Protein (SRP) selected from the amino acid
 CC sequences fully given in the specification and/or its homologues, a
 CC method of producing a transgenic plant with altered metabolic activity
 CC compared to a corresponding non-transformed wild type plant cell,
 CC modifying stress tolerance of a plant, detecting environmental stress in
 CC plant cells or plants, screening plant cells or plants for increased
 CC tolerance and/or resistance to environmental stress, breeding plant cells
 CC or plants towards increased tolerance and/or resistance to environmental
 CC stress, increasing tolerance of a plant to at least one abiotic stress,
 CC a plant transformed with the nucleic acid above and a seed of the plant.
 CC The altered metabolic activity and/or a SRP encoding nucleic acids or its
 CC homologues are useful as markers for selection of plants or plant cells
 CC with increased tolerance to environmental stress, or for detection of
 CC stress in plants or plant cells. The nucleic acids are useful for

CC producing transformed plants with altered metabolic activity resulting in
 CC increased tolerance and/or resistance to an environmental stress
 CC (drought, heat, cold and salt) as compared to a corresponding non-
 CC transformed wild-type plant cell. The present sequence is a yeast SRP of
 XX the invention.
 SQ Sequence 329 AA;
 Query Match 55.6%; Score 5; DB 8; Length 329;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 DDTFY 7
 Db 153 DDTFY 157
 RESULT 129
 ABU44842
 ID ABU44842 standard; protein; 330 AA.
 XX
 AC ABU44842;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #30369.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Salmonella paratyphi.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACA48712.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 72766; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX SQ Sequence 330 AA;

Query Match 55.6%; Score 5; DB 6; Length 330;

Best Local Similarity 100.0%; Pred. No. 5.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8

|||||

Db 178 DTFYY 182

RESULT 130

ABU50533

ID ABU50533 standard; protein; 330 AA.

AC ABU50533;

XX 19-JUN-2003 (first entry)

DT Protein encoded by Prokaryotic essential gene #36060.

DE Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Yersinia pestis.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA54403.

XX New antisense nucleic acids, useful for identifying proteins or screening

XX PT for homologous nucleic acids required for cellular proliferation to

XX PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 78457; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

XX CC the 6213 antisense sequences given in the specification where expression

XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:

XX CC (1) a vector comprising a promoter operably linked to the nucleic acid

XX CC encoding a polypeptide whose expression is inhibited by the antisense

XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX SQ Sequence 330 AA;

Query Match 55.6%; Score 5; DB 6; Length 330;

Best Local Similarity 100.0%; Pred. No. 5.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8

|||||

Db 179 DTFYY 183

RESULT 131

AAG14585

ID AAG14585 standard; protein; 331 AA.

AC AAG14585;

XX 17-OCT-2000 (first entry)

DT Arabidopsis thaliana protein fragment SEQ ID NO: 14505.

DE Protein identification; signal transduction pathway; metabolic pathway;

XX hybridisation assay; genetic mapping; gene expression control; promoter;

XX termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

XX 29-MAR-1999; 99US-0126785P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 08-APR-1999; 99US-0128714P.

XX 16-APR-1999; 99US-0129845P.

XX 19-APR-1999; 99US-0130077P.

XX 21-APR-1999; 99US-0130449P.

XX 23-APR-1999; 99US-0130510P.

XX 23-APR-1999; 99US-0130891P.

PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 17-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144323P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158039P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159283P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.

PR 18-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 26-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161933P.
 PR 23-OCT-1999; 99US-0162142P.

Query Match 55.6%; Score 5; DB 3; Length 331;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 179 KVDDT 183

RESULT 132
 ABU47384
 ID ABU47384 standard; protein; 331 AA.
 XX AC
 XX ABU47384;
 DT 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #32911.
 XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
 KW Salmomella typhimurium.
 OS
 XX WO200277183-A2.
 XX 03-OCT-2002.
 XX 21-MAR-2002; 2002WO-US009107.
 XX 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX (ELIT-) ELITRA PHARM INC.
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.
 DR N-PSDB; ACA51254.
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids, required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX Claim 25; SEQ ID NO 75308; 1766pp; English.
 PS The invention relates to an isolated nucleic acid comprising any one of
 XX the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 331 AA;
 Query Match 55.6%; Score 5; DB 6; Length 331;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
 Db 179 DTFYY 183

RESULT 133
 ABU15092
 ID ABU15092 standard; protein; 331 AA.
 XX AC
 XX ABU15092;
 DT 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #619.
 XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
 KW Escherichia coli.
 OS
 XX WO200277183-A2.
 XX 03-OCT-2002.
 XX 21-MAR-2002; 2002WO-US009107.
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX (ELIT-) ELITRA PHARM INC.
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.
 DR N-PSDB; ACA18962.

XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 43016; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 331 AA;

SQ

Query Match 55.6%; Score 5; DB 6; Length 331;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
|||
Db 179 DTFYY 183

RESULT 134
ABU21270

ID ABU21270 standard; protein; 337 AA.

XX AC ABU21270;

XX 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #6797.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Burkholderia fungorum.

XX WO200277183-A2.

PD 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlssen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.
DR N-PSDB; ACA25140.

XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 49194; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 337 AA;

SQ

Query Match 55.6%; Score 5; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDVT 5
|||
Db 117 KVDVT 121

RESULT 135
AAG53800

ID AAG53800 standard; protein; 347 AA.

XX AC AAG53800;

XX 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 68529.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.
OS EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-01231548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-01322484P.
PR 05-MAY-1999; 99US-01322485P.
PR 06-MAY-1999; 99US-01322486P.
PR 07-MAY-1999; 99US-01322487P.
PR 11-MAY-1999; 99US-01322863P.
PR 14-MAY-1999; 99US-01342566P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 18-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-01377502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139452P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145513P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.

```
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161320P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 55.6%; Score 5; DB 3; Length 347;
Best Local Similarity 100.0%; Pred. No. 6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 4 DTFY 8
Db 190 DTFY 194

RESULT 136
ADN00790
ID ADN00790 standard; protein; 348 AA.
XX AC
XX AC ADN00790;
XX DT
XX DT 15-JUL-2004 (first entry)
XX DE
XX DE Mycobacterium sapM-related P chrysoeum protein SeqID19.
KW promoter; mycobacterial secreted acid phosphatase; SAPM; sapM promoter;
KW antibacterial; fungicide; vaccine; pathogenic mycobacterial disease;
KW fungal infection.
XX OS
XX OS Penicillium chrysogenum.
XX PN
XX PN WO200403677-A2.
XX PD
XX PD 22-APR-2004.

PR 09-OCT-2003; 2003WO-CA001554.
PR 09-OCT-2002; 2002US-0416957P.
PR (LIUJ/) LIU J.
XX LIU J, Saleh MT, Alexander D;
XX WPI; 2004-364868/34.
DR N-PSDB; ADN00788.
XX New mycobacterial secreted acid phosphatase, useful in diagnosing,
PT treating or preventing a pathogenic mycobacterial disease or fungal
PT infection.
XX Disclosure; SEQ ID NO 19; 87pp; English.
XX This invention relates to a novel isolated DNA sequence which comprises a
CC promoter or a promoter fragment of a mycobacterial secreted acid
CC phosphatase (SAPM) gene, where the promoter or the promoter fragment is
CC sufficient to control expression of a nucleotide sequence of interest and
CC is inducible under low-pH conditions and where the promoter or the
CC promoter fragment hybridise to a sapM promoter, for example a
CC Mycobacterium tuberculosis sapM promoter, a M bovis sapM promoter, a M
CC avium sapM promoter or a M marinum sapM promoter, each comprising a
CC sequence of 500 bp, under high stringency hybridisation conditions. The
CC invention may be useful for the production of compounds with an
CC antibacterial or fungicide activity or for the production of a vaccine
CC against Mycobacterium species comprising a mycobacterial secreted acid
CC phosphatase (SAPM) or an antibody specific for a mycobacterial secreted
CC acid phosphatase. The DNA sequence, methods, compounds, vaccine and
CC compositions are useful in diagnosing, treating or preventing a
CC pathogenic mycobacterial disease or fungal infection. The present
CC sequence is that of a P chrysoeum protein fragment which is related to
CC the invention.
XX SQ Sequence 348 AA;

Query Match 55.6%; Score 5; DB 8; Length 348;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
Db 214 DDTFY 218

RESULT 137
AAG28320
ID AAG28320 standard; protein; 368 AA.
XX AC
XX AC AAG28320;
XX DT
XX DT 17-OCT-2000 (first entry)
XX DE
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 33493.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS
XX OS Arabidopsis thaliana.
XX PN
XX PN EP1033405-A2.
XX PD
XX PD 06-SEP-2000.
XX PF
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR
XX PR 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.
XX PR 09-MAR-1999; 99US-0123548P.
XX PR 23-MAR-1999; 99US-0125788P.
```

PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135333P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 17-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142292P.
PR 12-JUL-1999; 99US-0142377P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.

PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 03-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 16-AUG-1999; 99US-0148684P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 30-AUG-1999; 99US-0151080P.
PR 31-AUG-1999; 99US-0151303P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 16-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.

PR	08-OCT-1999;	99US-0158232P.	PR	21-APR-1999;	99US-0130449P.
PR	12-OCT-1999;	99US-0158369P.	PR	23-APR-1999;	99US-0130510P.
PR	13-OCT-1999;	99US-0159293P.	PR	28-APR-1999;	99US-0130891P.
PR	13-OCT-1999;	99US-0159294P.	PR	30-APR-1999;	99US-0131449P.
PR	13-OCT-1999;	99US-0159295P.	PR	30-APR-1999;	99US-0132048P.
PR	14-OCT-1999;	99US-0159329P.	PR	04-MAY-1999;	99US-0132407P.
PR	14-OCT-1999;	99US-0159330P.	PR	05-MAY-1999;	99US-0132484P.
PR	14-OCT-1999;	99US-0159331P.	PR	06-MAY-1999;	99US-0132485P.
PR	14-OCT-1999;	99US-0159637P.	PR	06-MAY-1999;	99US-0132486P.
PR	18-OCT-1999;	99US-0159638P.	PR	07-MAY-1999;	99US-0132487P.
PR	18-OCT-1999;	99US-0159584P.	PR	07-MAY-1999;	99US-0132863P.
PR	21-OCT-1999;	99US-0160741P.	PR	11-MAY-1999;	99US-0134256P.
PR	21-OCT-1999;	99US-0160767P.	PR	14-MAY-1999;	99US-0134218P.
PR	21-OCT-1999;	99US-0160768P.	PR	14-MAY-1999;	99US-0134219P.
PR	21-OCT-1999;	99US-0160770P.	PR	14-MAY-1999;	99US-0134221P.
PR	21-OCT-1999;	99US-0160814P.	PR	14-MAY-1999;	99US-0134370P.
PR	21-OCT-1999;	99US-0160815P.	PR	18-MAY-1999;	99US-0134768P.
PR	22-OCT-1999;	99US-0160980P.	PR	19-MAY-1999;	99US-0134941P.
PR	22-OCT-1999;	99US-0160981P.	PR	20-MAY-1999;	99US-0135124P.
PR	22-OCT-1999;	99US-0160989P.	PR	21-MAY-1999;	99US-0135353P.
PR	25-OCT-1999;	99US-0161404P.	PR	24-MAY-1999;	99US-0135629P.
PR	25-OCT-1999;	99US-0161405P.	PR	25-MAY-1999;	99US-0136021P.
PR	25-OCT-1999;	99US-0161406P.	PR	27-MAY-1999;	99US-0136392P.
PR	26-OCT-1999;	99US-0161359P.	PR	28-MAY-1999;	99US-0136782P.
PR	26-OCT-1999;	99US-0161360P.	PR	01-JUN-1999;	99US-0137222P.
PR	26-OCT-1999;	99US-0161361P.	PR	03-JUN-1999;	99US-0137528P.
PR	28-OCT-1999;	99US-0161920P.	PR	04-JUN-1999;	99US-0137502P.
PR	28-OCT-1999;	99US-0161992P.	PR	07-JUN-1999;	99US-0137724P.
PR	28-OCT-1999;	99US-0161993P.	PR	08-JUN-1999;	99US-0138094P.
PR	29-OCT-1999;	99US-0162142P.	PR	10-JUN-1999;	99US-0138540P.
Query Match 55.6%; Score 5; DB 3; Length 368;					99US-0138847P.
Best Local Similarity 100.0%; Pred.No. 6.4e-02;					99US-0139119P.
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					99US-0139452P.
QY	4 DTFYY 8		PR	16-JUN-1999;	99US-0139453P.
			PR	17-JUN-1999;	99US-0139459P.
Db	326 DTFYY 330		PR	18-JUN-1999;	99US-0139454P.
			PR	18-JUN-1999;	99US-0139455P.
			PR	18-JUN-1999;	99US-0139456P.
			PR	18-JUN-1999;	99US-0139457P.
RESULT 138			PR	18-JUN-1999;	99US-0139458P.
AAG28319			PR	18-JUN-1999;	99US-0139459P.
ID	AAG28319 standard; protein; 370 AA.		PR	18-JUN-1999;	99US-0139460P.
XX	AC		PR	18-JUN-1999;	99US-0139461P.
AC	AAG28319;		PR	18-JUN-1999;	99US-0139462P.
XX	DT		PR	18-JUN-1999;	99US-0139463P.
DT	17-OCT-2000 (first entry)		PR	18-JUN-1999;	99US-0139750P.
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 33492.		PR	18-JUN-1999;	99US-0139763P.
DE	Protein identification; signal transduction pathway; metabolic pathway;		PR	21-JUN-1999;	99US-0139817P.
KW	hybridisation assay; genetic mapping; gene expression control; promoter;		PR	22-JUN-1999;	99US-0139899P.
KW	termination sequence.		PR	23-JUN-1999;	99US-0140353P.
XX	XX		PR	23-JUN-1999;	99US-0140354P.
OS	Arabidopsis thaliana.		PR	24-JUN-1999;	99US-0140695P.
PN	EP1033405-A2.		PR	28-JUN-1999;	99US-0140823P.
XX	PD		PR	29-JUN-1999;	99US-0140991P.
XX	06-SEP-2000.		PR	30-JUN-1999;	99US-0141287P.
XX	25-FEB-2000; 2000EP-00301439.		PR	01-JUL-1999;	99US-0141842P.
PR	25-FEB-1999;	99US-0121825P.	PR	02-JUL-1999;	99US-0142154P.
PR	05-MAR-1999;	99US-0123180P.	PR	06-JUL-1999;	99US-0142055P.
PR	09-MAR-1999;	99US-0123548P.	PR	08-JUL-1999;	99US-0142390P.
PR	23-MAR-1999;	99US-0125788P.	PR	09-JUL-1999;	99US-0142803P.
PR	25-MAR-1999;	99US-0126264P.	PR	12-JUL-1999;	99US-0142920P.
PR	29-MAR-1999;	99US-0126785P.	PR	13-JUL-1999;	99US-0142977P.
PR	01-APR-1999;	99US-0127462P.	PR	14-JUL-1999;	99US-0143542P.
PR	06-APR-1999;	99US-0128234P.	PR	15-JUL-1999;	99US-0144005P.
PR	08-APR-1999;	99US-0128714P.	PR	16-JUL-1999;	99US-0144085P.
PR	16-APR-1999;	99US-0129845P.	PR	16-JUL-1999;	99US-0144086P.
PR	19-APR-1999;	99US-0130077P.	PR	19-JUL-1999;	99US-0144325P.
			PR	19-JUL-1999;	99US-0144331P.
			PR	19-JUL-1999;	99US-0144332P.
			PR	19-JUL-1999;	99US-0144333P.
			PR	19-JUL-1999;	99US-0144334P.
			PR	19-JUL-1999;	99US-0144335P.

PR 20-JUL-1999; 99US-0144352P.
 PR 20-JUL-1999; 99US-0144632P.
 PR 20-JUL-1999; 99US-0144884P.
 PR 21-JUL-1999; 99US-0144814P.
 PR 21-JUL-1999; 99US-0145086P.
 PR 21-JUL-1999; 99US-0145088P.
 PR 22-JUL-1999; 99US-0145085P.
 PR 22-JUL-1999; 99US-0145087P.
 PR 22-JUL-1999; 99US-0145089P.
 PR 22-JUL-1999; 99US-0145192P.
 PR 23-JUL-1999; 99US-0145145P.
 PR 23-JUL-1999; 99US-0145218P.
 PR 23-JUL-1999; 99US-0145224P.
 PR 26-JUL-1999; 99US-0145276P.
 PR 27-JUL-1999; 99US-0145913P.
 PR 27-JUL-1999; 99US-0145918P.
 PR 27-JUL-1999; 99US-0145919P.
 PR 28-JUL-1999; 99US-0145951P.
 PR 02-AUG-1999; 99US-0146386P.
 PR 02-AUG-1999; 99US-0146388P.
 PR 02-AUG-1999; 99US-0146389P.
 PR 03-AUG-1999; 99US-0147038P.
 PR 04-AUG-1999; 99US-0147204P.
 PR 04-AUG-1999; 99US-0147302P.
 PR 05-AUG-1999; 99US-0147182P.
 PR 05-AUG-1999; 99US-0147260P.
 PR 06-AUG-1999; 99US-0147303P.
 PR 06-AUG-1999; 99US-0147416P.
 PR 09-AUG-1999; 99US-0147493P.
 PR 09-AUG-1999; 99US-0147935P.
 PR 10-AUG-1999; 99US-0148171P.
 PR 11-AUG-1999; 99US-0148319P.
 PR 12-AUG-1999; 99US-0148341P.
 PR 13-AUG-1999; 99US-0148565P.
 PR 13-AUG-1999; 99US-0148684P.
 PR 16-AUG-1999; 99US-0149368P.
 PR 17-AUG-1999; 99US-0149175P.
 PR 18-AUG-1999; 99US-0149426P.
 PR 20-AUG-1999; 99US-0149722P.
 PR 20-AUG-1999; 99US-0149723P.
 PR 20-AUG-1999; 99US-0149929P.
 PR 23-AUG-1999; 99US-0149902P.
 PR 23-AUG-1999; 99US-0149910P.
 PR 25-AUG-1999; 99US-0150566P.
 PR 26-AUG-1999; 99US-0150884P.
 PR 27-AUG-1999; 99US-0151065P.
 PR 27-AUG-1999; 99US-0151066P.
 PR 27-AUG-1999; 99US-0151080P.
 PR 30-AUG-1999; 99US-0151303P.
 PR 31-AUG-1999; 99US-0151438P.
 PR 01-SEP-1999; 99US-0151930P.
 PR 07-SEP-1999; 99US-0152363P.
 PR 10-SEP-1999; 99US-0153070P.
 PR 13-SEP-1999; 99US-0153758P.
 PR 15-SEP-1999; 99US-0154018P.
 PR 16-SEP-1999; 99US-0154039P.
 PR 20-SEP-1999; 99US-0154779P.
 PR 22-SEP-1999; 99US-0155139P.
 PR 23-SEP-1999; 99US-0155486P.
 PR 24-SEP-1999; 99US-0155659P.
 PR 28-SEP-1999; 99US-0156458P.
 PR 23-SEP-1999; 99US-0156596P.
 PR 04-OCT-1999; 99US-0157117P.
 PR 05-OCT-1999; 99US-0157753P.
 PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158029P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.
 PR 14-OCT-1999; 99US-0159330P.

PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 28-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161992P.
 PR 29-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 55.8%; Score 5; DB 3; Length 370;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFY 8
 |||||
 Db 328 DTFY 332

RESULT 139

ADH87165

ID ADH87165 standard; protein; 370 AA.

XX ADH87165;

XX 22-APR-2004 (first entry)

XX Enterococcus faecalis polypeptide #1645.

XX Enterococcus faecalis infection; transcription regulatory element;
 antibacterial.

XX Enterococcus faecalis.

XX US6617156-B1.

XX 09-SEP-2003.

XX 13-AUG-1998; 98US-00134000.

XX 15-AUG-1997; 97US-0055778P.

XX (DOUC/) DOUCETTE-STAMM L A.
 (BUSH/) BUSH D.

XX Doucette-Stamm LA, Bush D;

XX WPI; 2003-895394/82.

XX N-PSDB; ADH83760.

XX New nucleic acid comprising a sequence encoding an Enterococcus faecalis
 polypeptide, useful for preparing a composition for diagnosing or
 treating E. faecalis infection.

XX Disclosure; SEQ ID NO 5050; 193pp; English.

XX The invention relates to Enterococcus faecalis polynucleotides and
 polypeptides. The invention also relates to a recombinant expression
 vector comprising a polynucleotide operably linked to a transcription

CC regulatory element, a cell comprising a recombinant vector, a method for
CC producing an E. faecalis polypeptide, an isolated nucleic acid comprising
CC a sequence not given in the specification, a recombinant vector
CC comprising the nucleic acid and a cell comprising the recombinant vector.
CC The polynucleotides can be used to detect the presence of E. faecalis in
CC a sample. The sequences are useful for preparing a composition for
CC diagnosing or treating Enterococcus faecalis infection. This sequence
CC represents an E. faecalis polypeptide of the invention.
XX
SQ Sequence 370 AA;

Query Match 55.6%; Score 5; DB 7; Length 370;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
DB 145 KVDDT 149
|||||

RESULT 140
AAB08467
ID AAB08467 standard; protein; 373 AA.
XX
AC AAB08467;
XX
XX
DT 20-DEC-2000 (first entry)
XX
DE Amino acid sequence of a lysophosphatidic acid acetyltransferase.

XX
KW Lysophosphatidic acid acetyltransferase; LPAAT; transgenic plant;
KW triacylglycerol; oil content.
XX
OS Glycine max.
XX
PN WO200049156-A2.
XX
PD 24-AUG-2000.
XX
PF 22-FEB-2000; 2000WO-US004526.
XX
PR 22-FEB-1999; 99US-0121119P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ, Ripp KG;
XX
DR WPI: 2000-558300/51.
DR N-PSDB; AAA64189.
XX
PT New nucleic acid fragment encoding a lysophosphatidic acid
PT acetyltransferase (LPAAT) isozyme, useful for creating transgenic plants
PT which encode LPAAT at higher or lower levels than normal.
XX
XX Claim 10; Page 82-83; 102pp; English.

PS The present sequence represents a lysophosphatidic acid acetyltransferase
CC (LPAAT) isoenzyme. The nucleic acid may be used to create transgenic
CC plants which encode LPAAT at higher or lower levels than normal or in
CC cell types or developmental stages in which they are not normally found.
CC This would have the effect of altering the level of specific
CC triacylglycerols in those cells, for e.g. overexpression of an LPAAT
CC similar to the maize LPAAT will result in higher oil content in the seed,
CC stem and leaf. LPAAT chimeric genes may be used for co-suppression of
CC genes encoding LPAAT. The polynucleotides may also be used as probes for
CC genetically and physically mapping the genes that are a part of, and as
CC markers for traits linked to those genes
XX
SQ Sequence 373 AA;

Query Match 55.6%; Score 5; DB 3; Length 373;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
DB 56 VDDTF 60
|||||

RESULT 141
ADD02198
ID ADD02198 standard; protein; 378 AA.
XX
AC ADD02198;
XX
DT 01-JAN-2004 (first entry)
XX
DE B2L viral envelope protein #1.
XX
KW B2L; viral envelope protein; Parapox virus; cell proliferative disorder;
KW immune response; inflammatory response; cancer; immunostimulant;
KW immunosuppressive; antiinflammatory; cytostatic.

XX
OS Parapoxvirus ovis strain NZ2.
XX
PN US2003109483-A1.
XX
PD 12-JUN-2003.
XX
PF 06-DEC-2002; 2002US-00313332.
XX
PR 07-DEC-2001; 2001US-0336694P.
XX
PA (CASS/) CASSELL D.
PA (TEPP/) TEPPER J S.
PA (SAMU/) SAMUELS I.
PA (DUBO/) DUBOIS-STRINGFELLOW N.

XX
PI Cassell D, Tepper JS, Samuels I, Dubois-Stringfellow N;
XX
DR WPI: 2003-801275/75.
DR N-PSDB; ADD02199.

PT Enhancing an immune response to endogenous antigens e.g. for treating
PT cancer, comprises administering a B2L Parapox viral envelope protein.
XX
XX Disclosure; SEQ ID NO 1; 22pp; English.

XX The invention relates to a method for enhancing an immune response to
CC endogenous antigens comprising administering a B2L viral envelope protein
CC of a Parapox virus to a subject. The method is used to enhance an immune
CC response to endogenous antigens, associated with a cell proliferative
CC disorder or infectious pathogens. The method is used to treat a patient
CC having a cell proliferative disorder, or to elicit an immune or
CC inflammatory response in a subject. The method is also used for
CC identifying compounds with the ability to modify a subject's immune
CC and/or inflammatory response. The method is used to treat cancer and can
CC enhance a subject's immune response to non-administered antigens. This
CC sequence represents a B2L protein of the invention. Note: The
CC specification states that this sequence is encoded by the DNA displayed
CC in SEQ ID NO:2, but this does not appear to be the case.

SQ Sequence 378 AA;
Query Match 55.6%; Score 5; DB 7; Length 378;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
DB 325 VDDTF 329
|||||

RESULT 142
ADD02200
ID ADD02200 standard; protein; 378 AA.

XX AC ADD02200;
 XX DT 01-JAN-2004 (first entry)
 XX DE B2L viral envelope protein #2.
 XX KW B2L; viral envelope protein; Parapox virus; cell proliferative disorder;
 XX KW immune response; inflammatory response; cancer; immunostimulant;
 XX KW immunosuppressive; antiinflammatory; cytostatic.
 XX OS Parapoxvirus ovis strain D1701.
 XX PN US2003109483-A1.
 XX PD 12-JUN-2003.
 XX PF 06-DEC-2002; 2002US-00313332.
 XX PR 07-DEC-2001; 2001US-0336694P.
 XX PA (CASS/) CASSELL D.
 XX PA (TEPP/) TEPPER J S.
 XX PA (SAMU/) SAMUELS I.
 XX PA (DUBO/) DUBOIS-STRINGFELLOW N.
 XX PI Cassell D, Tepper JS, Samuels I, Dubois-Stringfellow N;
 XX DR WPI; 2003-801275/75.
 XX DR N-PSDB; ADD02201.
 XX PT Enhancing an immune response to endogenous antigens e.g. for treating
 XX PT cancer, comprises administering a B2L Parapox viral envelope protein.
 XX PS Disclosure; SEQ ID NO 3; 22pp; English.
 XX CC The invention relates to a method for enhancing an immune response to
 XX CC endogenous antigens comprising administering a B2L viral envelope protein
 XX CC of a Parapox virus to a subject. The method is used to enhance an immune
 XX CC response to endogenous antigens, associated with a cell proliferative
 XX CC disorder or infectious pathogens. The method is used to treat a patient
 XX CC having a cell proliferative disorder, or to elicit an immune or
 XX CC inflammatory response in a subject. The method is also used for
 XX CC identifying compounds with the ability to modify a subject's immune
 XX CC and/or inflammatory response. The method is used to treat cancer and can
 XX CC enhance a subject's immune response to non-administered antigens. This
 XX CC sequence represents a B2L protein of the invention.
 XX SQ Sequence 378 AA;
 Query Match 55.6%; Score 5; DB 7; Length 378;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTF 6
 Db 325 VDDTF 329
 RESULT 143
 ADJ63965
 ID ADJ63965 standard; protein; 378 AA.
 XX AC ADJ63965;
 XX DT 06-MAY-2004 (first entry)
 XX DE Parapox virus B2L protein from parapox virus from strain D1701.
 XX KW Immune response; B2L viral envelope protein; Parapox virus; adjuvant;
 XX KW PP30 protein; virucide; cytostatic; tuberculostatic; virucide; anti-HIV;
 XX KW vaccine; tumour; flu; tuberculosis; respiratory syncytial virus; anthrax;
 XX KW HIV infection.

XX OS Orf virus; D1701.
 XX PH Key Location/Qualifiers
 XX FT Misc-difference 9 /note= "Encoded by GTG"
 XX FT
 XX PN US2003194737-A1.
 XX PD 16-OCT-2003.
 XX PF 15-APR-2003; 2003US-00414609.
 XX PR 15-APR-2002; 2002US-00123058.
 XX PA (JOHN/) JOHNSTON S A.
 XX PA (MCGU/) MCGUIRE M J.
 XX PI Johnston SA, McGuire MJ;
 XX DR WPI; 2003-844451/78.
 XX PT Enhancing an immune response to an antigen by administering to a subject
 XX PT mammal a B2L viral envelope protein of a Parapox virus and an antigen and
 XX PT detecting a resultant enhanced, specific immune response to the antigen.
 XX PS Disclosure; SEQ ID NO 4; 10pp; English.
 XX CC This invention relates to a novel composition for enhancing an immune
 XX CC response to an antigen comprising administering to a subject mammal a B2L
 XX CC viral envelope protein of a Parapox virus and an antigen, and detecting a
 XX CC resultant enhanced, specific immune response to the antigen. The B2L
 XX CC protein is unassociated with other envelope components naturally
 XX CC associated with the B2L protein in the virus, and acts as adjuvant to
 XX CC enhance the immune response to the antigen. The invention also discloses
 XX CC a pharmaceutical composition for enhancing an immune response to an
 XX CC antigen, the composition preferably comprises the PP30 protein of a
 XX CC Parapox virus or the nucleic acid encoding the protein and the antigen or
 XX CC the nucleic acid encoding the antigen. The composition of the invention or
 XX CC may have virucide, cytostatic, tuberculostatic, virucide or anti-HIV
 XX CC activity and may be used as a vaccine. The protein is PP30 protein of a
 XX CC Parapox virus. The method of the invention is useful for enhancing an
 XX CC immune response to an antigen for treating or preventing tumour, flu,
 XX CC tuberculosis, or respiratory syncytial virus, anthrax or HIV infections.
 XX CC The present sequence represents the parapoxvirus B2L viral envelope
 XX CC protein from Parapox virus strain D1701 used to create the composition of
 XX CC the invention.
 XX SQ Sequence 378 AA;
 Query Match 55.6%; Score 5; DB 7; Length 378;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTF 6
 Db 325 VDDTF 329
 RESULT 144
 ADJ63963
 ID ADJ63963 standard; protein; 378 AA.
 XX AC ADJ63963;
 XX DT 06-MAY-2004 (first entry)
 XX DE Parapox virus B2L protein.
 XX KW Immune response; B2L viral envelope protein; Parapox virus; adjuvant;
 XX KW PP30 protein; virucide; cytostatic; tuberculostatic; virucide; anti-HIV;
 XX KW vaccine; tumour; flu; tuberculosis; respiratory syncytial virus; anthrax;
 XX KW HIV infection; virus.

XX OS Orf virus; OV NZ2.
 XX PF US2003194737-A1.
 XX PN
 XX PD 16-OCT-2003.
 XX PF 15-APR-2003; 2003US-00414609.
 XX PR 15-APR-2002; 2002US-00123058.
 XX PA (JOHN/) JOHNSTON S A.
 XX PA (MCGU/) MCGUIRE M J.
 XX PI Johnston SA, Mcguire MJ;
 XX XX WPI; 2003-844451/78.
 XX DR N-PSDB; ADJ63962.
 XX XX
 PT Enhancing an immune response to an antigen by administering to a subject
 PT mammal a B2L viral envelope protein of a Parapox virus and an antigen and
 PT detecting a resultant enhanced, specific immune response to the antigen.
 XX
 PS Disclosure; SEQ ID NO 2; 10pp; English.
 XX
 CC This invention relates to a novel composition for enhancing an immune
 CC response to an antigen comprising administering to a subject mammal a B2L
 CC viral envelope protein of a Parapox virus and an antigen, and detecting a
 CC resultant enhanced, specific immune response to the antigen. The B2L
 CC protein is unassociated with other envelope components naturally
 CC associated with the B2L protein in the virus, and acts as adjuvant to
 CC enhance the immune response to the antigen. The invention also discloses
 CC a pharmaceutical composition for enhancing an immune response to an
 CC antigen, the composition preferably comprises the PP30 protein of a
 CC Parapox virus or the nucleic acid encoding the protein and the antigen or
 CC the nucleic acid encoding the antigen. The composition of the invention
 CC may have virucide, cytostatic, tuberculostatic, virucide or anti-HIV
 CC activity and may be used as a vaccine. The protein is PP30 protein of a
 CC Parapox virus. The method of the invention is useful for enhancing an
 CC immune response to an antigen for treating or preventing tumour, flu,
 CC tuberculosis, or respiratory syncytial virus, anthrax or HIV infections.
 CC The present sequence represents the parapoxvirus B2L viral envelope
 CC protein used to create the composition of the invention.
 XX
 SQ Sequence 378 AA;
 Query Match 55.6%; Score 5; DB 7; Length 378;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTF 6
 DB 325 VDDTF 329
 RESULT 145
 ADG46065
 ID ADG46065 standard; protein; 378 AA.
 XX
 AC ADG46065;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Parapoxvirus B2WL polypeptide #1.
 XX
 KW Immune system stimulation; immunostimulatory polypeptide; Parapoxvirus;
 KW B2WL; PP30; dendritic cell accumulation; skin; adjuvant activity;
 KW immune response; gene vaccine; immunostimulant.
 XX
 OS Orf virus; strain D1701.
 XX
 PN US2003194695-A1.
 XX

PD 16-OCT-2003.
 XX
 PF 15-APR-2002; 2002US-00123058.
 XX
 PR 15-APR-2002; 2002US-00123058.
 XX
 PA (JOHN/) JOHNSTON S A.
 PA (MCGU/) MCGUIRE M J.
 XX
 PI Johnston SA, Mcguire MJ;
 XX
 XX WPI; 2004-041264/04.
 DR N-PSDB; ADG46064.
 XX
 XX Stimulation of an immune system involves use of an immunostimulatory
 PT polypeptide from parapox virus.
 XX
 PS Claim 3; SEQ ID NO 2; 26pp; English.
 XX
 CC The present invention relates to a method of stimulation the immune
 CC system. The method involves administration of an immunostimulatory
 CC polypeptide from Parapoxvirus. Two immunostimulatory peptides are
 CC identified in the present invention and designated B2WL and PP30. Also
 CC disclosed are the polynucleotide sequences encoding them. The B2WL
 CC polynucleotide induces dendritic cell accumulation when expressed in
 CC skin, and the PP30 polynucleotide exhibits adjuvant activity in the
 CC absence of stimulating dendritic cell accumulation at the site of
 CC inoculation. When co-inoculated, both genes acts as adjuvants in
 CC stimulating an immune response. The sequences of the invention are useful
 CC for stimulation of an immune system in a subject, preferably mammal,
 CC especially human or mouse. The method enhances immune response induced by
 CC gene vaccines. The present sequence represents Parapoxvirus B2WL
 CC polypeptide.
 XX
 SQ Sequence 378 AA;
 Query Match 55.6%; Score 5; DB 8; Length 378;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTF 6
 DB 325 VDDTF 329
 RESULT 146
 ADG46067
 ID ADG46067 standard; protein; 378 AA.
 XX
 AC ADG46067;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Parapoxvirus B2WL polypeptide #2.
 XX
 KW Immune system stimulation; immunostimulatory polypeptide; Parapoxvirus;
 KW B2WL; PP30; dendritic cell accumulation; skin; adjuvant activity;
 KW immune response; gene vaccine; immunostimulant.
 XX
 OS Orf virus; strain D1701.
 XX
 PN US2003194695-A1.
 XX
 PD 16-OCT-2003.
 XX
 PF 15-APR-2002; 2002US-00123058.
 XX
 PR 15-APR-2002; 2002US-00123058.
 XX
 XX (JOHN/) JOHNSTON S A.
 XX (MCGU/) MCGUIRE M J.
 XX
 PI Johnston SA, Mcguire MJ;
 XX

XX WPI; 2004-041264/04.
 DR N-PSDB; ADG46066.
 XX
 PT Stimulation of an immune system involves use of an immunostimulatory
 PT polypeptide from parapox virus.
 XX
 PS Claim 3; SEQ ID NO 4; 26pp; English.
 XX
 CC The present invention relates to a method of stimulation the immune
 CC system. The method involves administration of an immunostimulatory
 CC polypeptide from Parapoxvirus. Two immunostimulatory peptides are
 CC identified in the present invention and designated B2WL and PP30. Also
 CC polynucleotide are the polynucleotide sequences encoding them. The B2WL
 CC polynucleotide induces dendritic cell accumulation when expressed in
 CC skin, and the PP30 polynucleotide exhibits adjuvant activity in the
 CC absence of stimulating dendritic cell accumulation at the site of
 CC inoculation. When co-inoculated, both genes acts as adjuvants in
 CC stimulating an immune response. The sequences of the invention are useful
 CC for stimulation of an immune system in a subject, preferably mammal,
 CC especially human or mouse. The method enhances immune response induced by
 CC gene vaccines. The present sequence represents Parapoxvirus B2WL
 CC polypeptide.
 XX
 SQ Sequence 378 AA;

Query Match 55.6%; Score 5; DB 8; Length 378;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 Db 325 VDDTF 329

RESULT 147
 ADK01346
 ID ADK01348 standard; protein; 378 AA.
 XX
 AC ADK01348;
 XX
 DT 03-JUN-2004 (first entry)
 DE D1701 B2L protein.
 XX
 KW B2L viral envelope protein; Parapoxvirus; immune response;
 KW tumour antigen; flu; tuberculosis; respiratory syncytial virus; anthrax;
 KW HIV; immunostimulant; virucide; anti-HIV; D1701.
 XX
 OS Parapoxvirus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 9 /note= "Encoded by GTG"
 FT
 XX US2004054159-A1.
 XX
 PD 18-MAR-2004.
 XX
 PF 15-APR-2003; 2003US-00414759.
 XX
 PR 07-DEC-2001; 2001US-0336694P.
 PR 06-DEC-2002; 2002WO-US038971.
 XX
 PA (JOHN/) JOHNSTON S A.
 PA (MCGU/) MCGUIRE M J.
 XX
 PI Johnston SA, Mcguire MJ;
 XX
 XX WPI; 2004-247782/23.
 DR N-PSDB; ADK01347.
 XX
 PT Enhancing an immune response to an antigen, useful in preventing and/or

PT treating flu, tuberculosis, respiratory syncytial virus, anthrax and HIV,
 PT by administering B2L viral envelope protein of a Parapox virus and an
 PT antigen.
 XX
 PS Disclosure; SEQ ID NO 4; 8pp; English.
 XX
 CC The invention relates to a method of enhancing an immune response to an
 CC antigen comprising administering to a mammal an amount of a B2L viral
 CC envelope protein of a Parapoxvirus and an antigen. The B2L protein acts
 CC as an adjuvant to enhance the immune response to the antigen. The antigen
 CC is a tumour antigen administered as an attenuated or killed pathogen
 CC comprising the antigen. The B2L protein and the antigen are administered
 CC sequentially or simultaneously as a fusion protein. The method and
 CC composition are useful in enhancing an immune response to an antigen such
 CC as a tumour antigen. The composition is useful in preventing and/or
 CC treating flu, tuberculosis, respiratory syncytial virus, anthrax and HIV.
 CC This sequence represents the D1701 B2L protein, used in the scope of the
 CC invention.
 XX
 SQ Sequence 378 AA;

Query Match 55.6%; Score 5; DB 8; Length 378;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 Db 325 VDDTF 329

RESULT 148
 ADK01346
 ID ADK01346 standard; protein; 378 AA.
 XX
 AC ADK01346;
 XX
 DT 03-JUN-2004 (first entry)
 DE Envelope antigen p37K polypeptide.
 XX
 KW B2L viral envelope protein; Parapoxvirus; immune response;
 KW tumour antigen; flu; tuberculosis; respiratory syncytial virus; anthrax;
 KW HIV; envelope antigen; p37K; immunostimulant; virucide; anti-HIV.
 XX
 OS Parapoxvirus.
 XX
 PN US2004054159-A1.
 XX
 PD 18-MAR-2004.
 XX
 PF 15-APR-2003; 2003US-00414759.
 XX
 PR 07-DEC-2001; 2001US-0336694P.
 PR 06-DEC-2002; 2002WO-US038971.
 XX
 PA (JOHN/) JOHNSTON S A.
 PA (MCGU/) MCGUIRE M J.
 XX
 PI Johnston SA, Mcguire MJ;
 XX
 XX WPI; 2004-247782/23.
 DR N-PSDB; ADK01345.
 XX
 PT Enhancing an immune response to an antigen, useful in preventing and/or
 PT treating flu, tuberculosis, respiratory syncytial virus, anthrax and HIV,
 PT by administering B2L viral envelope protein of a Parapox virus and an
 PT antigen.
 XX
 PS Disclosure; SEQ ID NO 2; 8pp; English.
 XX
 CC The invention relates to a method of enhancing an immune response to an
 CC antigen comprising administering to a mammal an amount of a B2L viral
 CC envelope protein of a Parapoxvirus and an antigen. The B2L protein acts

CC as an adjuvant to enhance the immune response to the antigen. The antigen
CC is a tumour antigen administered as an attenuated or killed pathogen
CC comprising the antigen. The B2L protein and the antigen are administered
CC sequentially or simultaneously as a fusion protein. The method and
CC composition are useful in enhancing an immune response to an antigen such
CC as a tumour antigen. The composition is useful in preventing and/or
CC treating flu, tuberculosis, respiratory syncytial virus, anthrax and HIV.
CC This sequence represents the envelope antigen p37K, used in the scope of
CC the invention.

XX SQ Sequence 378 AA;

Query Match 55.6%; Score 5; DB 8; Length 378;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 325 VDDTF 329

RESULT 149

ADT99512
ID ADT99512 standard; protein; 378 AA.

XX AC ADT99512;

XX DT 13-JAN-2005 (first entry)

XX DE Parapox ovis strain N22 B2L viral envelope protein.

XX KW Immune response; B2L; viral envelope protein; immunostimulatory protein;
KW PP30; tumour antigen; flu; tuberculosis; respiratory syncytial virus;
KW anthrax; vaccine; immunostimulant; virucide; antitubercular;
KW tuberculostatic; anti-HIV.

XX OS Parapox ovis.

XX PN US2004213807-A1.

XX PD 28-OCT-2004.

XX PF 28-MAY-2004; 2004US-00857546.

XX PR 07-DEC-2001; 2001US-0336694P.

XX PR 15-APR-2002; 2002US-00123058.

XX PR 06-DEC-2002; 2002WO-US038971.

XX PR 15-APR-2003; 2003US-00414609.

XX (JOHN/) JOHNSTON S A.

PA (MCGU/) MCGUIRE M J.

XX PI Johnston SA, Mcguire MJ;

XX WPI; 2004-765577/75.

XX DR N-PSDB; ADT99511.

XX PT Enhancing an immune response to an antigen comprises administering a
PT Parapox B2L protein and an antigen to the mammal.

XX PS Disclosure; SEQ ID NO 2; 10pp; English.

XX CC The present invention provides a method for enhancing a subject's immune
CC response to an administered antigen and/or an active component of a
CC vaccine by administering an amount of a B2L viral envelope protein and an
CC immunostimulatory protein PP30 of a Parapox virus. The method and
CC composition of the invention is useful for enhancing an immune response
CC to an antigen such as a tumour antigen. The invention is useful as an
CC adjuvant for vaccine for preventing and/or treating flu, tuberculosis,
CC respiratory syncytial virus, anthrax and human immunodeficiency virus
CC (HIV). The invention is also useful in the preparation of vaccine. The
CC present sequence is Parapox ovis B2L viral envelope protein.

SQ Sequence 378 AA;

Query Match 55.6%; Score 5; DB 8; Length 378;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 325 VDDTF 329

RESULT 150

ADT99514

ID ADT99514 standard; protein; 378 AA.

XX AC ADT99514;

XX DT 13-JAN-2005 (first entry)

XX DE Parapox ovis strain D1701 B2L viral envelope protein.

XX KW Immune response; B2L; viral envelope protein; immunostimulatory protein;
KW PP30; tumour antigen; flu; tuberculosis; respiratory syncytial virus;
KW anthrax; vaccine; immunostimulant; virucide; antitubercular;
KW tuberculostatic; anti-HIV.

XX OS Parapox ovis.

XX FH Key Location/Qualifiers

FT Misc-difference 9

FT /note= "Encoded by GTG"

XX US2004213807-A1.

XX PD 28-OCT-2004.

XX PF 28-MAY-2004; 2004US-00857546.

XX PR 07-DEC-2001; 2001US-0336694P.

XX PR 15-APR-2002; 2002US-00123058.

XX PR 06-DEC-2002; 2002WO-US038971.

XX PR 15-APR-2003; 2003US-00414609.

XX (JOHN/) JOHNSTON S A.

PA (MCGU/) MCGUIRE M J.

XX PI Johnston SA, Mcguire MJ;

XX WPI; 2004-765577/75.

XX DR N-PSDB; ADT99513.

XX PT Enhancing an immune response to an antigen comprises administering a
PT Parapox B2L protein and an antigen to the mammal.

XX PS Disclosure; SEQ ID NO 4; 10pp; English.

XX CC The present invention provides a method for enhancing a subject's immune
CC response to an administered antigen and/or an active component of a
CC vaccine by administering an amount of a B2L viral envelope protein and an
CC immunostimulatory protein PP30 of a Parapox virus. The method and
CC composition of the invention is useful for enhancing an immune response
CC to an antigen such as a tumour antigen. The invention is useful as an
CC adjuvant for vaccine for preventing and/or treating flu, tuberculosis,
CC respiratory syncytial virus, anthrax and human immunodeficiency virus
CC (HIV). The invention is also useful in the preparation of vaccine. The
CC present sequence is Parapox ovis B2L viral envelope protein.

XX SQ Sequence 378 AA;

Query Match 55.6%; Score 5; DB 8; Length 378;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
Db 325 VDDTF 329

Search completed: May 17, 2006, 06:20:35
Job time : 279 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2006, 06:24:29 ; Search time 24.5 Seconds
(without alignments)
35.345 Million cell updates/sec

Title: US-10-764-985-2

Perfect score: 9

Sequence: 1 KVDDTFYV 9

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR 80.*
1: Pirl.*
2: Pirl.*
3: Pirl.*
4: Pirl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	100.0	150	1 WZVZB1	vaccinia virus 18K
2	9	100.0	150	2 H36837	D8L protein - vari
3	9	100.0	150	2 H28446	hypothetical prote
4	9	100.0	150	2 F72151	Bl4L protein - var
5	7	77.8	770	2 S75042	hypothetical prote
6	6	66.7	206	2 C36365	transforming prote
7	6	66.7	400	2 B81169	tryptophan synthas
8	6	66.7	400	2 H81936	probable tryptopha
9	6	66.7	482	2 S31478	alpha-amylase (EC
10	6	66.7	485	2 C86143	hypothetical prote
11	6	66.7	535	2 T47790	hypothetical prote
12	6	66.7	1256	2 T26101	hypothetical prote
13	6	66.7	1286	2 T16507	hypothetical prote
14	5	55.6	72	2 S53874	endonuclease precu
15	5	55.6	90	2 D97355	hypothetical prote
16	5	55.6	118	2 S25001	ubiquitin/ribosoma
17	5	55.6	128	2 G85757	hypothetical prote
18	5	55.6	134	2 A59055	phospholipase A2 (
19	5	55.6	134	2 AC0079	hypothetical prote
20	5	55.6	139	2 I53298	cellular retinoic
21	5	55.6	140	2 T50420	shk1 kinase-bindin
22	5	55.6	156	1 UQ070A	ubiquitin / riboso
23	5	55.6	156	2 S25305	ubiquitin / riboso
24	5	55.6	211	2 A75176	dolichyl-phosphate
25	5	55.6	263	2 A83956	flagellar hook prote
26	5	55.6	264	2 B96612	hypothetical prote
27	5	55.6	275	2 C83482	2-phosphonacetald
28	5	55.6	279	2 H75326	tRNA (guanine-N1) -
29	5	55.6	284	2 T21974	hypothetical prote

30	5	55.6	284	2 AG3556	heat resistant agg
31	5	55.6	297	2 T09542	endonuclease G (EC
32	5	55.6	300	2 B56118	vetispiradiene syn
33	5	55.6	304	2 AH0763	probable transcrip
34	5	55.6	306	2 G97132	uncharacterized ph
35	5	55.6	311	2 T49312	hypothetical prote
36	5	55.6	313	2 AD1285	glycerate dehydrog
37	5	55.6	313	2 AG1656	glycerate dehydrog
38	5	55.6	313	2 S51729	NSP3 protein - hum
39	5	55.6	315	2 AG0503	probable regulator
40	5	55.6	316	1 F64966	probable transcrip
41	5	55.6	316	2 A99881	probable transcrip
42	5	55.6	316	2 F85826	probable transcrip
43	5	55.6	317	2 T29624	hypothetical prote
44	5	55.6	329	1 NCBYN1	nuclease NUC1 (EC
45	5	55.6	330	2 T33944	hypothetical prote
46	5	55.6	330	2 AI0491	probable membrane
47	5	55.6	331	2 D91184	hypothetical prote
48	5	55.6	331	2 B86031	hypothetical prote
49	5	55.6	331	2 S47782	hypothetical 37.6K
50	5	55.6	350	2 C56118	vetispiradiene syn
51	5	55.6	358	2 AC2367	glucose-1-phosphat
52	5	55.6	372	2 JC1069	nonstructure prote
53	5	55.6	372	2 C83766	adenine glycosylas
54	5	55.6	399	2 G83857	tryptophan synthas
55	5	55.6	406	2 JS0343	tryptophan synthas
56	5	55.6	412	2 JN0319	acid phosphatase (
57	5	55.6	417	2 JC2389	acid phosphatase (
58	5	55.6	422	2 B31776	hypothetical prote
59	5	55.6	425	2 T36585	probable membrane
60	5	55.6	426	2 E86575	phosphate permease
61	5	55.6	426	2 D72049	phosphate permease
62	5	55.6	435	2 G87334	acyl-CoA dehydroge
63	5	55.6	440	2 JS0374	hypothetical 51.6K
64	5	55.6	452	2 H81777	UDP-N-acetylmutamo
65	5	55.6	455	2 D81202	UDP-N-acetylmutamo
66	5	55.6	465	2 T00090	glycosyltransferas
67	5	55.6	468	2 T24724	hypothetical prote
68	5	55.6	475	2 T01260	probable ammonium
69	5	55.6	483	2 JC7179	acid phosphatase (
70	5	55.6	483	2 T47974	hypothetical prote
71	5	55.6	483	2 D86385	hypothetical prote
72	5	55.6	484	2 S40051	starch synthase (E
73	5	55.6	486	2 AB1584	hypothetical prote
74	5	55.6	492	2 A82632	ammonium transport
75	5	55.6	506	2 G90430	conserved hypotet
76	5	55.6	508	2 T22836	hypothetical prote
77	5	55.6	518	2 S49620	phytoene dehydroge
78	5	55.6	518	2 T50745	phytoene dehydroge
79	5	55.6	520	2 A56118	vetispiradiene syn
80	5	55.6	524	2 A32617	phytoene dehydroge
81	5	55.6	528	2 T34417	delayed rectifier
82	5	55.6	535	2 F90418	ABC transporter, p
83	5	55.6	540	2 S54586	probable membrane
84	5	55.6	545	2 T06264	3-dehydroquinatate d
85	5	55.6	547	2 I39593	exaA protein - Aer
86	5	55.6	548	2 T51035	hypothetical prote
87	5	55.6	550	2 T03714	5-epi-aristolochin
88	5	55.6	566	2 D90250	glycogen synthase
89	5	55.6	572	1 ERBP22	DNA-directed DNA p
90	5	55.6	574	2 T37452	68K ankyrin-like p
91	5	55.6	574	2 JQ1811	B17R protein - vac
92	5	55.6	574	2 H42527	B18R protein - vac
93	5	55.6	574	2 A36857	B19R protein - var
94	5	55.6	574	2 T28615	hypothetical prote
95	5	55.6	574	2 C72174	D8R protein - vari
96	5	55.6	579	1 ERBP29	DNA-directed DNA p
97	5	55.6	579	2 S46210	3-dehydroquinatate d
98	5	55.6	617	2 JC5721	vacuolar protein s
99	5	55.6	628	2 T45864	probable tyrosine
100	5	55.6	683	2 AC0741	oligopeptidase B (
101	5	55.6	683	2 AB0217	oligopeptidase B (
102	5	55.6	686	2 C90948	proteinase II (imp

103	5	55.6	686	2	G85796	proteinase II [imp	176	4	44.4	85	2	F96949	hypothetical prote
104	5	55.6	696	2	A12849	GGDEF family prote	177	4	44.4	85	2	AG2583	hypothetical prote
105	5	55.6	696	2	G97626	hypothetical prote	178	4	44.4	85	2	F97664	hypothetical prote
106	5	55.6	705	2	T51034	hypothetical prote	179	4	44.4	85	2	F97365	hypothetical prote
107	5	55.6	724	1	B32571	ribosomal protein	180	4	44.4	86	2	G98244	hypothetical prote
108	5	55.6	735	2	I51901	ribosomal protein	181	4	44.4	86	2	T41003	transcription init
109	5	55.6	735	2	A53300	ribosomal protein	182	4	44.4	87	2	A84679	hypothetical prote
110	5	55.6	739	2	A81430	outer membrane pro	183	4	44.4	87	2	B45823	shiga-like toxin I
111	5	55.6	752	1	A34571	ribosomal protein	184	4	44.4	87	2	S52290	HLA-A30 variant ex
112	5	55.6	752	2	T27276	hypothetical prote	185	4	44.4	87	2	T44104	hypothetical prote
113	5	55.6	778	2	D87965	protein Y63D3A.6b	186	4	44.4	87	2	T18045	hypothetical prote
114	5	55.6	807	2	T00990	hypothetical prote	187	4	44.4	89	1	JN0726	Shiga-like toxin I
115	5	55.6	841	2	S69563	suppressor protein	188	4	44.4	89	1	XVEPH9	Shiga-like toxin c
116	5	55.6	938	2	T01809	hypothetical prote	189	4	44.4	89	1	XVEBBD	Shigella toxin cha
117	5	55.6	955	2	S44622	C50C3.3 protein -	190	4	44.4	89	2	S58344	Shiga-like toxin I
118	5	55.6	956	2	B71468	probable insulinas	191	4	44.4	89	2	F90779	Shiga toxin 2 subu
119	5	55.6	971	2	T39912	conserved hypothet	192	4	44.4	89	2	H85640	Shiga toxin 1 subu
120	5	55.6	971	2	T43656	mating-type switch	193	4	44.4	89	2	E91000	Shiga toxin 1 subu
121	5	55.6	973	2	B89009	protein T27C4.4 [i	194	4	44.4	89	2	G85845	Shiga toxin I subu
122	5	55.6	1045	2	B83393	RND multidrug effl	195	4	44.4	89	2	I69156	Shiga-like toxin I
123	5	55.6	1152	2	AE1852	hypothetical prote	196	4	44.4	89	2	S01033	Shiga-like toxin I
124	5	55.6	1185	2	AG2457	transcription-repa	197	4	44.4	89	2	B53887	Shiga-like toxin I
125	5	55.6	1245	2	D71613	GAF domain protein	198	4	44.4	89	2	A47759	retrovirus-related
126	5	55.6	1269	2	T14476	p51A protein - sli	199	4	44.4	91	2	T28436	hypothetical prote
127	5	55.6	1294	2	S58307	hypothetical 149.2	200	4	44.4	91	2	T15032	hypothetical prote
128	5	55.6	1308	2	E71622	probable membrane	201	4	44.4	91	2	S07895	hypothetical prote
129	5	55.6	1338	2	T40993	protein kinase cek	202	4	44.4	93	2	A60232	T-cell surface gly
130	5	55.6	1361	2	S50943	hypothetical prote	203	4	44.4	93	2	T44779	hypothetical prote
131	5	55.6	1552	2	G86344	T22111.2 protein -	204	4	44.4	94	2	G75143	hypothetical prote
132	5	55.6	1614	2	T29861	hypothetical prote	205	4	44.4	94	2	A81453	ferredoxin Cj033c
133	5	55.6	1679	2	S48385	hypothetical prote	206	4	44.4	96	1	I64010	C4-dicarboxylate t
134	5	55.6	1860	2	T17485	peptide synthetase	207	4	44.4	97	2	S72333	hypothetical prote
135	5	55.6	2025	2	T03884	hypothetical prote	208	4	44.4	97	2	T29534	hypothetical prote
136	5	55.6	3085	2	T00327	polyprotein - infe	209	4	44.4	98	2	S17604	Ig heavy chain V r
137	5	55.6	3871	2	T22812	hypothetical prote	210	4	44.4	98	2	E64763	probable alpha hel
138	5	55.6	10797	2	T30192	probable peptide s	211	4	44.4	98	2	D90680	probable alpha hel
139	4	44.4	25	2	B53415	lectin chain B - I	212	4	44.4	98	2	H85530	hypothetical prote
140	4	44.4	33	2	C64536	hypothetical prote	213	4	44.4	98	2	T14691	hypothetical prote
141	4	44.4	37	2	I56058	cell surface glyco	214	4	44.4	99	2	T09998	12-oxophytodienoat
142	4	44.4	37	2	S21665	S-layer protein -	215	4	44.4	99	2	A5819	nonhistone chromos
143	4	44.4	37	2	E72269	hypothetical prote	216	4	44.4	99	2	AG1090	hypothetical prote
144	4	44.4	38	2	T31381	lebetin 2 isoform	217	4	44.4	99	2	AG3070	hypothetical prote
145	4	44.4	46	2	B81717	hypothetical protei	218	4	44.4	99	2	B98216	hypothetical prote
146	4	44.4	49	2	JH0643	GTP-binding protei	219	4	44.4	100	2	H95366	NADH2 dehydrogenas
147	4	44.4	50	2	A60718	phospholipase A2 h	220	4	44.4	100	2	T49323	hypothetical prote
148	4	44.4	50	2	B60718	phospholipase A2 h	221	4	44.4	101	2	B97800	hypothetical prote
149	4	44.4	53	2	B84236	hypothetical prote	222	4	44.4	101	2	T26137	hypothetical prote
150	4	44.4	58	2	S05489	alpha-amylase (EC	223	4	44.4	103	2	AH2487	hypothetical prote
151	4	44.4	58	2	S76577	hypothetical prote	224	4	44.4	103	2	H9764	conserved hypothet
152	4	44.4	61	2	F98014	hypothetical prote	225	4	44.4	104	1	K9RB	Ig kappa-B9 chain
153	4	44.4	63	2	G84589	hypothetical prote	226	4	44.4	104	2	H51204	hypothetical prote
154	4	44.4	63	2	AD3041	hypothetical prote	227	4	44.4	104	2	T18823	hypothetical prote
155	4	44.4	64	2	H81811	hypothetical prote	228	4	44.4	105	2	S06985	probable nitrogen
156	4	44.4	64	2	T34580	hypothetical prote	229	4	44.4	106	2	E84056	thioredoxin H1 BH3
157	4	44.4	65	2	S51099	MHC class I histoc	230	4	44.4	107	2	B53307	thioredoxin - Stre
158	4	44.4	65	2	A81810	hypothetical prote	231	4	44.4	107	2	A69825	hypothetical prote
159	4	44.4	66	2	S03855	hypothetical prote	232	4	44.4	107	2	A82040	hypothetical prote
160	4	44.4	67	2	I53485	GTP-binding protei	233	4	44.4	107	2	D87337	hypothetical prote
161	4	44.4	67	2	T44097	hypothetical prote	234	4	44.4	108	2	A84658	hypothetical prote
162	4	44.4	67	2	S66426	plasma-sensitive	235	4	44.4	109	2	T17831	hypothetical prote
163	4	44.4	67	2	F97130	probable transcrip	236	4	44.4	110	2	C85063	hypothetical prote
164	4	44.4	69	2	AH2888	hypothetical prote	237	4	44.4	110	2	F89797	hypothetical prote
165	4	44.4	71	2	H65284	conserved hypothet	238	4	44.4	111	2	S69911	Ig V-D-J region (R
166	4	44.4	72	2	A65292	archaeal histone A	239	4	44.4	112	2	S51123	genome polyprotein
167	4	44.4	74	2	B90467	conserved hypothet	240	4	44.4	112	2	A90595	ribosome-binding f
168	4	44.4	76	2	A69033	hypothetical prote	241	4	44.4	112	2	AI3327	hypothetical cytos
169	4	44.4	76	2	T14724	hypothetical prote	242	4	44.4	113	2	G86823	nitrogen regulator
170	4	44.4	80	2	S78295	acyl carrier prote	243	4	44.4	113	2	T06155	hypothetical prote
171	4	44.4	80	2	B84285	hypothetical prote	244	4	44.4	113	2	S09830	hypothetical prote
172	4	44.4	81	2	C72349	acyl carrier prote	245	4	44.4	113	2	G96942	hypothetical prote
173	4	44.4	81	2	C81337	hypothetical prote	246	4	44.4	114	2	S26319	Ig heavy chain V r
174	4	44.4	83	2	B84679	hypothetical prote	247	4	44.4	114	2	T44547	hypothetical prote
175	4	44.4	83	2	F89920	conserved hypothet	248	4	44.4	114	2	T49086	hypothetical prote

249	4	44.4	114	2	E90274	hypothetical prote	322	4	44.4	140	2	T28576	6R protein - vario
250	4	44.4	115	2	S78053	ig heavy chain-V-D	323	4	44.4	140	2	F64516	hypothetical prote
251	4	44.4	115	2	S60397	hypothetical prote	324	4	44.4	140	2	F90342	hypothetical prote
252	4	44.4	115	2	AD3601	hypothetical prote	325	4	44.4	140	2	F97027	hypothetical prote
253	4	44.4	115	2	AB1172	hypothetical prote	326	4	44.4	141	2	S06483	hemoglobin I, extr
254	4	44.4	116	2	E69393	probable erpK prot	327	4	44.4	141	2	T26567	hypothetical prote
255	4	44.4	116	2	A10746	flagellar transcri	328	4	44.4	142	1	F70437	nucleoside-diphosp
256	4	44.4	116	2	H97213	reductase/isomeras	329	4	44.4	142	1	JC5612	troponin I beta -
257	4	44.4	116	2	T05517	absicisic acid-indu	330	4	44.4	142	2	JC5611	troponin I alpha -
258	4	44.4	117	2	JK0053	lysozyme (EC 3.2.1	331	4	44.4	142	2	C70059	hypothetical prote
259	4	44.4	117	2	B97063	uncharacterized pr	332	4	44.4	142	2	H89829	conserved hypotet
260	4	44.4	117	2	AB3201	hypothetical prote	333	4	44.4	142	4	S13768	MHC class I hiatoc
261	4	44.4	118	2	T23280	interphotoreceptor	334	4	44.4	143	2	A95333	hypothetical prote
262	4	44.4	118	2	160377	RNA polymerase II	335	4	44.4	144	2	H82837	conserved hypotet
263	4	44.4	118	2	160377	hypothetical prote	336	4	44.4	144	2	C95308	hypothetical prote
264	4	44.4	118	2	159405	ribosomal protein	337	4	44.4	145	2	B98057	hypothetical prote
265	4	44.4	118	2	G87180	hypothetical prote	338	4	44.4	146	2	I47196	ig heavy chain var
266	4	44.4	119	2	S29887	hypothetical prote	339	4	44.4	146	2	H72167	A35R protein - var
267	4	44.4	119	2	C95877	hypothetical prote	340	4	44.4	146	2	I46506	zona pellucida bin
268	4	44.4	120	2	T17514	ybfg protein - Esc	341	4	44.4	147	2	F98018	flavodoxin [import
269	4	44.4	120	2	A64804	chemotaxis respons	342	4	44.4	147	2	H95150	flavodoxin [import
270	4	44.4	121	2	B69380	hypothetical prote	343	4	44.4	147	2	A43547	T-cell surface gly
271	4	44.4	121	2	F97650	flagellar protein	344	4	44.4	147	2	AH2414	hypothetical prote
272	4	44.4	122	2	AC0222	inter-alpha-trypsi	345	4	44.4	147	2	G48552	ORF-US441 - infect
273	4	44.4	123	2	A29652	hypothetical prote	346	4	44.4	147	2	T40381	hypothetical prote
274	4	44.4	123	2	H70482	hypothetical prote	347	4	44.4	147	2	E82923	early glycoprotein
275	4	44.4	123	2	H71558	hypothetical prote	348	4	44.4	148	1	VGBE48	probable flavodoxi
276	4	44.4	124	2	D64549	hypothetical prote	349	4	44.4	148	2	AF1288	probable flavodoxi
277	4	44.4	124	2	AB01465	dihydroneopterin a	350	4	44.4	148	2	AE1660	6-pyruvoyltetrahyd
278	4	44.4	124	2	AE0561	conserved hypotet	351	4	44.4	148	2	AI3263	hypothetical prote
279	4	44.4	124	2	F85543	hypothetical prote	352	4	44.4	148	2	S78271	probable phage tai
280	4	44.4	124	2	B90893	hypothetical prote	353	4	44.4	148	2	AE1036	probable phage tai
281	4	44.4	124	2	D64776	hypothetical prote	354	4	44.4	148	2	B71529	hypothetical prote
282	4	44.4	124	2	F42520	hypothetical prote	355	4	44.4	148	2	CGWN2C	globin IIC, extrac
283	4	44.4	125	2	S72665	ig V-D-J region (R	356	4	44.4	149	1	GMWN2C	transcription regu
284	4	44.4	126	2	T10191	hypothetical prote	357	4	44.4	149	2	D84292	hypothetical prote
285	4	44.4	126	2	S53585	hypothetical prote	358	4	44.4	150	2	T33928	iron-sulfur cofact
286	4	44.4	127	2	B61558	60S ribosomal prot	359	4	44.4	151	2	C64064	early glycoprotein
287	4	44.4	127	2	AG1024	hypothetical prote	360	4	44.4	152	1	VGBEY9	hypothetical prote
288	4	44.4	127	2	AH3491	hypothetical cytos	361	4	44.4	153	2	D96906	galactoside O-acet
289	4	44.4	128	2	S58156	hypothetical prote	362	4	44.4	153	2	E86872	protein K04F1.8 [i
290	4	44.4	129	2	JE0400	hypothetical prote	363	4	44.4	153	2	E88955	hypothetical prote
291	4	44.4	129	2	G98225	ribosomal protein	364	4	44.4	153	2	T12454	probable ubiquitin
292	4	44.4	130	2	H97605	hypothetical prote	365	4	44.4	155	2	T04026	probable ubiquitin
293	4	44.4	130	2	A83400	hypothetical prote	366	4	44.4	155	2	JS0657	ubiquitin / riboso
294	4	44.4	130	2	A48892	absicisic acid-indu	367	4	44.4	155	2	S40239	ubiquitin/riboso
295	4	44.4	130	2	T22920	hypothetical prote	368	4	44.4	155	2	S40240	ubiquitin/ribosoma
296	4	44.4	131	2	QJ1767	SalLIR protein - v	369	4	44.4	155	2	JH0227	ubiquitin / riboso
297	4	44.4	132	1	JC4159	ribosomal protein	370	4	44.4	155	2	JH0226	leu ribosomal prot
298	4	44.4	132	1	R3HU12	ribosomal protein	371	4	44.4	155	2	C75145	probable ribosomal
299	4	44.4	132	1	R3MS12	ribosomal protein	372	4	44.4	155	2	G71184	hypothetical prote
300	4	44.4	132	1	R3RT12	ribosomal protein	373	4	44.4	155	2	T35423	hypothetical prote
301	4	44.4	132	2	I51557	ribosomal protein	374	4	44.4	155	2	H89787	ubiquitin extensio
302	4	44.4	132	2	A69844	hypothetical prote	375	4	44.4	156	2	T52335	ubiquitin extensio
303	4	44.4	132	2	C91173	chemotaxis signal	376	4	44.4	156	2	T52334	ubiquitin prote
304	4	44.4	133	2	A11658	glutathione transf	377	4	44.4	156	2	T35689	hypothetical prote
305	4	44.4	134	2	AE3490	hit1 protein [impo	378	4	44.4	156	2	A86473	17.2K hypothetical
306	4	44.4	134	2	C90490	conserved hypotet	379	4	44.4	157	2	S22489	IGe-dependent hist
307	4	44.4	134	2	A95304	conserved hypotet	380	4	44.4	157	2	F72274	type IV pilin-rela
308	4	44.4	135	2	P80057	ig heavy chain pre	381	4	44.4	157	2	F81274	probable flagellar
309	4	44.4	135	2	C90699	hypothetical prote	382	4	44.4	157	2	F82941	hypothetical UU033
310	4	44.4	135	2	E64781	hypothetical prote	383	4	44.4	157	2	G83772	hypothetical prote
311	4	44.4	135	2	F85549	hypothetical prote	384	4	44.4	157	2	T35638	hypothetical prote
312	4	44.4	136	2	T15031	hypothetical prote	385	4	44.4	157	2	C71060	hypothetical prote
313	4	44.4	136	2	C95291	hypothetical prote	386	4	44.4	158	2	T33718	probable transcrip
314	4	44.4	137	2	H86700	flavodoxin [import	387	4	44.4	158	2	AH1930	hypothetical prote
315	4	44.4	137	2	B72335	(3R)-hydroxymyrist	388	4	44.4	158	2	F90273	hypothetical prote
316	4	44.4	137	2	H95190	conserved domain p	389	4	44.4	158	2	E86993	hypothetical prote
317	4	44.4	138	1	RJHU2	retinoic acid-bind	390	4	44.4	158	2	T22645	hypothetical prote
318	4	44.4	138	2	B97224	ferric uptake regu	391	4	44.4	159	2	S32014	dihydrofolate redu
319	4	44.4	138	2	T12631	DrS12 protein - co	392	4	44.4	159	2	S77852	probable phenylala
320	4	44.4	140	1	S57774	thioredoxin m prec	393	4	44.4	161	2	B86678	hypothetical prote
321	4	44.4	140	2	H36851	RNA-binding ribonu	394	4	44.4	161	2	T32499	hypothetical prote

395	4	44.4	162	2	B70144	transcription fact	468	4	44.4	187	1	S77378	polypeptide deform
396	4	44.4	162	2	I58408	IK factor - human	469	4	44.4	187	2	AH2190	polypeptide deform
397	4	44.4	163	2	PC4186	hemagglutinin 2 ch	470	4	44.4	188	2	S55057	SSX1 protein - hum
398	4	44.4	163	2	D84320	hypothetical prote	471	4	44.4	188	2	D87694	hypothetical prote
399	4	44.4	165	2	AC2463	hypothetical prote	472	4	44.4	188	2	G75326	probable 16S rRNA
400	4	44.4	165	2	C97624	petP protein limpo	473	4	44.4	189	2	E95000	peptidyl-tRNA hydr
401	4	44.4	165	2	AD2847	transcription regu	474	4	44.4	189	2	E97872	aminoacyl-tRNA hyd
402	4	44.4	166	2	I69004	histocompatibility	475	4	44.4	189	2	D84289	hypothetical prote
403	4	44.4	166	2	I69005	histocompatibility	476	4	44.4	189	2	T48779	ankyrin repeat-con
404	4	44.4	166	2	I69006	histocompatibility	477	4	44.4	190	2	B72416	conserved hypothet
405	4	44.4	166	2	I69003	histocompatibility	478	4	44.4	190	2	H83172	hypothetical prote
406	4	44.4	167	2	T05686	TCTP protein homol	479	4	44.4	190	2	E83103	hypothetical prote
407	4	44.4	167	2	T06567	IGF-dependent hist	480	4	44.4	190	2	H84412	hypothetical prote
408	4	44.4	167	2	G70436	hypothetical prote	481	4	44.4	190	2	C90529	nuclease, lipoprot
409	4	44.4	167	2	F90090	60S ribosomal prot	482	4	44.4	191	2	A00016	conserved hypothet
410	4	44.4	168	2	B86861	hypothetical prote	483	4	44.4	191	2	T19026	hypothetical prote
411	4	44.4	168	2	S68355	heme d1 synthesis	484	4	44.4	191	2	A96765	hypothetical prote
412	4	44.4	168	2	T45305	hypothetical prote	485	4	44.4	191	2	AB1800	hypothetical prote
413	4	44.4	169	2	G64250	plasmid surface ex	486	4	44.4	192	2	B48111	EF-hand protein EF
414	4	44.4	169	2	A64396	hypothetical prote	487	4	44.4	192	2	G95072	conserved hypothet
415	4	44.4	169	2	AE1166	transcription regu	488	4	44.4	192	2	D37940	conserved hypothet
416	4	44.4	170	2	G90157	conserved hypothet	489	4	44.4	192	2	E75318	transcription term
417	4	44.4	171	1	A42514	dual specificity p	490	4	44.4	192	2	E64942	hypothetical 21.4
418	4	44.4	171	1	B47452	dual specificity p	491	4	44.4	192	2	B90944	hypothetical prote
419	4	44.4	171	1	I36845	dual specificity p	492	4	44.4	192	2	F85792	hypothetical prote
420	4	44.4	171	1	QQVZHL	dual specificity p	493	4	44.4	193	2	H84051	RNA polymerase ECF
421	4	44.4	171	1	T28522	probable dual spec	494	4	44.4	194	2	F69840	conserved hypothet
422	4	44.4	171	2	B72161	JLL protein - vari	495	4	44.4	195	2	D83237	hypothetical prote
423	4	44.4	171	2	G83829	hypothetical prote	496	4	44.4	195	2	AC2527	hypothetical prote
424	4	44.4	172	2	S73542	MG428 homolog C12	497	4	44.4	195	2	C83076	type 4 fibrinai bi
425	4	44.4	172	2	F83696	hypothetical prote	498	4	44.4	196	2	S40728	hypothetical prote
426	4	44.4	173	2	AF0743	crossover junction	499	4	44.4	197	2	C42148	GTP-binding protei
427	4	44.4	173	2	A85799	crossover junction	500	4	44.4	197	2	E69415	conserved hypothet
428	4	44.4	173	2	D38113	crossover junction	501	4	44.4	197	2	H83910	hypothetical prote
429	4	44.4	173	2	E90950	Holliday junction	502	4	44.4	197	2	T24133	hypothetical prote
430	4	44.4	174	2	D97760	NADH2 dehydrogenas	503	4	44.4	197	2	E84606	probable WRKY-type
431	4	44.4	174	2	G70877	probable rexf prot	504	4	44.4	197	2	T33525	hypothetical prote
432	4	44.4	174	2	T02683	hypothetical prote	505	4	44.4	198	2	S48994	hypothetical prote
433	4	44.4	175	2	F82529	hypothetical prote	506	4	44.4	199	2	AB3195	conserved hypothet
434	4	44.4	176	2	AD0716	probable cytochrom	507	4	44.4	201	2	A53688	5-formyltetrahydro
435	4	44.4	176	2	F84110	hypothetical prote	508	4	44.4	201	2	G64013	hypothetical prote
436	4	44.4	176	2	AG2403	hypothetical prote	509	4	44.4	201	2	AC1785	hydrolase (esteras
437	4	44.4	177	2	AB3221	oxidoreductase wit	510	4	44.4	201	2	S16899	alanine-tRNA ligas
438	4	44.4	177	2	E71327	hypothetical prote	511	4	44.4	202	2	E97556	clpp (AF218420) - i
439	4	44.4	177	2	G96794	probable calmoduli	512	4	44.4	202	2	AC2776	ATP-dependent Clp
440	4	44.4	177	2	T06170	resistance protein	513	4	44.4	202	2	H86689	prophage ps2 prote
441	4	44.4	177	2	D95278	conserved hypothet	514	4	44.4	203	2	H89892	orotate phosphorib
442	4	44.4	177	2	T31499	hypothetical prote	515	4	44.4	204	2	T14834	plastoquinol-plast
443	4	44.4	178	2	G84357	probable acetyltra	516	4	44.4	204	2	D72864	Acorf-115 protein
444	4	44.4	179	2	G83451	hypothetical prote	517	4	44.4	204	2	T41853	ACMPV orf115 - Bo
445	4	44.4	180	2	H84154	hypothetical prote	518	4	44.4	204	2	E70525	hypothetical prote
446	4	44.4	181	2	I79640	MHC cell surface a	519	4	44.4	205	2	T11657	rno GDP dissociati
447	4	44.4	181	2	I59188	MHC cell surface g	520	4	44.4	205	2	T10384	hypothetical prote
448	4	44.4	181	2	A05087	lectin beta-1 chai	521	4	44.4	205	2	A83427	homoserine kinase
449	4	44.4	181	2	A05088	lectin beta-2 chai	522	4	44.4	205	2	JC2558	flagellar filament
450	4	44.4	181	2	E84676	hypothetical prote	523	4	44.4	206	2	JN0874	GTP-binding protei
451	4	44.4	182	2	A59411	human leukocyte an	524	4	44.4	206	2	I37529	HLA-Cw7 - human (f
452	4	44.4	182	2	D70859	hypothetical prote	525	4	44.4	206	2	I37528	HLA-Cw1 - human (f
453	4	44.4	183	2	B83240	hypothetical prote	526	4	44.4	206	2	D95082	amino acid ABC tra
454	4	44.4	183	2	T21289	hypothetical prote	527	4	44.4	206	2	C84408	hypothetical prote
455	4	44.4	183	2	AD1474	probable secreted,	528	4	44.4	206	2	T38251	hypothetical prote
456	4	44.4	183	2	T47707	hypothetical prote	529	4	44.4	207	2	T01366	hypothetical prote
457	4	44.4	183	2	G97035	secreted protein,	530	4	44.4	207	2	A56385	nitrophorin 1 prec
458	4	44.4	184	2	E98229	sarcosine oxidase,	531	4	44.4	207	2	D72215	hypothetical prote
459	4	44.4	184	2	AB1056	sarcosine oxidase	532	4	44.4	208	2	S40207	GTP-binding protei
460	4	44.4	184	2	B86192	hypothetical prote	533	4	44.4	208	2	A48567	calmodulin-ubiquit
461	4	44.4	185	2	S67036	SPF2 protein - yea	534	4	44.4	209	2	A86455	hypothetical prote
462	4	44.4	186	2	F89949	DNA-3-methyladenin	535	4	44.4	209	2	S71156	hypothetical prote
463	4	44.4	186	2	S35057	NADH2 dehydrogenas	536	4	44.4	209	2	H69872	conserved hypothet
464	4	44.4	186	2	E75515	conserved hypothet	537	4	44.4	209	2	A85623	hypothetical prote
465	4	44.4	186	2	B84074	hypothetical prote	538	4	44.4	209	2	C90759	hypothetical prote
466	4	44.4	186	2	AB1493	probable transcrip	539	4	44.4	209	2	F64836	probable membrane
467	4	44.4	186	2	AB1134	probable transcrip	540	4	44.4	209	2	C64317	hypothetical prote

541	4	44.4	210	2	P86551	hypothetical prote	614	4	44.4	221	2	A82331	hypothetical prote
542	4	44.4	210	2	G84899	hypothetical prote	615	4	44.4	221	2	C64040	hypothetical prote
543	4	44.4	210	2	H72460	hypothetical prote	616	4	44.4	222	1	KIBYA	adenylate kinase (
544	4	44.4	211	2	F75474	hypothetical prote	617	4	44.4	222	2	S26193	plastoquinol-plast
545	4	44.4	211	2	D96960	uncharacterized pr	618	4	44.4	222	2	S76297	plastoquinol-plast
546	4	44.4	211	2	T01627	probable ATP bindi	619	4	44.4	222	2	S22470	plastoquinol-plast
547	4	44.4	211	2	AB3020	conserved hypothet	620	4	44.4	222	2	T03540	cobalamin biosynth
548	4	44.4	211	2	T34501	hypothetical prote	621	4	44.4	222	2	B97118	hypothetical prote
549	4	44.4	212	2	D84203	hypothetical prote	622	4	44.4	222	2	AF0658	phase shock protei
550	4	44.4	212	2	AB2992	hypothetical prote	623	4	44.4	222	2	A99864	phase shock protei
551	4	44.4	212	2	H98291	hypothetical prote	624	4	44.4	222	2	B90096	hypothetical prote
552	4	44.4	213	1	JQ1727	22K protein - cani	625	4	44.4	222	2	A83996	dolichyl-phosphate
553	4	44.4	213	2	T07603	NADH2 dehydrogenas	626	4	44.4	222	2	H85754	phase shock protei
554	4	44.4	213	2	T44818	NADH2 dehydrogenas	627	4	44.4	222	2	C64879	hemagglutinin HA2
555	4	44.4	213	2	A26130	translation initia	628	4	44.4	223	2	PQ0514	hypothetical prote
556	4	44.4	214	2	H86692	hypothetical prote	629	4	44.4	223	2	F75051	hypothetical prote
557	4	44.4	214	2	D64442	conserved hypothet	630	4	44.4	223	2	E95862	hypothetical prote
558	4	44.4	214	2	B87424	outer membrane pro	631	4	44.4	224	2	C85571	L4 ribosomal prote
559	4	44.4	215	1	A30807	plastoquinol-plast	632	4	44.4	224	2	H72055	ribosomal protein
560	4	44.4	215	1	CBKL6P	plastoquinol-plast	633	4	44.4	224	2	S37862	hypothetical prote
561	4	44.4	215	1	CBLV6	plastoquinol-plast	634	4	44.4	224	2	C48652	transfer protein s
562	4	44.4	215	1	CBNT6	plastoquinol-plast	635	4	44.4	225	2	D90570	hypothetical prote
563	4	44.4	215	1	CBSP6	plastoquinol-plast	636	4	44.4	225	2	S36621	probable drought-i
564	4	44.4	215	1	CBZM6R	plastoquinol-plast	637	4	44.4	225	2	F97349	response regulator
565	4	44.4	215	1	S09186	plastoquinol-plast	638	4	44.4	225	2	S29950	surface glycoprote
566	4	44.4	215	1	S21253	plastoquinol-plast	639	4	44.4	225	2	S29953	surface glycoprote
567	4	44.4	215	1	S34548	plastoquinol-plast	640	4	44.4	225	2	S29947	surface glycoprote
568	4	44.4	215	1	XSAC2	plastoquinol-plast	641	4	44.4	225	2	AH0538	hypothetical prote
569	4	44.4	215	2	S73262	chloramphenicol O-	642	4	44.4	226	2	G83293	probable two-compo
570	4	44.4	215	2	S78307	plastoquinol-plast	643	4	44.4	226	2	S29948	surface glycoprote
571	4	44.4	215	2	S14961	plastoquinol-plast	644	4	44.4	226	2	AD2198	hypothetical prote
572	4	44.4	215	2	T07266	plastoquinol-plast	645	4	44.4	226	2	B82417	Cbby family protei
573	4	44.4	215	2	T07512	plastoquinol-plast	646	4	44.4	226	2	A70436	hypothetical prote
574	4	44.4	215	2	T06963	plastoquinol-plast	647	4	44.4	226	2	D82597	phase-related prot
575	4	44.4	215	2	AF2233	plastoquinol-plast	648	4	44.4	226	2	F71108	hypothetical prote
576	4	44.4	215	2	B26473	chloramphenicol O-	649	4	44.4	226	2	S29952	surface glycoprote
577	4	44.4	215	2	A49758	chloramphenicol O-	650	4	44.4	226	2	S29951	surface glycoprote
578	4	44.4	215	2	F96746	probable drought i	651	4	44.4	228	2	AD1052	tRNA (guanine-N1) -
579	4	44.4	215	2	S48826	S0S ribosomal prot	652	4	44.4	228	2	H97373	hypothetical prote
580	4	44.4	215	2	F97825	NADH2 dehydrogenas	653	4	44.4	228	2	A13106	transcription regu
581	4	44.4	215	2	G70575	hypothetical prote	654	4	44.4	228	2	C98180	probable transcrip
582	4	44.4	215	2	G97590	probable membrane	655	4	44.4	229	1	P8XR10	nonstructural prot
583	4	44.4	215	2	AF2812	conserved hypothet	656	4	44.4	229	1	P8XR10	nonstructural prot
584	4	44.4	215	2	H97181	uncharacterized pr	657	4	44.4	229	2	A20969	IG kappa chain pre
585	4	44.4	216	2	T48378	GTP-binding protei	658	4	44.4	229	2	H83892	two-component resp
586	4	44.4	216	2	A71672	ribosomal protein	659	4	44.4	229	2	S12593	nonstructural prot
587	4	44.4	216	2	AG2591	peptide methionine	660	4	44.4	229	2	S44640	hypothetical prote
588	4	44.4	217	2	T12965	GTP-binding protei	661	4	44.4	229	2	S58210	bradyzoite-specifi
589	4	44.4	217	2	T43082	transfer complex p	662	4	44.4	230	2	T28284	hypothetical prote
590	4	44.4	217	2	E70126	hypothetical prote	663	4	44.4	230	2	C97104	hypothetical prote
591	4	44.4	217	2	A82467	hypothetical prote	664	4	44.4	231	2	S58245	BC17A protein - hu
592	4	44.4	217	2	C70629	probable mutT3 pro	665	4	44.4	231	2	D90427	hypothetical prote
593	4	44.4	218	2	S37658	drought-induced pr	666	4	44.4	231	2	H70157	hypothetical prote
594	4	44.4	218	2	I72808	MHC class I HLA-J	667	4	44.4	231	2	G98264	hypothetical prote
595	4	44.4	218	2	S52286	NADH2 dehydrogenas	668	4	44.4	232	1	S04149	plastoquinol-plast
596	4	44.4	218	2	H85643	hypothetical prote	669	4	44.4	232	2	D97683	trNA (guanine-N1) -
597	4	44.4	218	2	F90783	hypothetical prote	670	4	44.4	232	2	AD2908	tRNA-(guanine-N1) -
598	4	44.4	219	1	H69098	phosphate transpor	671	4	44.4	232	2	F35009	DNA-binding respon
599	4	44.4	219	2	T35128	hypothetical prote	672	4	44.4	232	2	D97881	response regulator
600	4	44.4	219	2	B29224	GTP-binding protei	673	4	44.4	232	1	LNLWBA	lectin precursor [
601	4	44.4	219	2	S47177	GTP-binding protei	674	4	44.4	233	1	FVVFBA	flavin precursor -
602	4	44.4	219	2	S47177	lactoylglutathione	675	4	44.4	233	1	D69630	menaquinone biosyn
603	4	44.4	219	2	T08330	hypothetical prote	676	4	44.4	233	1	H84322	30S ribosomal prot
604	4	44.4	220	1	NXEC	exclusion-determin	677	4	44.4	233	2	T02590	DNA binding protei
605	4	44.4	220	2	G72472	hypothetical prote	678	4	44.4	233	2	C90427	hypothetical prote
606	4	44.4	220	2	B84304	hypothetical prote	679	4	44.4	233	2	T41980	hypothetical prote
607	4	44.4	220	2	A97216	superoxide dismuta	680	4	44.4	234	2	S58581	plastoquinol-plast
608	4	44.4	220	2	S48450	hypothetical prote	681	4	44.4	234	2	D81342	trNA (guanine-N1-)
609	4	44.4	220	2	T09108	RNA binding protei	682	4	44.4	234	2	F70360	3-deoxy-manno-occu
610	4	44.4	221	2	F70243	hypothetical prote	683	4	44.4	234	2	T07686	transcription fact
611	4	44.4	221	2	S69682	hypothetical prote	684	4	44.4	234	2	G83111	HAD superfamily hy
612	4	44.4	221	2	G83998	mutants block spor	685	4	44.4	234	2	E96957	
613	4	44.4	221	2			686	4	44.4	234	2		

687	4	44.4	234	2	AF2214	760	4	44.4	249	2	AI1196	B. subtilis yjch p
688	4	44.4	235	2	E69814	761	4	44.4	249	2	A81892	probable transposase
689	4	44.4	235	2	E72217	762	4	44.4	250	2	S07237	hypothetical prote
690	4	44.4	235	2	AC1800	763	4	44.4	250	2	G84054	hypothetical prote
691	4	44.4	235	2	D84919	764	4	44.4	250	2	F97036	hypothetical prote
692	4	44.4	236	2	I57681	765	4	44.4	251	2	T43928	tryptophan synthas
693	4	44.4	236	2	G90007	766	4	44.4	251	2	S69021	hypothetical prote
694	4	44.4	236	2	T02432	767	4	44.4	251	2	A84807	probable acid phos
695	4	44.4	236	2	T36579	768	4	44.4	251	2	T14407	pectin esterase ho
696	4	44.4	236	2	T50280	769	4	44.4	251	2	B1298	hypothetical prote
697	4	44.4	237	2	S64718	770	4	44.4	251	2	F70683	probable lipoprote
698	4	44.4	237	2	T27198	771	4	44.4	251	2	AH2520	hypothetical prote
699	4	44.4	238	2	AC2043	772	4	44.4	251	2	H90568	conserved hypotet
700	4	44.4	238	2	D49316	773	4	44.4	252	2	AC2291	tRNA methyltransfe
701	4	44.4	238	2	B84951	774	4	44.4	252	2	T35989	probable translati
702	4	44.4	239	2	B89967	775	4	44.4	252	2	H69491	cell division initi
703	4	44.4	239	2	E64961	776	4	44.4	252	2	E83747	transcription anti
704	4	44.4	239	2	B85815	777	4	44.4	252	2	A64492	toxin sensitivity
705	4	44.4	239	2	C90967	778	4	44.4	253	2	AF0916	uridine phosphoryl
706	4	44.4	239	2	F96908	779	4	44.4	253	2	T46830	uridine phosphoryl
707	4	44.4	239	2	A75164	780	4	44.4	253	2	S05491	uridine phosphoryl
708	4	44.4	239	2	G89867	781	4	44.4	253	2	G86070	uridine phosphoryl
709	4	44.4	239	2	E84232	782	4	44.4	253	2	A98224	uridine phosphoryl
710	4	44.4	239	2	F86738	783	4	44.4	253	2	AI0460	uridine phosphoryl
711	4	44.4	239	2	F97542	784	4	44.4	253	2	T36867	hypothetical prote
712	4	44.4	239	2	T16829	785	4	44.4	254	2	B72366	conserved hypotet
713	4	44.4	241	1	BVFCPU	786	4	44.4	254	2	E90054	hypothetical prote
714	4	44.4	241	2	AH3270	787	4	44.4	255	2	I54307	MHC H1A-A30US heav
715	4	44.4	241	2	B82879	788	4	44.4	255	2	F89769	hypothetical prote
716	4	44.4	241	2	D86057	789	4	44.4	255	2	T46946	phosphonoacetaldeh
717	4	44.4	241	2	D91211	790	4	44.4	255	2	AH2479	transcription regu
718	4	44.4	241	2	PQ0624	791	4	44.4	256	2	T12396	NADH2 dehydrogenas
719	4	44.4	241	2	PQ0623	792	4	44.4	256	2	T16661	hypothetical prote
720	4	44.4	241	2	PQ0620	793	4	44.4	256	2	F84612	hypothetical prote
721	4	44.4	241	2	H81327	794	4	44.4	257	2	T40880	hypothetical prote
722	4	44.4	242	1	BVFCRO	795	4	44.4	257	1	SNBY3	proteasome endopep
723	4	44.4	242	2	AI0828	796	4	44.4	258	1	A43692	T1 protein - rabbi
724	4	44.4	242	2	D85902	797	4	44.4	258	2	AG0459	Sec-independent pr
725	4	44.4	242	2	G91057	798	4	44.4	258	2	B82249	uridine phosphoryl
726	4	44.4	242	2	PQ0625	799	4	44.4	259	1	PMWSEB	bisphosphoglycerat
727	4	44.4	242	2	PQ0626	800	4	44.4	259	2	T12386	NADH2 dehydrogenas
728	4	44.4	242	2	H83829	801	4	44.4	259	2	C64059	uridine phosphoryl
729	4	44.4	242	2	AB1091	802	4	44.4	259	2	G83966	dihydroxotrate deh
730	4	44.4	242	2	AI1454	803	4	44.4	259	2	C81168	conserved hypotet
731	4	44.4	242	2	PQ0621	804	4	44.4	259	2	F81937	hypothetical prote
732	4	44.4	243	2	T26432	805	4	44.4	260	1	KLBOB	calcium-binding pr
733	4	44.4	243	2	I54459	806	4	44.4	260	2	T12395	NADH2 dehydrogenas
734	4	44.4	244	2	T29079	807	4	44.4	260	2	T12387	NADH2 dehydrogenas
735	4	44.4	244	2	T41594	808	4	44.4	260	2	T12394	NADH2 dehydrogenas
736	4	44.4	244	2	E64490	809	4	44.4	260	2	T12390	NADH2 dehydrogenas
737	4	44.4	244	2	A39365	810	4	44.4	260	2	T12397	NADH2 dehydrogenas
738	4	44.4	245	2	E97085	811	4	44.4	260	2	T12393	NADH2 dehydrogenas
739	4	44.4	245	2	A83856	812	4	44.4	260	2	T14435	NADH2 dehydrogenas
740	4	44.4	245	2	E69511	813	4	44.4	260	2	T12392	NADH2 dehydrogenas
741	4	44.4	246	2	G83959	814	4	44.4	260	2	I52551	carbonate dehydrat
742	4	44.4	246	2	B69311	815	4	44.4	260	2	H97357	stage 0 sporulatio
743	4	44.4	246	2	S47805	816	4	44.4	260	2	A70329	hypothetical prote
744	4	44.4	246	2	F72769	817	4	44.4	260	2	G75301	hypothetical prote
745	4	44.4	246	2	T25532	818	4	44.4	260	2	E90984	probable glycosyl
746	4	44.4	247	2	AF5712	819	4	44.4	260	2	T28182	hypothetical prote
747	4	44.4	247	2	AF2182	820	4	44.4	260	2	H85829	glycosyl transfera
748	4	44.4	247	2	T33288	821	4	44.4	260	2	T12398	NADH2 dehydrogenas
749	4	44.4	247	2	B86157	822	4	44.4	260	2	T12391	calcium-binding pr
750	4	44.4	248	2	ACO630	823	4	44.4	260	2	A34955	calcium-binding pr
751	4	44.4	248	2	D69460	824	4	44.4	261	1	KLRTB	calcium-binding pr
752	4	44.4	248	2	B81077	825	4	44.4	261	1	S00234	calcium-binding pr
753	4	44.4	248	2	H81864	826	4	44.4	261	1	A33470	fibroin light chai
754	4	44.4	248	2	S75632	827	4	44.4	262	2	H85376	hypothetical prote
755	4	44.4	248	2	T18315	828	4	44.4	263	2	T04634	hypothetical prote
756	4	44.4	248	2	E64898	829	4	44.4	263	2	E83923	hypothetical prote
757	4	44.4	248	2	A86213	830	4	44.4	265	2	T40259	hypothetical prote
758	4	44.4	248	2	AH3073	831	4	44.4	265	2	T28102	hypothetical prote
759	4	44.4	249	2	D64310	832	4	44.4	265	2		

833	4	44.4	266	2	T09281	embryonic abundant	906	4	44.4	282	2	B71601	probable integral
834	4	44.4	266	2	E71230	hypothetical prote	907	4	44.4	282	2	H97226	protein containing
835	4	44.4	267	2	B84213	hypothetical prote	908	4	44.4	283	2	T24646	hypothetical prote
836	4	44.4	267	2	T46202	endoxyluglucan tra	909	4	44.4	283	2	H65154	probable transpos
837	4	44.4	268	2	C81325	probable periplasm	910	4	44.4	283	2	D64448	hypothetical prote
838	4	44.4	269	1	R5BYL3	ribosomal protein	911	4	44.4	283	2	B98040	pyridoxal/pyridoxi
839	4	44.4	269	2	S61555	xyloglucan endo-1,	912	4	44.4	283	2	E85884	pyridoxal/pyridoxi
840	4	44.4	269	2	S73816	MG374 homolog G12	913	4	44.4	283	2	A65016	pyridoxal kinase (
841	4	44.4	269	2	AH0555	phosphonoacetaldeh	914	4	44.4	284	2	S77554	hypothetical prote
842	4	44.4	269	2	A82240	conserved hypoteth	915	4	44.4	284	2	T39813	hypothetical prote
843	4	44.4	269	2	T36910	MHC class I histoc	916	4	44.4	284	2	S08385	nodO protein - Rhi
844	4	44.4	270	1	HLRU28	hydrolase (esteras	917	4	44.4	284	2	A43721	nodule formation p
845	4	44.4	270	2	AD1409	probable enoyl-CoA	918	4	44.4	285	2	T20237	hypothetical prote
846	4	44.4	270	2	G83418	hypothetical prote	919	4	44.4	285	2	G87298	short chain dehydr
847	4	44.4	270	2	AF2159	hypothetical prote	920	4	44.4	285	2	A69748	hypothetical prote
848	4	44.4	270	2	F64460	hypothetical prote	921	4	44.4	285	2	T23183	hypothetical prote
849	4	44.4	270	2	T22213	conserved hypoteth	922	4	44.4	286	2	G75407	transaldolase - De
850	4	44.4	270	2	AE1127	conserved hypoteth	923	4	44.4	286	2	G85230	hypothetical prote
851	4	44.4	270	2	AI1487	conserved hypoteth	924	4	44.4	286	2	F84403	hypothetical prote
852	4	44.4	271	2	B84138	biotin synthetasis B	925	4	44.4	286	2	B71663	hypothetical prote
853	4	44.4	271	2	AB2956	cell division inhi	926	4	44.4	286	2	T39404	hypothetical prote
854	4	44.4	271	2	C98327	cell division inhi	927	4	44.4	286	2	A90281	ABC transporter, A
855	4	44.4	271	2	A96011	probable cell divi	928	4	44.4	287	2	D83856	hypothetical prote
856	4	44.4	271	2	H84337	spermidine/purasc	929	4	44.4	287	2	AF3372	hypothetical prote
857	4	44.4	271	2	B82438	phosphonoacetaldeh	930	4	44.4	288	2	D97113	ABC transporter AT
858	4	44.4	271	2	C96010	conserved hypoteth	931	4	44.4	288	2	F84042	probable Grpase (Y
859	4	44.4	272	2	AB1458	dipeptide ABC tran	932	4	44.4	288	2	T21770	hypothetical prote
860	4	44.4	272	2	C86539	CT041 hypothetical	933	4	44.4	289	2	H84205	hypothetical prote
861	4	44.4	272	2	C72084	conserved hypoteth	934	4	44.4	289	2	E81259	hypothetical prote
862	4	44.4	273	1	HLHUAM	MHC class I histoc	935	4	44.4	290	2	F89952	hypothetical prote
863	4	44.4	273	1	HLHU69	MHC class I histoc	936	4	44.4	290	2	C72259	hypothetical prote
864	4	44.4	273	2	I38509	MHC class I histoc	937	4	44.4	290	2	AF1133	hypothetical prote
865	4	44.4	273	2	T34740	hypothetical prote	938	4	44.4	291	2	AC1302	hypothetical prote
866	4	44.4	273	2	D90516	esterase/lipase 1	939	4	44.4	291	2	AC1674	hypothetical prote
867	4	44.4	273	2	T39446	conserved hypoteth	940	4	44.4	291	2	S67672	hypothetical prote
868	4	44.4	274	1	HLHU32	MHC class I histoc	941	4	44.4	291	2	S48990	hypothetical prote
869	4	44.4	274	2	I68774	MHC HLA-B39 chain	942	4	44.4	291	2	T00855	hypothetical prote
870	4	44.4	274	2	I54463	MHC HLA-B38 chain	943	4	44.4	292	2	D98096	conserved hypoteth
871	4	44.4	274	2	SI6647	sporulation dipept	944	4	44.4	292	2	B95232	conserved hypoteth
872	4	44.4	274	2	JC4294	ammonia monooxygen	945	4	44.4	292	2	T02737	probable ubiquitin
873	4	44.4	274	2	G84353	hypothetical prote	946	4	44.4	292	2	B0501	conserved hypoteth
874	4	44.4	274	2	D97653	hypothetical prote	947	4	44.4	292	2	S64361	hypothetical prote
875	4	44.4	274	2	AB2877	conserved hypoteth	948	4	44.4	293	2	E49539	hypothetical prote
876	4	44.4	274	2	T22214	hypothetical prote	949	4	44.4	293	1	DNCHFM	conserved hypoteth
877	4	44.4	274	2	S24439	class I histocompa	950	4	44.4	294	2	G83962	hypothetical prote
878	4	44.4	275	1	LNPM	lectin precursor -	951	4	44.4	295	1	S29399	homeotic protein m
879	4	44.4	275	2	S05299	hypothetical prote	952	4	44.4	295	2	D69534	conserved hypoteth
880	4	44.4	276	2	T18742	hypothetical prote	953	4	44.4	296	2	A41730	nucleophosmin NO38
881	4	44.4	276	2	A84361	hypothetical prote	954	4	44.4	296	2	PC1085	coat protein homol
882	4	44.4	276	2	F95936	conserved hypoteth	955	4	44.4	296	2	B40257	RNA15 protein - Ye
883	4	44.4	277	2	T34779	tRNA (guanine-N1) -	956	4	44.4	297	1	I39938	N-acetyluramoyl-L
884	4	44.4	277	2	T51975	proteasome endopep	957	4	44.4	297	2	G69950	6-phosphogluconate
885	4	44.4	277	2	C84463	hypothetical prote	958	4	44.4	297	2	S33927	interphotoreceptor
886	4	44.4	277	2	C90574	ABC transporter pe	959	4	44.4	297	2	A69968	phage-related lyti
887	4	44.4	277	2	B86397	protein H04J21.2 [960	4	44.4	297	2	D83825	hypothetical prote
888	4	44.4	277	2	T17911	hypothetical prote	961	4	44.4	297	2	AH2358	hypothetical prote
889	4	44.4	277	2	E97703	hypothetical prote	962	4	44.4	298	1	A69879	conserved hypoteth
890	4	44.4	278	1	S39900	multicatalytic end	963	4	44.4	298	2	S44994	class I histocompa
891	4	44.4	278	2	T51974	proteasome endopep	964	4	44.4	298	2	T24029	hypothetical prote
892	4	44.4	278	2	G89827	conserved hypoteth	965	4	44.4	298	2	H83863	modulation of CheA
893	4	44.4	279	2	C81381	orotidine 5'-phosp	966	4	44.4	298	2	B75096	glycosyl transfera
894	4	44.4	279	2	T09620	probable lectin 2	967	4	44.4	298	2	B83984	6-phosphogluconate
895	4	44.4	279	2	JC4327	uridine phosphoryl	968	4	44.4	298	2	B35272	osteoinductive fac
896	4	44.4	280	2	E75216	hypothetical prote	969	4	44.4	298	2	JC4130	osteoglycin precur
897	4	44.4	280	2	C71453	hypothetical prote	970	4	44.4	298	2	C55223	minor tail protein
898	4	44.4	281	1	S26018	NADH2 dehydrogenas	971	4	44.4	298	2	E90172	hypothetical prote
899	4	44.4	281	2	D70213	outer membrane pro	972	4	44.4	298	2	AD2715	ABC transporter, m
900	4	44.4	281	2	G70309	protoporphyrinogen	973	4	44.4	299	2	D97403	rbsk protein (AJ00
901	4	44.4	282	2	AC2294	hypothetical prote	974	4	44.4	299	2	AD2621	ribokinase [import
902	4	44.4	282	2	S61663	probable membrane	975	4	44.4	299	2	C97030	arginase [imported
903	4	44.4	282	2	T39471	hypothetical prote	976	4	44.4	299	2	I46937	tissue factor path
904	4	44.4	282	2	T03250	calmodulin-binding	977	4	44.4	299	2	A35272	osteoinductive fac
905	4	44.4	282	2	F82867	conserved hypoteth	978	4	44.4	300	2	S12143	lipoprotein-associ

979 4 44.4 300 2 B49238 gamma-hemolysin ga
980 4 44.4 301 2 AD0660 probable transcript
981 4 44.4 301 2 H69508 formylmethanofuran
982 4 44.4 301 2 C69524 deoxyhypusine synt
983 4 44.4 301 2 T24651 hypothetical prote
984 4 44.4 302 1 PAF1A phosphoprotein pho
985 4 44.4 302 2 B35961 hypothetical 21k p
986 4 44.4 302 2 H90717 hypothetical prote
987 4 44.4 302 2 A71709 hypothetical prote
988 4 44.4 302 2 T21843 hypothetical prote
989 4 44.4 303 2 B45067 laminin B1 chain -
990 4 44.4 304 2 A49185 interphotoreceptor
991 4 44.4 304 2 T28891 hypothetical prote
992 4 44.4 304 2 D59100 hypothetical prote
993 4 44.4 304 2 A86842 conserved hypothet
994 4 44.4 304 2 B86641 hypothetical prote
995 4 44.4 305 2 T08836 probable metallopr
996 4 44.4 305 2 D75306 purine nucleoside
997 4 44.4 305 2 F69748 hypothetical prote
998 4 44.4 305 2 B82873 conserved hypothet
999 4 44.4 305 2 T23929 hypothetical prote
1000 4 44.4 306 2 S47906 PAD synthetase - Y

ALIGNMENTS

RESULT 1
WZVZB1
vaccinia virus 18K HindIII-C protein - vaccinia virus (strain Ankara and WR)
N:Alternate names: C7L protein; host range protein
C:Species: vaccinia virus
A:Variety: strain Ankara
C:Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: A33348; G42503; T30771
R:Kotwal, G.J.; Moss, B.
Virology 167, 524-537, 1988
A:Title: Analysis of a large cluster of nonessential genes deleted from a vaccinia virus
A:Reference number: A94385; MUID:89073756; PMID:2849238
A:Accession: A33348
A:Molecule type: DNA
A:Residues: 1-150 <KOT>
A:Cross-references: UNIPROT:P17363; UNIPARC:UPI00000001F9; GB:M22812; NID:G335691; PIDN:
A:Experimental source: strain WR
R:Johnson, G.P.
submitted to GenBank, June 1990
A:Reference number: A33172
A:Accession: G42503
A:Molecule type: DNA
A:Residues: 1-150 <JOH>
A:Cross-references: UNIPARC:UPI00000001F9
A:Experimental source: strain Copenhagen
R:Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dorner, F.
submitted to the EMBL Data Library, March 1997
A:Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain
A:Reference number: Z20877
A:Accession: T30771
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-150 <ANT>
A:Cross-references: UNIPARC:UPI00000001F9; EMBL:U94848; PIDN:AAB96405.1
A:Experimental source: strain Ankara
C:Genetics:
A>Note: MVA018L
C:Superfamily: host range protein, vaccinia C7L type
C:Keywords: early protein

Query Match 100.0%; Score 9; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDTFYV 9
|||||||

Db 74 KVDDTFYV 82
RESULT 2
H36837
D8L protein - variola virus (strain India-1967)
C:Species: variola virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: H36837
R:Blinov, V.M.
submitted to GenBank, November 1992
A:Reference number: A36859
A:Accession: H36837
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-150 <BLI>
A:Cross-references: UNIPROT:P33860; UNIPARC:UPI00000000732; GB:X69198; NID:G456758; PIDN:
C:Superfamily: host range protein, vaccinia C7L type

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYV 9
|||||||
Db 74 KVDDTFYV 82

RESULT 3
T28446
hypothetical protein D111 - variola major virus
C:Species: variola major virus
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28446
R:Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
Nature 366, 748-751, 1993
A:Title: Potential virulence determinants in terminal regions of variola smallpox virus
A:Reference number: Z20488; MUID:94088747; PMID:8264798
A:Accession: T28446
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-150 <MAS>
A:Cross-references: UNIPROT:P33860; UNIPARC:UPI00000000732; EMBL:L22579; NID:G623595; PID
A:Experimental source: strain "Bangladesh-1975"
C:Superfamily: host range protein, vaccinia C7L type

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYV 9
|||||||
Db 74 KVDDTFYV 82

RESULT 4
F72151
B14L protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004
C:Accession: F72151
R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar
submitted to GenBank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A:Reference number: A72150
A:Accession: F72151
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-150 <SCH>
A:Cross-references: UNIPROT:P33860; UNIPARC:UPI00000000732; GB:Y16780; NID:G5830555; PIDN:
A:Experimental source: strain Garcia-1966
C:Genetics:
A:Gene: B14L

C;Superfamily: host range protein, vaccinia C7L type

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDPTFYV 9
Db 74 KVDPTFYV 82

RESULT 5

S75042

hypothetical protein sl11608 - *Synechocystis* sp. (strain PCC 6803)

C;Species: *Synechocystis* sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C;Accession: S75042

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimo, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

s.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S75042

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-770 <KAN>

A;Cross-references: UNIPROT:P73845; UNIPARC:UPI00000C0DCB; EMBL:D90910; GB:AB001339; NID

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match

Best Local Similarity 77.8%; Score 7; DB 2; Length 770;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 8

Db 286 VDDTFY 292

RESULT 6

C36365

transforming protein homolog MRAS3 - *Rhizomucor racemosus*

C;Species: *Rhizomucor racemosus*

C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004

C;Accession: C36365

R;Casale, W.L.; McConnell, D.G.; Wang, S.Y.; Lee, Y.J.; Linz, J.E.

Mol. Cell. Biol. 10, 6654-6663, 1990

A;Title: Expression of a gene family in the dimorphic fungus *Mucor racemosus* which exhib

A;Reference number: A36365; MUID:91061774; PMID:1701021

A;Accession: C36365

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-206 <CAS>

A;Cross-references: UNIPROT:P22280; UNIPARC:UPI000017642D; GB:M55177

C;Superfamily: ras transforming protein; translation elongation factor Tu homology

C;Keywords: GTP binding; nucleotide binding; P-loop

F;11-126/Domain: translation elongation factor Tu homology <ETU>

F;17-24/Region: nucleotide-binding motif A (P-loop)

F;123-126/Region: GTP-binding NKAD motif

F;153-155/Region: GTP-binding SKA/L motif

F;23,24,42,123,124,126,153/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #sta

Query Match

Best Local Similarity 66.7%; Score 6; DB 2; Length 206;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7

Db 160 VDDTFY 165

RESULT 7

B81169

tryptophan synthase, beta chain NMB0699 [imported] - *Neisseria meningitidis* (strain MCS

C;Species: *Neisseria meningitidis*

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: B81169

R;Retzein, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V

A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MCS8.

A;Reference number: AB1000; MUID:20175755; PMID:10710307

A;Accession: B81169

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-400 <TET>

A;Cross-references: UNIPROT:Q9K0B5; UNIPARC:UPI000013751E; GB:AE002424; GB:AE002098; NI

A;Experimental source: serogroup B, strain MCS9

C;Genetics:

A;Gene: NMB0699

C;Superfamily: tryptophan synthase beta chain; tryptophan synthase beta chain homology

Query Match

Best Local Similarity 66.7%; Score 6; DB 2; Length 400;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7

Db 186 VDDTFY 191

RESULT 8

H81936

probable tryptophan synthase (EC 4.2.1.20) beta chain NMA0904 [imported] - *Neisseria me*

C;Species: *Neisseria meningitidis*

C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C;Accession: H81936

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More

r; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandrea

Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.

A;Reference number: AB1775; MUID:20222556; PMID:10761919

A;Accession: H81936

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-400 <PAB>

A;Cross-references: UNIPROT:Q9JVC0; UNIPARC:UPI000013751D; GB:AL162754; GB:AL157959; NI

A;Experimental source: serogroup A, strain Z2491

C;Genetics:

A;Gene: trpB; NMA0904

C;Superfamily: tryptophan synthase beta chain; tryptophan synthase beta chain homology

C;Keywords: carbon-oxygen lyase; hydro-lyase

Query Match

Best Local Similarity 66.7%; Score 6; DB 2; Length 400;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7

Db 186 VDDTFY 191

RESULT 9

S31478

alpha-amylase (EC 3.2.1.1) - *Thermoactinomyces vulgaris*

C;Species: *Thermoactinomyces vulgaris*

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004

C;Accession: S31478

R;Hofemeister, B.; Koenig, S.; Hoang, V.; Engel, J.; Mayer, G.; Heese, O.; Hansen, G.; I

submitted to the EMBL Data Library, December 1992

A;Description: The gene amyTV coding for a non-glucoamylase from *Thermoactin*

A;Reference number: S31478

A;Accession: S31478

A:Molecule type: DNA
A:Residues: 1-482 <HOF>
A:Cross-references: UNIPROT:Q60051; UNIPARC:UPI00000B6F58; EMBL:X69807; NID:g48289; PIDN
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: cyclomaltoextrin glucanotransferase/alpha-amylase; alpha-amylase core ho
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:194-319/Domain: alpha-amylase core homology <MY>

Query Match 66.7%; Score 6; DB 2; Length 482;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
|||||
Db 409 VDDTFY 414

RESULT 10
C86143
hypothetical protein F6F3.10 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: C86143
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C86143
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-485 <STO>
A:Cross-references: UNIPROT:Q9LNU3; UNIPARC:UPI000009E0F7; GB:AE005172; NID:g9665144; PI
C:Genetics:
A:Map position: 1

Query Match 66.7%; Score 6; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
|||||
Db 327 DTFYV 332

RESULT 11
T47790
hypothetical protein F17J16.130 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47790
R:D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.; I
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24476
A:Accession: T47790
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-535 <DAN>
A:Cross-references: UNIPROT:Q9LYS8; UNIPARC:UPI00000AC14B; EMBL:AL163527
C:Experimental source: cultivar Columbia; BAC clone F17J16
C:Genetics:
A:Map position: 3
A>Note: F17J16.130

Query Match 66.7%; Score 6; DB 2; Length 535;

Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
|||||
Db 374 DTFYV 379

RESULT 12
T26101
hypothetical protein W02B8.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26101
R:Sims, M.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z20151
A:Accession: T26101
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1256 <WIL>
A:Cross-references: UNIPROT:Q9XVH4; UNIPARC:UPI0000081416; EMBL:Z81136; PIDN:CAB03458.1;
A:Experimental source: clone W02B8
C:Genetics:
A:Gene: CESP:W02B8.2
A:Map position: 2
A:Introns: 27/3; 327/3; 670/3; 949/3; 1073/3

Query Match 66.7%; Score 6; DB 2; Length 1256;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
|||||
Db 1096 DTFYV 1101

RESULT 13
T16507
hypothetical protein F59A6.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16507
R:Nhan, M.
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid F59A6.
A:Reference number: Z18526
A:Accession: T16507
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1286 <NHA>
A:Cross-references: UNIPROT:Q21025; UNIPARC:UPI000008155B; EMBL:U41994; NID:g1123047; PI
C:Genetics:
A:Gene: CESP:F59A6.5
A:Introns: 35/3; 335/3; 685/3; 973/3; 1097/3

Query Match 66.7%; Score 6; DB 2; Length 1286;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
|||||
Db 1120 DTFYV 1125

RESULT 14
SS3874
endonuclease precursor - human
C:Species: Homo sapiens (man)
C:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: SS3874
R:Gerschenson, M.; Houmiel, K.L.; Low, R.L.
Nucleic Acids Res. 23, 88-97, 1995

A;Title: Endonuclease G from mammalian nuclei is identical to the major endonuclease of
 A;Reference number: S53874; MUID:95175374; PMID:7870594
 A;Accession: S53874

A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-72 <GER>
 A;Cross-references: UNIPARC:UPI000017C100

Query Match 55.6%; Score 5; DB 2; Length 72;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFY 7
 |||||
 Db 20 DDTFY 24

RESULT 15

D97355
 hypothetical protein CAC3711 [imported] - Clostridium acetobutylicum
 C;Species: Clostridium acetobutylicum
 C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C;Accession: D97355
 R;Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
 A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: D97355
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-90 <KUR>

A;Cross-references: UNIPROT:Q04353; UNIPARC:UPI0000139447; GB:AE001437; PIDN:AAK81631.1;
 A;Experimental source: Clostridium acetobutylicum ATCC824
 C;Genetics:
 A;Gene: CAC3711

Query Match 55.6%; Score 5; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
 |||||
 Db 56 KVDDT 60

RESULT 16

S25001
 ubiquitin/ribosomal protein S27a fusion protein - garden asparagus
 C;Species: Asparagus officinalis (garden asparagus)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C;Accession: S25001
 R;Davies, K.M.; King, G.A.

A;Description: Isolation and characterization of asparagus officinalis L. cDNA clones en
 A;Reference number: S25001

A;Accession: S25001
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-118 <DAV>

A;Cross-references: UNIPROT:P31753; UNIPROT:P03993; UNIPARC:UPI00001699FA; EMBL:X66875;
 C;Superfamily: ubiquitin / rat ribosomal protein S27a; ribosomal protein S27a homology;
 C;Keywords: nucleus

F;1-40/Domain: ubiquitin homology (fragment) <UBH>
 F;1-40/Product: ubiquitin (fragment) #status predicted <UBI>
 F;41-118/Product: ribosomal protein S27a #status predicted <RIBP>
 F;65-115/Domain: ribosomal protein S27a homology <RIB>

Query Match 55.6%; Score 5; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5

Db 71 KVDDT 75
 |||||

RESULT 17

G85757
 hypothetical protein Z2511 [imported] - Escherichia coli (strain O157:H7, substrain EDL
 C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C;Accession: G85757
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca

Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: G85757
 A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-128 <STO>
 A;Cross-references: UNIPROT:Q8X3T8; UNIPARC:UPI00000D0EB0; GB:AE005174; NID:g12515499;
 A;Experimental source: strain O157:H7, substrain EDL933
 C;Genetics:
 A;Gene: Z2511

Query Match 55.6%; Score 5; DB 2; Length 128;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
 |||||
 Db 14 KVDDT 18

RESULT 18

A59055
 Phospholipase A2 (EC 3.1.1.4), venom - Indian honeybee
 N;Alternate names: allergen api cl

C;Species: Apis mellifera cerana (Indian honeybee)
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 16-Aug-2004
 C;Accession: A59055
 R;Hoffman, D.R.; Schmidt, J.O.

submitted to the Protein Sequence Database, July 1999
 A;Description: Venom phospholipase A2.

A;Reference number: A59055
 A;Accession: A59055
 A;Status: preliminary

A;Molecule type: protein
 A;Residues: 1-134 <HOF>

A;Cross-references: UNIPARC:UPI0000050AE5
 A;Experimental source: venom
 C;Function:

A;Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl
 C;Superfamily: Phospholipase A2
 C;Keywords: calcium; carboxylic ester hydrolase; glycoprotein; lipid degradation; metal
 F;1-134/Product: phospholipase A2 #status experimental <MAT>
 F;8,10,12,35/Binding site: calcium (Trp, Gly, Gly, Asp) #status predicted
 F;9-31,30-70,37-63,61-95,105-113/Disulfide bonds: #status predicted
 F;13/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;34,64/Active site: His, Asp #status predicted

Query Match 55.6%; Score 5; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFY 7
 |||||
 Db 64 DDTFY 68

RESULT 19

AC0079
 hypothetical protein YPO0641 [imported] - Yersinia pestis (strain CO92)
 C;Species: Yersinia pestis

C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AC00079
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell, Nature 413, 523-527, 2001
 A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AC00079
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-134 <KUR>
 A:Cross-references: UNIPROT:Q8Z174; UNIPARC:UPI00000CD6PF; GB:AL590842; PIDN:CAC89494.1;
 C:Genetics:
 A:Gene: YPO0641

Query Match 55.6%; Score 5; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 8
 Db 91 DTFY 95

RESULT 20
 I53298
 cellular retinoic acid-binding protein II - rat
 C:Species: *Rattus norvegicus* (Norway rat)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C:Accession: I53298
 R:Bucco, R.A.; Melner, M.H.; Gordon, D.S.; Leers-Sucheta, S.; Ong, D.E. Endocrinology 136, 2730-2740, 1995
 A:Title: Inducible expression of cellular retinoic acid-binding protein II in rat ovary.
 A:Reference number: I53298; MUID:95269720; PMID:7750498
 A:Accession: I53298
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-139 <RES>
 A:Cross-references: UNIPROT:P51673; UNIPARC:UPI0000167AAC; EMBL:U23407; NID:g727432; PID
 A:Gene: CRABP II
 C:Superfamily: myelin P2 protein

Query Match 55.6%; Score 5; DB 2; Length 139;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DTFY 7
 Db 49 DTFY 53

RESULT 21
 shk1 kinase-binding protein 5. [imported] - fission yeast (*Schizosaccharomyces pombe*)
 C:Species: *Schizosaccharomyces pombe*
 C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
 C:Accession: T50420
 R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrrell, B.G. submitted to the EMBL Data Library, February 2000
 A:Reference number: Z25039
 A:Accession: T50420
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-140 <SEE>
 A:Cross-references: UNIPROT:Q9US59; UNIPARC:UPI000006A970; EMBL:AL157991; PIDN:CAB76222.
 A:Experimental source: strain 972h(-); cosmid c24B10
 C:Genetics:
 A:Gene: SPDB:SPCC24B10.13
 A:Map position: 3

Query Match 55.6%; Score 5; DB 2; Length 140;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 Db 41 VDDTF 45

RESULT 22
 UQ070A
 ubiquitin / ribosomal protein S27a - tomato
 N:Alternate names: ubiquitin fusion protein ubi3
 N:Contains: ribosomal protein S27a; ubiquitin
 C:Species: *Lycopersicon esculentum* (tomato)
 C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
 C:Accession: S18351; S27280; S14656
 R:Hoffman, N.E.; Ko, K.; Milkowski, D.; Pichersky, E. Plant Mol. Biol. 17, 1189-1201, 1991
 A:Title: Isolation and characterization of tomato cDNA and genomic clones encoding the
 A:Reference number: S18351; MUID:92032784; PMID:1657246
 A:Accession: S18351
 A:Molecule type: DNA
 A:Residues: 1-156 <HOF1>
 A:Cross-references: UNIPROT:P27083; UNIPROT:P03993; UNIPARC:UPI000016DE25; EMBL:X58253;
 A:Accession: S27280
 A:Molecule type: mRNA
 A:Residues: 1-156 <HOF2>
 A:Cross-references: UNIPARC:UPI000016DE25; GB:X58253; NID:g19396; PIDN:CAA41207.1; PID:9
 C:Genetics:
 A:Gene: UBI3
 A:Map position: 1
 C:Superfamily: ubiquitin / rat ribosomal protein S27a; ribosomal protein S27a homology;
 C:Keywords: protein biosynthesis; protein degradation; ribosome
 F:1-76/Product: ubiquitin #status predicted <MAT1>
 F:1-76/Domains: ubiquitin homology <UBH>
 F:77-156/Product: ribosomal protein S27a #status predicted <MAT2>
 F:101-151/Domains: ribosomal protein S27a homology <RIB>

Query Match 55.6%; Score 5; DB 1; Length 156;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 107 KVDDT 111

RESULT 23
 S25305
 ubiquitin / ribosomal protein S27a - potato
 N:Contains: ribosomal protein S27a; ubiquitin
 C:Species: *Solanum tuberosum* (potato)
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
 C:Accession: S25305; S19798
 R:Garbarino, J.E.; Rockhold, D.R.; Belknap, W.R. Plant Mol. Biol. 20, 235-244, 1992
 A:Title: Expression of stress-responsive ubiquitin genes in potato tubers.
 A:Reference number: S25305; MUID:93004476; PMID:1327270
 A:Accession: S25305
 A:Molecule type: mRNA
 A:Residues: 1-156 <GAR>
 A:Cross-references: UNIPARC:UPI000016DE25; EMBL:Z11669; NID:g21600; PIDN:CRA77735.1; PID
 C:Superfamily: ubiquitin / rat ribosomal protein S27a; ribosomal protein S27a homology;
 C:Keywords: protein biosynthesis; ribosome
 F:1-76/Product: ubiquitin #status predicted <UBI>
 F:1-76/Domains: ubiquitin homology <UBH>
 F:77-156/Product: ribosomal protein S27a #status predicted <MAT>
 F:101-151/Domains: ribosomal protein S27a homology <RIB>

Query Match 55.6%; Score 5; DB 2; Length 156;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 107 KVDDT 111

RESULT 24
 A75176
 dolichyl-phosphate mannose synthase related protein PAB1981 - Pyrococcus abyssi (strain
 C;Species: Pyrococcus abyssi
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C;Accession: A75176
 R;anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
 A;Reference number: A75001
 A;Accession: A75176
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-211 <KAW>
 A;Cross-references: UNIPROT:Q9V162; UNIPARC:UPI0000034682; GB:AJ248284; GB:AL096836; NID
 A;Experimental source: strain Orsay
 C;Genetics:
 A;Gene: PAB1981
 C;Superfamily: Methanobacterium thermoautotrophicum dolichyl-phosphate mannose synthase

Query Match 55.6%; Score 5; DB 2; Length 211;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 139 KVDDT 143

RESULT 25
 A83956
 flagellar hook protein flgE [imported] - Bacillus halodurans (strain C-125)
 C;Species: Bacillus halodurans
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C;Accession: A83956
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: A83956
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-263 <STO>
 A;Cross-references: UNIPROT:Q9KA41; UNIPARC:UPI00000C3EF4; GB:AP001515; GB:BA0000004; NID
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: flgE
 C;Superfamily: rod protein flgF

Query Match 55.6%; Score 5; DB 2; Length 263;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 8
 Db 108 DTFY 112

RESULT 26
 B96612
 hypothetical protein F12K22.17 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: B96612
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: B96612
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-264 <STO>
 A;Cross-references: UNIPROT:Q9FVSO; UNIPARC:UPI00000A44DB; GB:AE005173; NID:gl1079522;
 C;Genetics:
 A;Gene: F12K22.17
 A;Map position: 1

Query Match 55.6%; Score 5; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 107 KVDDT 111

RESULT 27
 C83482
 2-phosphonoacetaldehyde hydrolase PA1311 [imported] - Pseudomonas aeruginosa (strain PA
 C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C;Accession: C83482
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
 A;Reference number: A82950; MUID:20437337; PMID:10984043
 A;Accession: C83482
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-275 <STO>
 A;Cross-references: UNIPROT:Q9I433; UNIPARC:UPI00000C5306; GB:AE004560; GB:AE004091; NID
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: phnX; PA1311

Query Match 55.6%; Score 5; DB 2; Length 275;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 186 KVDDT 190

RESULT 28
 H75326
 tRNA (guanine-N1)-methyltransferase - Deinococcus radiodurans (strain R1)
 C;Species: Deinococcus radiodurans
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
 C;Accession: H75326
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A;Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.
 A;Reference number: A75250; MUID:20036896; PMID:10567266
 A;Accession: H75326
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-279 <WHI>
 A;Cross-references: UNIPROT:Q9RSW0; UNIPARC:UPI0000137411; GB:AE002038; GB:AE000513; NID
 A;Experimental source: strain R1

C;Genetics:	
A;Gene: DR2011	
A;Map position: 1	
C;Superfamily: tRNA-(miG37) methyltransferase	
Query Match 55.6%; Score 5; DB 2; Length 279;	
Best Local Similarity 100.0%; Pred. No. 1.1e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 KVDUT 5	
DB 49 KVDUT 53	
RESULT 29	
T21974	
hypothetical protein F38H4.5 - Caenorhabditis elegans	
C;Species: Caenorhabditis elegans	
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004	
C;Accession: T21974	
R;Lennard, N.	
submitted to the EMBL Data Library, July 1996	
A;Reference number: Z19496	
A;Accession: T21974	
A;Status: preliminary; translated from GB/EMBL/DBJ	
A;Molecule type: DNA	
A;Residues: 1-284 <WIL>	
A;Cross-references: UNIPROT:Q20180; UNIPARC:UPI0000074C84; EMBL:Z77660; PIDN:CAB01173.1;	
A;Experimental source: clone F38H4	
C;Genetics:	
A;Gene: CBSP:F38H4.5	
A;Map position: 4	
A;Introns: 25/3; 221/3	
C;Superfamily: scyllo-inosamine-4-phosphate amidinotransferase	
Query Match 55.6%; Score 5; DB 2; Length 284;	
Best Local Similarity 100.0%; Pred. No. 1.1e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 3 DDTFY 7	
DB 168 DDTFY 172	
RESULT 30	
AG3556	
heat resistant agglutinin 1 precursor [imported] - Brucella melitensis (strain 16M)	
C;Species: Brucella melitensis	
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004	
C;Accession: AG3556	
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, .; Mazur, M.; Goltzman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002	
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis	
A;Reference number: AD3252; PMID:11756688	
A;Accession: AG3556	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-284 <KUR>	
A;Cross-references: UNIPROT:Q8YD01; UNIPARC:UPI0000058467; GB:AE008918; PIDN:AAL53618.1;	
A;Experimental source: strain 16M	
C;Genetics:	
A;Gene: BMELI0376	
A;Map position: 11	
Query Match 55.6%; Score 5; DB 2; Length 284;	
Best Local Similarity 100.0%; Pred. No. 1.1e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 2 VDDTF 6	
DB 75 VDDTF 79	

RESULT 31	
T09542	
endonuclease G (EC 3.1.30.-) precursor - human	
C;Species: Homo sapiens (man)	
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 12-Jul-2004	
C;Accession: T09542	
R;Zeviani, M.	
submitted to the EMBL Data Library, August 1998	
A;Reference number: Z16729	
A;Accession: T09542	
A;Status: preliminary; translated from GB/EMBL/DBJ	
A;Molecule type: mRNA	
A;Residues: 1-297 <ZEV>	
A;Cross-references: UNIPROT:Q14249; UNIPARC:UPI0000161B77; EMBL:X79444; NID:el315166; P1	
C;Genetics:	
A;Map position: 9q34.1	
A;Genome: nuclear	
C;Function:	
A;Description: involved in the replication and transcription of the mitochondrial genome	
C;Superfamily: nuclease NUC1	
C;Keywords: endonuclease; hydrolase; mitochondrion	
Query Match 55.6%; Score 5; DB 2; Length 297;	
Best Local Similarity 100.0%; Pred. No. 1.1e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 3 DDTFY 7	
DB 156 DDTFY 160	
RESULT 32	
BS6118	
vetispiradiene synthase 2 - Hyoscyamus muticus (fragment)	
C;Species: Hyoscyamus muticus	
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004	
C;Accession: BS6118	
R;Back, K.; Chappell, J.	
J. Biol. Chem. 270, 7375-7381, 1995	
A;Title: Cloning and bacterial expression of a sesquiterpene cyclase from Hyoscyamus muticus	
A;Reference number: A56118; MUID:95221394; PMID:7706281	
A;Accession: BS6118	
A;Status: preliminary	
A;Molecule type: mRNA	
A;Residues: 1-300 <BAC>	
A;Cross-references: UNIPROT:Q39379; UNIPARC:UPI00000A5CCF; GB:U20189; NID:g763424; PIDN:	
C;Superfamily: vetispiradiene synthase 1	
Query Match 55.6%; Score 5; DB 2; Length 300;	
Best Local Similarity 100.0%; Pred. No. 1.1e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 2 VDDTF 6	
DB 53 VDDTF 57	
RESULT 33	
AH0763	
probable transcription regulator STY2278 [imported] - Salmonella enterica subsp. enteric	
C;Species: Salmonella enterica subsp. enterica serovar Typhi	
A;Note: this species has also been called Salmonella typhi	
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002	
C;Accession: AH0763	
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, ., S.; Moule, S.; O'Garra, P.	
Nature 413, 848-852, 2001	
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;	
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov	
A;Reference number: AB0502; MUID:21534947; PMID:11677608	
A;Accession: AH0763	

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-304 <PAR>
A:Cross-references: UNIPARC:UPI0000059C58; GB:AL513382; PIDN:CAD02430.1; PID:g16503297;
C:Genetics:
A:Gene: STY2278
C:Superfamily: probable transcription regulator ybbs

Query Match 55.6%; Score 5; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||||
Db 99 VDDTF 103

RESULT 34
G97132
uncharacterized phage related protein [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: G97132
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium CLO
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: G97132
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-306 <KUR>
A:Cross-references: UNIPROT:Q97HX0; UNIPARC:UPI00000CA335; GB:AE001437; PIDN:AAK79850.1;
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1886

Query Match 55.6%; Score 5; DB 2; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||
Db 111 KVDDT 115

RESULT 35
T49912
hypothetical protein T24H18.150 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T49912
R;Bevan, M.; Robben, J.; Gymnoprrez, B.; Volckaert, G.; Bancroft, I.; Mewes, H.W.; Rudd, submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25024
A:Accession: T49912
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-311 <BEV>
A:Cross-references: UNIPROT:Q9SLXU1; UNIPARC:UPI0000005377; EMBL:AL353013; GSPDB:GN00063;
A:Experimental source: cultivar Columbia; BAC clone T24H18
C:Genetics:
A:Gene: ATSP:T24H18.150
A:Map position: 5
A:Introns: 56/3; 80/3; 110/3; 125/1; 160/3; 192/3; 256/2; 279/3

Query Match 55.6%; Score 5; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||
Db 160 KVDDT 164

RESULT 36
AD1285
glycerate dehydrogenases homolog lml684 [imported] - Listeria monocytogenes (strain EG
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
C:Accession: AD1285
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Faihi, H
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A:Title: Comparative Genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1285
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-313 <GLA>
A:Cross-references: UNIPROT:Q8Y6K0; UNIPARC:UPI00000553E0; GB:NC_003210; PIDN:CAC99762.
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lml684
C:Superfamily: Phosphoglycerate dehydrogenase

Query Match 55.6%; Score 5; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 8
|||||
Db 24 DTFY 28

RESULT 37
AG1656
glycerate dehydrogenases homolog lin1792 [imported] - Listeria innocua (strain Clp1126
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
C:Accession: AG1656
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Faihi, H
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A:Title: Comparative Genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1656
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-313 <GLA>
A:Cross-references: UNIPROT:Q92AX6; UNIPARC:UPI00000CC675; GB:AL592022; PIDN:CAC97023.1
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lin1792
C:Superfamily: Phosphoglycerate dehydrogenase

Query Match 55.6%; Score 5; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 23 DDTFY 27

RESULT 38
SS1729
NSP3 protein - human rotavirus (strain S2)
N:Alternate names: NS34 protein
C:Species: human rotavirus

A,Variety: strain S2
 C,Date: 07-May-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
 C,Accession: S51729
 R,Rao, C.D.; Das, M.; Rao, B.S.; Gowda, K.
 submitted to the EMBL Data Library, September 1994
 A,Reference number: S51709
 A,Accession: S51729
 A,Status: preliminary
 A,Molecule type: mRNA
 A,Residues: 1-313 <RAO>
 A,Cross-references: UNIPROT:Q82052; UNIPARC:UPI00000EC0A9; EMBL:X81428; NID:G607093; PID:
 C,Superfamily: rotavirus nonstructural protein

Query Match 55.6%; Score 5; DB 2; Length 313;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 154 VDDTF 158

RESULT 39
 AG0503
 probable regulatory protein STY0014 [imported] - Salmonella enterica subsp. enterica ser
 C,Species: Salmonella enterica subsp. enterica serovar Typhi
 A,Note: this species has also been called Salmonella typhi
 C,Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C,Accession: AG0503
 R,Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Connerthon, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A,Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A,Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A,Reference number: AB0502; MUID:21534947; PMID:11677608
 A,Accession: AG0503
 A,Status: preliminary
 A,Molecule type: DNA
 A,Residues: 1-315 <PAR>
 A,Cross-references: UNIPARC:UPI000005996F; GB:AL513382; PIDN:CAD01167.1; PID:g16501297;
 C,Genetics:
 A,Gene: STY0014

Query Match 55.6%; Score 5; DB 2; Length 315;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 84 VDDTF 88

RESULT 40
 F64966
 probable transcription regulator yeeY - Escherichia coli (strain K-12)
 C,Species: Escherichia coli
 C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
 C,Accession: F64966
 R,Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 .A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A,Title: The complete genome sequence of Escherichia coli K-12.
 A,Reference number: A64720; MUID:97426617; PMID:9278503
 A,Accession: F64966
 A,Status: nucleic acid sequence not shown; translation not shown
 A,Molecule type: DNA
 A,Residues: 1-316 <BLAT>
 A,Cross-references: UNIPARC:UPI00001680FE; GB:AE000293; GB:U00096; NID:G2367127; PIDN:AP
 A,Experimental source: strain K-12, substrain MG1655
 C,Genetics:
 A,Gene: yeeY
 C,Superfamily: probable transcription regulator ybbs

C,Keywords: DNA binding; nucleotide binding; P-loop; transcription regulation
 F:307-314/Region: nucleotide-binding motif A (P-loop)

Query Match 55.6%; Score 5; DB 1; Length 316;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 106 VDDTF 110

RESULT 41
 A99981
 probable transcription regulator LYSR-type [imported] - Escherichia coli (strain O157:H7
 C,Species: Escherichia coli
 C,Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C,Accession: A99981
 R,Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A,Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
 A,Reference number: A99629; MUID:21156231; PMID:11258796
 A,Accession: A99981
 A,Status: preliminary
 A,Molecule type: DNA
 A,Residues: 1-316 <HAY>
 A,Cross-references: UNIPROT:Q8X4U0; UNIPARC:UPI00000D0D78; GB:BA000007; PIDN:BA836240.1;
 A,Experimental source: strain O157:H7, substrain RIMD 0509952
 C,Genetics:
 A,Gene: ECs2817
 C,Superfamily: probable transcription regulator ybbs

Query Match 55.6%; Score 5; DB 2; Length 316;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 106 VDDTF 110

RESULT 42
 F85826
 probable transcription regulator LYSR-type yeeY [imported] - Escherichia coli (strain O1
 C,Species: Escherichia coli
 C,Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C,Accession: F85826
 R,Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A,Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A,Reference number: A85480; MUID:21074935; PMID:11206551
 A,Accession: F85826
 A,Status: preliminary
 A,Molecule type: DNA
 A,Residues: 1-316 <STO>
 A,Cross-references: UNIPROT:Q8X4U0; UNIPARC:UPI00000D0D78; GB:AE005174; NID:g12516196;
 A,Experimental source: strain O157:H7, substrain EDL933
 C,Genetics:
 A,Gene: yeeY
 C,Superfamily: probable transcription regulator ybbs

Query Match 55.6%; Score 5; DB 2; Length 316;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 106 VDDTF 110

RESULT 43

T29624

hypothetical protein K09E3.5 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T29624
 R:Johnson, D.; Gattung, S.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of *C. elegans* cosmid K09E3.
 A:Reference number: Z20655
 A:Accession: T29624
 A:Molecule type: DNA
 A:Residues: 1-317 <JOH>
 A:Cross-references: UNIPROT:Q21395; UNIPARC:UPI0000079763; EMBL:U41033; PIDN:AAA82372.1;
 C:Genetics:
 A:Gene: CESP:K09E3.5
 A:Introns: 75/1; 238/3
 C:Superfamily: *Caenorhabditis elegans* hypothetical protein C08A9.6

Query Match 55.6%; Score 5; DB 2; Length 317;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 148 VDDTF 152

RESULT 44

NCBYN1
 nuclease NUC1 (EC 3.1.1.30.-) precursor, mitochondrial - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: protein HR329; protein J0310; protein YUL208c
 C:Species: *Saccharomyces cerevisiae*
 C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
 C:Accession: S05888; S50777; S46621; S56995; S56998; S45165
 R:Vincenot, R.D.; Hofmann, T.J.; Zassenhaus, H.P.
 Nucleic Acids Res. 16, 3297-3312, 1988
 A:Title: Sequence and expression of NUC1, the gene encoding the mitochondrial nuclease
 A:Reference number: S05885; MUID:88233924; PMID:2836792
 A:Accession: S05888
 A:Molecule type: DNA
 A:Residues: 1-329 <VIN>
 A:Cross-references: UNIPROT:P08456; UNIPARC:UPI0000052ED4; EMBL:X06670; NID:G4062; PIDN:
 R:Vandenbol, M.; Durand, P.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.
 Yeast 10, 1657-1662, 1994
 A:Title: Sequence analysis of a 40.2 kb DNA fragment located near the left telomere of Y
 A:Reference number: S50701, MUID:95242842; PMID:7725802
 A:Accession: S50777
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-329 <VAV>
 A:Cross-references: UNIPARC:UPI0000052ED4; EMBL:Z34098; NID:G496934; PIDN:CAA84003.1; PI
 R:Purnelle, B.; Coster, F.; Goffeau, A.
 Yeast 10, 1235-1249, 1994
 A:Title: The sequence of a 36 kb segment on the left arm of yeast chromosome X identifies
 a gene ACO1 and two homologues to chromosome III genes.
 A:Reference number: S46621; MUID:95274326; PMID:7754713
 A:Accession: S46621
 A>Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-329 <PUR>
 A:Cross-references: UNIPARC:UPI0000052ED4; EMBL:X77688; NID:G1183992; PIDN:CAA54748.1; R
 R:Purnelle, B.; Coster, F.; Goffeau, A.
 submitted to the Protein Sequence Database, September 1995
 A:Reference number: S56977
 A:Accession: S56995
 A:Molecule type: DNA
 A:Residues: 1-329 <PUW>
 A:Cross-references: UNIPARC:UPI0000052ED4; EMBL:Z49483; NID:G1015588; PIDN:CAA89505.1; R
 R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
 submitted to the Protein Sequence Database, September 1995
 A:Reference number: S56835

A:Accession: S56998

A:Molecule type: DNA
 A:Residues: 1-329 <VAN>
 A:Cross-references: UNIPARC:UPI0000052ED4; EMBL:Z49483; NID:G1015588; PIDN:CAA89505.1;
 C:Genetics:
 A:Gene: SGD:NUC1; MIPS:YJL208C
 A:Cross-references: SGD:S0003744; MIPS:YJL208C
 A:Map position: 10L
 A:Genome: nuclear
 C:Complex: homodimer
 C:Function:
 A:Description: nuclease
 A>Note: the protein has both RNase and DNase activity
 C:Superfamily: nuclease NUC1
 C:Keywords: homodimer; hydrolase; membrane protein; mitochondrion
 F:138/Active site: His #status predicted

Query Match 55.6%; Score 5; DB 1; Length 329;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 |||||
 Db 153 DDTFY 157

RESULT 45

T33944
 hypothetical protein C01B4.6 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T33944
 R:Smith, A.; Wamsley, P.; Fronick, W.
 submitted to the EMBL Data Library, February 1999
 A:Description: The sequence of *C. elegans* cosmid C01B4.
 A:Reference number: Z21443
 A:Accession: T33944
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-330 <SMI>
 A:Cross-references: UNIPROT:Q9UAT6; UNIPARC:UPI000007A31B; EMBL:AF125952; PIDN:AAD14698
 A:Experimental source: strain Bristol N2; clone C01B4
 C:Genetics:
 A:Gene: CESP:C01B4.6
 A:Map position: 5
 A:Introns: 49/1; 100/3; 133/3; 304/3
 C:Superfamily: aldose 1-epimerase

Query Match 55.6%; Score 5; DB 2; Length 330;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 189 VDDTF 193

RESULT 46

A10491
 probable membrane protein YPO4045 [imported] - *Yersinia pestis* (strain CO92)
 C:Species: *Yersinia pestis*
 C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: A10491
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;
 Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: A10491

A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-330 <KUR>

A:Cross-references: UNIPROT:Q8Z9Y6; UNIPARC:UPI00000DCDAD; GB:AL590842; PIDN:CAC93501.1;
C:Gene: YPO4045

Query Match 55.6%; Score 5; DB 2; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
|||
Db 179 DTFYY 183

RESULT 47

D91184
hypothetical protein EC64444 [imported] - Escherichia coli (strain O157:H7, substrain R1
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: D91184

R;Hayashi, T.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
gagawara, N.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno

A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D91184
A>Status: preliminary
A:Molecule type: DNA

A:Residues: 1-331 <HAY>

A:Cross-references: UNIPROT:Q8XDM7; UNIPARC:UPI00000D033C; GB:BA000007; PIDN:BAB37867.1;
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: EC64444

Query Match 55.6%; Score 5; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
|||
Db 179 DTFYY 183

RESULT 48

B86031
hypothetical protein yiaH [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: B86031

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: B86031

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-331 <STO>

A:Cross-references: UNIPROT:Q8XDM7; UNIPARC:UPI00000D033C; GB:AE005174; NID:gl2518299; E
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yiaH

Query Match 55.6%; Score 5; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
|||
Db 179 DTFYY 183

RESULT 49

S47782

hypothetical 37.6K protein (glyO-xyLB intergenic region) - Escherichia coli (strain K-1.
N:Alternate names: hypothetical protein o331

C:Species: Escherichia coli

C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004

C:Accession: S47782; C65155

R;Plunkett, G.

submitted to the EMBL Data Library, March 1994

A:Reference number: S47666

A:Accession: S47782

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-331 <PLU>

A:Cross-references: UNIPROT:P37669; UNIPARC:UPI000013B368; EMBL:U00039; NID:g466582; PID

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: C65155

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-331 <BLAT>

A:Cross-references: UNIPARC:UPI000013B368; GB:AE000433; GB:U00096; NID:g1789977; PIDN:AA

A:Experimental source: strain K-12, substrain MGI655

C:Genetics:
A:Gene: yiaH

Query Match 55.6%; Score 5; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
|||
Db 179 DTFYY 183

RESULT 50

C56118

vetispiradiene synthase 2 - Hyoscyamus muticus (fragment)

C:Species: Hyoscyamus muticus

C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C:Accession: C56118

R;Back, K.; Chappell, J.

J. Biol. Chem. 270, 7375-7381, 1995

A:Title: Cloning and bacterial expression of a sesquiterpene cyclase from Hyoscyamus mut

A:Reference number: A56118; MUID:95221394; PMID:7706281

A:Accession: C56118

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-350 <BAC>

A:Cross-references: UNIPROT:Q39980; UNIPARC:UPI00000A52B1; GB:U20190; NID:g763426; PIDN:

A:Note: authors translated the codon GAA for residue 181 as Val, and GCA for residue 182

C:Superfamily: vetispiradiene synthase 1

Query Match 55.6%; Score 5; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 102 VDDTF 106

RESULT 51

AC2367

glucose-1-phosphate thymidyltransferase [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AC2367

R;kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC2367
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-358 <KUR>
A;Cross-references: UNIPROT:Q8YNS0; UNIPARC:UPI000000CEB4C; GB:BA0000019; PIDN:BAB76190.1;
A;Experimental source: strain PCC 7120
C;Genetics:
C;Superfamily: mannose-1-phosphate guanylyltransferase

Query Match 55.6%; Score 5; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
DB 147 KVDDT 151
|||||

RESULT 52
JC1069
nonstructure protein - rice dwarf virus
C;Species: rice dwarf virus
C;Date: 09-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 20-Sep-1999
C;Accession: JC1069
R;Chu, R.Y.; Zhang, X.; Pan, N.S.; Chen, Z.L.
Acta Bot. Sin. 35, 115-120, 1993
A;Title: The cDNA cloning and nucleotide sequence of the gene encoding nonstructure protein
A;Reference number: JC1069
A;Accession: JC1069
A;Molecule type: mRNA
A;Residues: 1-372 <CHU>
C;Genetics:
A;Cross-references: UNIPARC:UPI00001786F4
A;Map position: segment 10
C;Superfamily: wound tumor virus nonstructural protein Pns11

Query Match 55.6%; Score 5; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
DB 159 DTFYY 163
|||||

RESULT 53
C83766
adenine glycosylase BH0931 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: C83766
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83766
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-372 <STO>
A;Cross-references: UNIPROT:Q9KEC2; UNIPARC:UPI000000C3A35; GB:AP001510; GB:BA0000004; NID
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0931
C;Superfamily: A/G-specific adenine glycosylase

Query Match 55.6%; Score 5; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5

DB 361 KVDDT 365
|||||

RESULT 54
G83857

tryptophan synthase (beta subunit) trpB [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G83857
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83857
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-399 <STO>
A;Cross-references: UNIPROT:Q9KCB0; UNIPARC:UPI00001374FD; GB:AP001512; GB:BA0000004; NID
A;Experimental source: strain C-125
C;Genetics:
A;Gene: trpB
C;Superfamily: tryptophan synthase beta chain; tryptophan synthase beta chain homology

Query Match 55.6%; Score 5; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DTFY 7
DB 186 DTFY 190
|||||

RESULT 55
JS0343

tryptophan synthase (EC 4.2.1.20) beta chain - Lactobacillus casei
C;Species: Lactobacillus casei
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: S42346; JS0343
R;Natori, Y.; Kano, Y.; Imamoto, F.
J. Biochem. 107, 248-255, 1990
A;Title: Nucleotide sequences and genomic constitution of five tryptophan genes of Lactobacillus casei
A;Reference number: S42346; MUID:90299861; PMID:2113923
A;Accession: S42346
A;Molecule type: DNA
A;Residues: 1-406 <NAT>
A;Cross-references: UNIPROT:P17167; UNIPARC:UPI0000137513; EMBL:D00496; NID:g216754; PI
A;Experimental source: isolate RNL7
C;Genetics:
A;Gene: trpB
C;Function:
A;Description: catalyzes conversion of indoleglycerol phosphate and serine to tryptophan
A;Pathway: tryptophan biosynthesis
A;Note: cofactor pyridoxal phosphate; last step in pathway
C;Superfamily: tryptophan synthase beta chain; tryptophan synthase beta chain homology
C;Keywords: carbon-oxygen lyase; hydro-lyase; phosphoprotein; pyridoxal phosphate; tryp
F13-397/Domain: tryptophan synthase beta chain homology <TRPB>
F;96/Active site: His #status predicted
F;97/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 55.6%; Score 5; DB 2; Length 406;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DTFY 7
DB 192 DTFY 196
|||||

RESULT 56
JN0319

acid phosphatase (EC 3.1.3.2) precursor, phosphate-repressible - Penicillium chrysogenum
C;Species: Penicillium chrysogenum

C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
A:Accession: JN0319; PU0032
R:Haas, H.; Redl, B.; Friedlin, E.; Stoeffler, G.
Gene 113, 129-133, 1992
A:Title: Isolation and analysis of the *Penicillium chrysogenum* *phoA* gene encoding a secreted phosphatase
A:Reference number: JN0319; MUID:92225342; PMID:1563629
A:Accession: JN0319
A:Molecule type: DNA
A:Residues: 1-412 <HAA>
A:Cross-references: UNIPROT:P37274; UNIPARC:UPI00001319B2; GB:M80366; NID:g169175; PIDN:PI00032
A:Accession: PU0032
A:Molecule type: protein
A:Residues: 49-75;132-150;185-202;240-273;316-344;368-396 <HAAL>
A:Cross-references: UNIPARC:UPI0000179849; UNIPARC:UPI000017984A; UNIPARC:UPI000017984B;
C:Genetics:
A:Gene: *phoA*
A:Introns: 64/3
C:Keywords: glycoprotein; phosphoric monoester hydrolase
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-411/Product: acid phosphatase #status predicted <MAT>
F:74,121,186,217,332,343/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 55.6%; Score 5; DB 2; Length 412;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 278 DDTFY 282

RESULT 57
JC2389
acid phosphatase (EC 3.1.3.2) - *Aspergillus ficuum*
C:Species: *Aspergillus ficuum*
C>Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 12-Sep-1997
A:Accession: JC2389; PC2243
R:Erlich, K.C.; Montalbano, B.G.; Mullaney, E.J.; Dischinger Jr., H.C.; Ullah, A.H.J.
Biochem. Biophys. Res. Commun. 204, 63-68, 1994
A:Title: An acid phosphatase from *Aspergillus ficuum* has homology to *Penicillium chrysogenum*
A:Reference number: JC2389; MUID:95032134; PMID:7945393
A:Accession: JC2389
A:Molecule type: DNA
A:Residues: 1-417 <EHRL>
A:Cross-references: UNIPARC:UPI00001319B1; GB:L20566; NID:g304094; PID:g304095
A:Accession: PC2243
A:Molecule type: protein
A:Residues: 32-180;204-220;252-297;325-413 <EHR2>
A:Cross-references: UNIPARC:UPI0000179845; UNIPARC:UPI0000179846; UNIPARC:UPI0000179847;
C:Genetics:
A:Gene: *APPhoA*
A:Introns: 64/3
C:Keywords: glycoprotein; phosphoric monoester hydrolase
F:215-216/Region: catalytic #status predicted
F:122,187,209,218,333,383/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 55.6%; Score 5; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 279 DDTFY 283

RESULT 58
B31776
hypothetical protein (LAC12 3' region) - yeast (*Kluyveromyces marxianus* var. *Lactis*)
C:Species: *Kluyveromyces marxianus* var. *Lactis*, *Candida sphaerica*
C>Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
A:Accession: B31776
R:Chang, Y.D.; Dickson, R.C.
J. Biol. Chem. 263, 16696-16703, 1988

A:Title: Primary structure of the lactose permease gene from the yeast *Kluyveromyces fragilis*
A:Reference number: A92683; MUID:89034156; PMID:3053697
A:Accession: B31776
A:Molecule type: DNA
A:Residues: 1-422 <CHA>
A:Cross-references: UNIPROT:P08540; UNIPARC:UPI0000168907; GB:X06997; NID:g2856; PIDN:PI00032

Query Match 55.6%; Score 5; DB 2; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 293 DDTFY 297

RESULT 59
T36585
probable membrane protein - *Streptomyces coelicolor*
C:Species: *Streptomyces coelicolor*
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
A:Accession: T36585
R:Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1999
A:Reference number: Z21575
A:Accession: T36585
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-425 <OLI>
A:Cross-references: UNIPROT:Q9X8T4; UNIPARC:UPI00000DB069; EMBL:AL049826; PIDN:CAB42736
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: *SCOREDB:SCH24.20C*

Query Match 55.6%; Score 5; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||||
Db 359 VDDTF 363

RESULT 60
E86575
phosphate permease [imported] - *Chlamydomonas reinhardtii* (strain J138)
C:Species: *Chlamydomonas reinhardtii*, *Chlamydomonas reinhardtii*
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
A:Accession: E86575
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishiguro, M.
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of *Chlamydomonas reinhardtii* J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: E86575
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <STO>
A:Cross-references: UNIPROT:Q9Z7M4; UNIPARC:UPI0000165655; GB:BA000008; NID:g8979052; PIDN:PI00032
A:Experimental source: strain J138
C:Genetics:
A:Gene: *Ygo4*

Query Match 55.6%; Score 5; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYIV 9
|||||
Db 223 TFYIV 227

RESULT 61
D72049

phosphate permease - Chlamydophila pneumoniae (strain CWL029)
 C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: D72049
 R;Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
 A:Title: Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.
 A:Reference number: A72000; MUID:99206606; PMID:10192388
 A:Accession: D72049
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-426 <ARN>
 A:Cross-references: UNIPROT:Q9Z7M4; UNIPARC:UPI00000139BC5; GB:AE001650; GB:AE001363; NID: A:Experimental source: strain CWL029
 C:Genetics:
 A:Gene: Y9o4

Query Match 55.6%; Score 5; DB 2; Length 426;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFFYV 9
 |||||
 Db 223 TFFYV 227

RESULT 62
 G87334
 acyl-CoA dehydrogenase family protein [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C:Accession: G87334
 R;Nierman, W.C.; Feildblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: G87334
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-435 <STO>
 A:Cross-references: UNIPROT:Q9AAB4; UNIPARC:UPI000000C712A; GB:AE005673; NID:g13421911; H C:Genetics:
 A:Gene: CC0690
 C:Superfamily: acyl-CoA dehydrogenase

Query Match 55.6%; Score 5; DB 2; Length 435;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 75 VDDTF 79

RESULT 63
 JS0374
 hypothetical 51.6K protein - soybean chlorotic mottle virus
 C:Species: soybean chlorotic mottle virus
 A:Note: host Glycine max (soybean)
 C:Accession: JS0374
 R;Hasegawa, A.; Verver, J.; Shimada, A.; Saito, M.; Goldbach, R.; van Kammen, A.; Miki, Nucleic Acids Res. 17, 993-10013, 1989
 A:Title: The complete sequence of soybean chlorotic mottle virus DNA and the identification
 A:Reference number: JS0372; MUID:90098857; PMID:2602148
 A:Accession: JS0374
 A:Molecule type: DNA
 A:Residues: 1-440 <HAS>
 A:Cross-references: UNIPARC:UPI000017A805; GB:X15828; NID:g58833; PIDN:CAA33828.1; PID:9 C:Keywords: DNA binding; zinc finger

Query Match 55.6%; Score 5; DB 2; Length 440;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 8
 |||||
 Db 147 DTFYV 151

RESULT 64

H81777
 UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diamino-pimelate-D-alanyl-D-alanine ligase (E
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-Oct-2004
 C:Accession: H81777
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: A81775; MUID:20222556; PMID:10761919
 A:Accession: H81777
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-452 <PAR>
 A:Cross-references: UNIPROT:Q9JSZ1; UNIPARC:UPI000000C4D1F; GB:AL162758; GB:AL157959; NID: A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: murF; NMA2068
 C:Superfamily: UDP-N-acetylmuramate-alanine ligase
 C:Keywords: ligase

Query Match 55.6%; Score 5; DB 2; Length 452;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 |||||
 Db 80 KVDDT 84

RESULT 65

D81202
 UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase NMB
 C:Species: Neisseria meningitidis
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
 C:Accession: D81202
 R;Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M. Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.; V A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A:Reference number: A81000; MUID:20175755; PMID:10710307
 A:Accession: D81202
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-455 <TET>
 A:Cross-references: UNIPROT:Q9K0Y8; UNIPARC:UPI000000C449F; GB:AE002397; GB:AE002098; NID: A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NMB0416
 C:Superfamily: UDP-N-acetylmuramate-alanine ligase

Query Match 55.6%; Score 5; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 |||||
 Db 80 KVDDT 84

RESULT 66

T00090
glycosyltransferase rgpEc - Streptococcus mutans
C:Species: Streptococcus mutans
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C:Accession: T00090
R:Yamashita, Y.; Teukioka, Y.; Tomihisa, K.; Nakano, Y.; Koga, T.
J. Bacteriol. 181, 5803-5807, 1998
A:Title: Genes involved in cell wall localization and side chain formation of rhamnose-9
A:Reference number: Z14108
A:Accession: T00090
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-465 <YAM>
A:Cross-references: UNIPROT:O82877; UNIPARC:UPI00000BAC49; EMBL:AB010970; NID:dl1224517;
A:Experimental source: strain XC
C:Genetics:
A:Gene: rgpEc

Query Match 55.6%; Score 5; DB 2; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
DB 183 VDDTF 187

RESULT 67
T24724
hypothetical protein T09A5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T24724
R:Lightning, J.
submitted to the EMBL Data Library, August 1994
A:Reference number: Z19928
A:Accession: T24724
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-468 <WIL>
A:Cross-references: UNIPARC:UPI00001779A5; EMBL:Z36753; PIDN:CAA85338.1; GSPDB:GN000020;
A:Experimental source: clone T09A5
C:Genetics:
A:Gene: CESP:T09A5.3
A:Map position: 2
A:Introns: 35/2; 84/3; 126/2; 156/3; 198/1; 237/2; 282/1; 348/3; 391/1; 429/3
C:Superfamily: acetylcholine receptor

Query Match 55.6%; Score 5; DB 2; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TPYYV 9
DB 246 TPYYV 250

RESULT 68
T01260
probable ammonium transport protein F16M14.22 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01260; T02516; B84803
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, July 1998
A:Description: Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence.
A:Reference number: Z14213
A:Accession: T01260
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-475 <ROU>
A:Cross-references: UNIPROT:Q9MGN7; UNIPARC:UPI0000048613; EMBL:AC003028; NID:g3335356;
A:Experimental source: cultivar Columbia

R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
submitted to the EMBL Data Library, August 1998
A:Description: Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence.
A:Reference number: Z14676
A:Accession: T02516
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-434 <RO2>
A:Cross-references: UNIPARC:UPI0000178E16; EMBL:AC004683; NID:g333954421; PID:g33395443
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB4420; MUID:20083487; PMID:10617197
A:Accession: B84803
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-475 <STO>
A:Cross-references: UNIPARC:UPI0000048613; GB:AE002093; NID:g6598436; PIDN:AAC28754.2;
C:Genetics:
A:Gene: At2G38290
A:Map position: 2
A:Introns: 104/3; 201/3; 297/1; 331/3
C:Superfamily: ammonium transporter nrgA

Query Match 55.6%; Score 5; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
DB 331 KVDDT 335

RESULT 69
JC7179
acid phosphatase (EC 3.1.3.2) Pho610 - Yeast (Kluyveromyces marxianus)
N:Alternate names: Pho610 protein
C:Species: Kluyveromyces marxianus
C:Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 09-Jul-2004
C:Accession: JC7179
R:Yoda, K.; Ko, J.H.; Nagamatsu, T.; Lin, Y.; Kaibara, C.; Kawada, T.; Tomishige, N.; Ha
Biosci. Biotechnol. Biochem. 64, 142-148, 2000
A:Title: Molecular characterization of a novel yeast cell-wall acid phosphatase cloned f
A:Reference number: JC7179; MUID:20169637; PMID:10705459
A:Accession: JC7179
A:Molecule type: DNA
A:Residues: 1-483 <YOD>
A:Cross-references: UNIPROT:Q7M4U8; UNIPARC:UPI000017984F; GB:E02615
A:Experimental source: strain Y-610
C:Comment: This enzyme, highly glycosylated, is a covalently-linked cell-wall protein ha
rganic compounds.
C:Genetics:
A:Gene: pho610
C:Keywords: cell wall; endoplasmic reticulum; glycoprotein; phosphoric monoester hydrola

Query Match 55.6%; Score 5; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
DB 294 DDTFY 298

RESULT 70
T47974
hypothetical protein F15G16.210 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47974

R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet
 Submitted to the Protein Sequence Database, January 2000
 A;Reference number: Z24480
 A;Accession: T47974
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-483 <DEH>
 A;Cross-references: UNIPROT:Q9M356; UNIPARC:UPI000009B4DF; EMBL:AL132959
 A;Experimental source: cultivar Columbia; BAC clone F15G16
 C;Genetics:
 A;Map position: 3
 A;Note: F15G16.210

Query Match 55.6%; Score 5; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 8
 |||||
 Db 326 DTFY 330

RESULT 71

D86385
 hypothetical protein F2J7.6 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: D86385
 R;Theologia, A.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: D86385
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-483 <STO>
 A;Cross-references: UNIPROT:Q9C6M0; UNIPARC:UPI00000AC338; GB:AR005172; NID:g10092330; F
 C;Genetics:
 A;Map position: 1

Query Match 55.6%; Score 5; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 8
 |||||
 Db 326 DTFY 330

RESULT 72

S40051
 starch synthase (EC 2.4.1.21) glgA - Bacillus subtilis
 N;Alternate names: starch (bacterial glycogen) synthase glgA
 C;Species: Bacillus subtilis
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C;Accession: S40051; E69632; S36627
 R;Kiel, J.A.K.W.; Boels, J.M.; Beldman, G.; Venema, G.
 Mol. Microbiol. 11, 203-218, 1994
 A;Title: Glycogen in Bacillus subtilis: molecular characterization of an operon encoding
 A;Reference number: S40048; MUID:94195107; PMID:8145641
 A;Accession: S40051
 A;Molecule type: DNA
 A;Residues: 1-484 <KIE>
 A;Cross-references: UNIPROT:P39125; UNIPARC:UPI000006096A; EMBL:Z25795; NID:g397487; PID
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.;
 Nature 390, 249-256, 1997
 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galie
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F
 Koester, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
 A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
 A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowaka, A.; Sero
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
 A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A;Reference number: A69580; MUID:98044033; PMID:9384377
 A;Accession: E69632
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-484 <KUN>
 A;Cross-references: UNIPARC:UPI000006096A; GB:Z99119; GB:AL009136; NID:g2635411; PIDN:C
 A;Experimental source: strain 168
 C;Genetics:

A;Gene: glgA

A;Start codon: TTG

C;Superfamily: starch synthase

C;Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 55.6%; Score 5; DB 2; Length 484;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DTFY 7
 |||||
 Db 250 DTFY 254

RESULT 73

AB1584
 hypothetical protein lin1211 [imported] - Listeria innocua (strain Clip11262)
 C;Species: Listeria innocua
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AB1584
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fsihi, H.
 Science 294, 849-852, 2001
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M
 ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fsihi, H.
 Science 294, 849-852, 2001
 A;Title: Comparative genomics of Listeria species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AB1584
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-486 <GLA>
 A;Cross-references: UNIPROT:Q92CG1; UNIPARC:UPI00000CC4D0; GB:AL592022; PIDN:CAC96442.1
 A;Experimental source: strain Clip11262
 C;Genetics:

A;Gene: lin1211

Query Match 55.6%; Score 5; DB 2; Length 486;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 8
 |||||
 Db 251 DTFY 255

RESULT 74

A82632
 ammonium transporter XFL844 [imported] - Xylella fastidiosa (strain 9a5c)
 C;Species: Xylella fastidiosa
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: A82632

R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82515; MUID:20365717; PMID:10910347
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: A82632
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-492 <SIM>
 A:Cross-references: UNIPROT:Q9PCD7; UNIPARC:UPI00000C2857; GB:AE004005; GB:AE003849; NID:
 A:Experimental source: strain 9a5c
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canargo, L.E.A.; Carriaro, D.M.; Carrer, H
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.B.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigh
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tsuchioka, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF1844
 C:Superfamily: ammonium transporter nrgA

Query Match 55.6%; Score 5; DB 2; Length 492;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 393 KVDDT 397

RESULT 75
 G90430
 conserved hypothetical protein [imported] - Sulfolobus solfataricus
 C:Species: Sulfolobus solfataricus
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 28-Jul-2003
 A:Accession: G90430
 R:She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
 arett, R.A.; Regan, M.A.; Senses, C.W.; Van der Oost, J.
 submitted to GenBank, April 2001
 A:Description: Sulfolobus solfataricus complete genome.
 A:Reference number: A99139
 A:Accession: G90430
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-506 <KUR>
 A:Cross-references: UNIPARC:UPI00000647AB; GB:AE006641; NID:g13815879; PIDN:AAK42702.1;
 C:Genetics:
 A:Gene: SS02575
 C:Superfamily: glycy1 monoaminopeptidase

Query Match 55.6%; Score 5; DB 2; Length 506;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 272 KVDDT 276

RESULT 76
 T22836
 hypothetical protein F57B7.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T22836
 R:Lenhard, N
 submitted to the EMBL Data Library, June 1996
 A:Reference number: Z19623
 A:Accession: T22836
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-508 <WIL>
 A:Cross-references: UNIPROT:Q20930; UNIPARC:UPI000017BA38; EMBL:Z74037; PIDN:CAA98493.1
 A:Experimental source: clone F57B7
 C:Genetics:
 A:Gene: CESP:F57B7.4
 A:Map position: 5
 A:Introns: 45/3; 137/2; 221/2; 256/2; 306/2; 409/3; 451/3

Query Match 55.6%; Score 5; DB 2; Length 508;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 Db 175 VDDTF 179

RESULT 77
 S49620
 phytoene dehydrogenase (EC 1.3.-.-) - Rhodobacter sphaeroides
 N:Alternate names: phytoene desaturase
 C:Species: Rhodobacter sphaeroides
 C:Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
 A:Accession: S49620
 R:Lang, H.P.; Cogdell, R.J.; Takaichi, S.; Hunter, C.N.
 submitted to the EMBL Data Library, November 1994
 A:Description: The complete DNA sequence, specific TMS insertion map and gene assignment
 A:Reference number: S49619
 A:Accession: S49620
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-518 <LAN>
 A:Cross-references: UNIPROT:P54980; UNIPARC:UPI00001284C3; EMBL:X82458; NID:g575405; PTI
 C:Genetics:
 A:Gene: ctri
 C:Superfamily: phytoene dehydrogenase
 C:Keywords: oxidoreductase

Query Match 55.6%; Score 5; DB 2; Length 518;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 Db 379 DDTFY 383

RESULT 78
 TS0745
 phytoene dehydrogenase (EC 1.3.-.-) [imported] - Rhodobacter sphaeroides
 C:Species: Rhodobacter sphaeroides
 C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
 A:Accession: TS0745
 R:Choudhary, M.; Kaplan, S.
 Nucleic Acids Res. 28, 862-867, 2000
 A:Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides
 A:Reference number: Z25222; MUID:20115911; PMID:10648776
 A:Accession: TS0745
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-518 <CHO>
 A:Cross-references: UNIPROT:P54980; UNIPARC:UPI000016E416; EMBL:AF195122; PIDN:AAF24289
 A:Experimental source: strain 2.4.1
 C:Genetics:
 A:Gene: ctri
 C:Superfamily: phytoene dehydrogenase

C;Keywords: oxidoreductase

Query Match 55.6%; Score 5; DB 2; Length 518;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||

Db 379 DDTFY 383

RESULT 79

A56118 vetiipiradiene synthase 1 - Hyoscyamus muticus (fragment)

C;Species: Hyoscyamus muticus
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56118

R;Back, K.; Chappell, J.

J. Biol. Chem. 270, 7375-7381, 1995

A;Title: Cloning and bacterial expression of a sesquiterpene cyclase from Hyoscyamus muticus
A;Reference number: A56118; MUID:95221394; PMID:7706281

A;Accession: A56118

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-520 <BAC>

A;Cross-references: UNIPROT:Q39978; UNIPARC:UPI00000A1DF5; GB:U20188; NID:g763422; PIDN:C;Superfamily: vetiipiradiene synthase 1

Query Match 55.6%; Score 5; DB 2; Length 520;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||||

Db 272 VDDTF 276

RESULT 80

A32617

phytoene dehydrogenase (EC 1.3.-.-) - Rhodobacter capsulatus

N;Alternate names: phytoene desaturase

C;Species: Rhodobacter capsulatus

C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004

C;Accession: A32617; S04402

R;Bartley, G.B.; Scolnik, P.A.

J. Biol. Chem. 264, 13109-13113, 1989

A;Title: Carotenoid biosynthesis in photosynthetic bacteria. Genetic characterization of the carotenoid biosynthetic gene cluster

A;Reference number: A32617; MUID:89327279; PMID:2546948

A;Accession: A32617

A;Molecule type: DNA

A;Residues: 1-524 <BAR>

A;Cross-references: UNIPROT:P17054; UNIPARC:UPI00001284C2; GB:J04969; NID:g340554; PIDN:C;Superfamily: phytoene dehydrogenase

R;Armstrong, G.A.; Alberti, M.; Leach, F.; Hearst, J.E.

Mol. Gen. Genet. 216, 254-268, 1989

A;Title: Nucleotide sequence, organization, and nature of the protein products of the carotenoid biosynthetic gene cluster

A;Reference number: S04401; MUID:89313663; PMID:2747617

A;Accession: S04402

A;Molecule type: DNA

A;Residues: 1-524 <ARM>

A;Cross-references: UNIPARC:UPI00001284C2; EMBL:X52291; NID:g45996; PIDN:CAA36533.1; PIDN:C;Superfamily: carotenoid biosynthesis; oxidoreductase

A;Note: translation of codons 1-33 is not given

A;Note: the authors translated the codon GTG for residue 34 as Met

C;Genetics:

A;Gene: crtI

C;Superfamily: phytoene dehydrogenase

C;Keywords: carotenoid biosynthesis; oxidoreductase

Query Match 55.6%; Score 5; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||

Db 378 DDTFY 382

RESULT 81

T34417

delayed rectifier channel protein homolog exp-2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C;Accession: T34417

R;Fulton, B.; Wohldmann, P.

submitted to the EMBL Data Library, July 1998

A;Description: The sequence of C. elegans cosmid F12F3.

A;Reference number: Z21521

A;Accession: T34417

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-528 <FUL>

A;Cross-references: UNIPROT:P91256; UNIPARC:UPI0000164218; EMBL:U80022; PIDN:AAC25887.1

A;Experimental source: strain Bristol N2; clone F12F3

C;Genetics:

A;Gene: exp-2; CESP:F12F3.1

A;Map position: 5

A;Introns: 42/2; 135/3; 173/3; 213/3; 271/3; 469/1

Query Match

55.6%; Score 5; DB 2; Length 528;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||

Db 213 KVDDT 217

RESULT 82

F90418

ABC transporter, probable SSO2468 [imported] - Sulfolobus solfataricus

C;Species: Sulfolobus solfataricus

C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C;Accession: F90418

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan

Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,

arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A;Description: Sulfolobus solfataricus complete genome.

A;Reference number: A99139

A;Accession: F90418

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-535 <KUR>

A;Cross-references: UNIPROT:Q97VY5; UNIPARC:UPI000006475A; GB:AE006641; NID:g13815769;

C;Genetics:

A;Gene: SSO2468

Query Match

55.6%; Score 5; DB 2; Length 535;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYV 9
|||||

Db 399 TFYV 403

RESULT 83

S54586

probable membrane protein YMR279c - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein YMR279c

C;Species: Saccharomyces cerevisiae

C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C;Accession: S54586

R;Pearson, D.; Bowman, S.

submitted to the EMBL Data Library, May 1995

A;Reference number: S54582

A;Accession: S54586

A:Molecule type: DNA
A:Residues: 1-540 <PEA>
A:Cross-references: UNIPROT:Q03263; UNIPARC:UPI000013B942; EMBL:Z49704; NID:G825540; PID
A:Experimental source: strain AB972
C:Genetics:
A:Gene: MIPS:YMR279C
A:Cross-references: SGD:S0004892
A:Map position: 13R
C:Superfamily: aminotriazole resistance protein YML116w
C:Keywords: transmembrane protein
F:109-125/Domain: transmembrane #status predicted <TM1>
F:139-155/Domain: transmembrane #status predicted <TM2>
F:174-190/Domain: transmembrane #status predicted <TM3>
F:233-249/Domain: transmembrane #status predicted <TM4>
F:268-284/Domain: transmembrane #status predicted <TM5>
F:298-314/Domain: transmembrane #status predicted <TM6>
F:335-351/Domain: transmembrane #status predicted <TM7>
F:377-393/Domain: transmembrane #status predicted <TM8>
F:400-416/Domain: transmembrane #status predicted <TM9>
F:435-451/Domain: transmembrane #status predicted <TM10>
F:503-519/Domain: transmembrane #status predicted <TM11>
Query Match 55.6%; Score 5; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TFYYV 9
Db 353 TFYYV 357
RESULT 84
T06264
N:Contains: 3-dehydroquininate dehydratase (EC 4.2.1.10) / shikimate 5-dehydrogenase (EC 1.1.1.25) - b
C:Species: Lycopersicon esculentum (tomato)
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T06264
R:Bischoff, M.
submitted to the EMBL Data Library, November 1997
A:Description: Lycopersicon esculentum dehydroquininate dehydratase/shikimate:NADP oxidore
A:Reference number: Z15575
A:Accession: T06264
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-545 <BIS>
A:Cross-references: UNIPROT:Q65917; UNIPARC:UPI00000A2F9F; EMBL:AF033194; NID:G3169882;
A:Experimental source: strain UC82b
C:Superfamily: 3-dehydroquininate dehydratase / shikimate dehydrogenase; 3-dehydroquininate
C:Keywords: carbon-oxygen lyase; hydro-lyase; oxidoreductase
F:24-254/Domain: 3-dehydroquininate dehydratase homology <DQ>
F:324-525/Domain: shikimate dehydrogenase homology <SKD>
Query Match 55.6%; Score 5; DB 2; Length 545;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDT 5
Db 470 KVDDT 474
RESULT 85
I39593
exeA protein - Aeromonas hydrophila
C:Species: Aeromonas hydrophila
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: I39593
R:Jahagirdar, R.; Howard, S.P.
J. Bacteriol. 176, 6819-6826, 1994
A:Title: Isolation and characterization of a second exe operon required for extracellular
A:Reference number: I39593; MUID:95050248; PMID:7961440
A:Accession: I39593

A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-547 <RES>
A:Cross-references: UNIPROT:P45754; UNIPARC:UPI000012BC18; EMBL:X81473; NID:G551215; PT
C:Superfamily: Aeromonas hydrophila exeA protein
Query Match 55.6%; Score 5; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDT 5
Db 314 KVDDT 318
RESULT 86
TS1035
hypothetical protein B15120.50 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C:Accession: TS1035
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, July 2000
A:Reference number: Z25286
A:Accession: TS1035
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-548 <SCH>
A:Cross-references: UNIPROT:Q9P3K6; UNIPARC:UPI000006AF57; EMBL:AL389900; GSPDB:GN00116,
A:Experimental source: BAC clone B15120; strain OR74A
C:Genetics:
A:Gene: NCSP:B15120.50
A:Map position: 6
Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TFYYV 9
Db 252 TFYYV 256
RESULT 87
T03714
5-epi-aristolochene synthase - common tobacco
N:Alternate names: sesquiterpene cyclase
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03714
R:Facchini, P.J.; Chappell, J.
Proc. Natl. Acad. Sci. U.S.A. 89, 11088-11092, 1992
A:Title: Gene family for an elicitor-induced sesquiterpene cyclase in tobacco.
A:Reference number: Z15024; MUID:93066390; PMID:1438319
A:Accession: T03714
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-550 <FAC>
A:Cross-references: UNIPROT:Q40577; UNIPARC:UPI000014C8BF; EMBL:L04680; NID:G170342; PID
A:Experimental source: strain NK326
C:Genetics:
A:Introns: 37/3; 126/1; 251/2; 324/2; 370/3; 452/3
C:Function:
A:Description: mediates the conversion of the isoprenoid intermediate farnesyl diphosphat
C:Superfamily: vetispiradiene synthase 1
Query Match 55.6%; Score 5; DB 2; Length 550;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTF 6
Db 302 VDDTF 306

RESULT 88

D90250
glycogen synthase [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: D90250
R;She, Q.; Singh, R.K.; Confalonieri, P.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: D90250
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-566 <KUR>
A:Cross-references: UNIPROT:Q97ZD3; UNIPARC:UPI0000064308; GB:AE006641; NID:gl3814171; F
C:Genetics:
A:Gene: SSO0987

Query Match 55.6%; Score 5; DB 2; Length 566;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5

|||||
Db 516 KVDDT 520

RESULT 89

ERBP22
DNA-directed DNA polymerase (EC 2.7.7.7) - phage PZA
N:Alternate names: gene 2 protein (gp2)
C:Species: phage PZA
A:Note: host Bacillus subtilis
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 31-Dec-2004
C:Accession: D24528
R;Paces, V.; Vilek, C.; Urbanek, P.; Hostomsky, Z.
Gene 38, 45-56, 1985
A:Title: Nucleotide sequence of the major early region of Bacillus subtilis phage PZA,
A:Reference number: A91538; MUID:86056991; PMID:3934048
A:Accession: D24528
A:Molecule type: DNA
A:Residues: 1-572 <PAC>
A:Cross-references: UNIPROT:P06950; UNIPARC:UPI00001297E3; GB:M11813; GB:M13904; GB:M139
C:Genetics:
A:Gene: 2

C:Superfamily: DNA polymerase, Bacillus phage type
C:Keywords: DNA binding; early protein; nucleotidyltransferase

Query Match 55.6%; Score 5; DB 1; Length 572;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6

|||||
Db 565 VDDTF 569

RESULT 90

T37452
68K ankryrin-like protein - vaccinia virus (strain Ankara)
C:Species: vaccinia virus
A:Variety: strain Ankara
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T37452
R;Antoine, G.; Scheifflinger, F.; Falkner, F.G.; Dörner, F.
submitted to the EMBL Data Library, March 1997
A:Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain
A:Reference number: Z20877
A:Accession: T37452

A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-574 <ANT>
A:Cross-references: UNIPROT:O57263; UNIPARC:UPI00000F7EC4; EMBL:U94848; PIDN:AA96556.1
A:Experimental source: strain Ankara
C:Genetics:
A:Note: MVA186R

Query Match 55.6%; Score 5; DB 2; Length 574;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7

|||||
Db 424 DDTFY 428

RESULT 91

QJ1811
B17R protein - vaccinia virus (strain WR)
C:Species: vaccinia virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: QJ1811
R;Smith, G.L.; Chan, Y.S.; Howard, S.T.
J. Gen. Virol. 72, 1349-1376, 1991
A:Title: Nucleotide sequence of 42kbp of vaccinia virus strain WR from near the right i
A:Reference number: QJ1767; MUID:91259063; PMID:2045793
A:Accession: QJ1811
A:Molecule type: DNA
A:Residues: 1-574 <SMI>
A:Cross-references: UNIPROT:Q01222; UNIPARC:UPI00013822A; DDBJ:D11079; NID:g222717; PI

Query Match 55.6%; Score 5; DB 2; Length 574;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7

|||||
Db 424 DDTFY 428

RESULT 92

H42527
B18R protein - vaccinia virus (strain Copenhagen)
C:Species: vaccinia virus
A:Note: host Homo sapiens (man)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
C:Accession: H42527
R;Johnson, G.P.
submitted to GenBank, June 1990
A:Reference number: A33172
A:Accession: H42527

A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-574 <JOH>
A:Cross-references: UNIPROT:P21076; UNIPARC:UPI0000138229

Query Match 55.6%; Score 5; DB 2; Length 574;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7

|||||
Db 424 DDTFY 428

RESULT 93

A36857
B19R protein - variola virus
N:Alternate names: B18R protein (COP)
C:Species: variola virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: A36857; S46876

R;Blinov, V.M.
 submitted to GenBank, November 1992
 A:Reference number: A36859
 A:Accession: A36857
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-574 <BLI>
 A:Cross-references: UNIPROT:P33824; UNIPARC:UPI000013822B; GB:X69198; NID:g456758; PIDN:
 A:Experimental source: strain India-1967, ssp. major, isolate Ind3
 R;Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Froil
 submitted to the EMBL Data Library, April 1992
 A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
 A:Reference number: S46868
 A:Accession: S46876
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-574 <COL>
 A:Cross-references: UNIPARC:UPI000013822B; EMBL:X67117; NID:g516428; PIDN:CAA47528.1; PI
 A:Experimental source: strain India-1967, isolate Ind3

Query Match 55.6%; Score 5; DB 2; Length 574;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 |||||
 Db 424 DDTFY 428

RESULT 94

T28615
 hypothetical protein B16R - variola major virus
 C:Species: variola major virus
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T28615
 R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
 Nature 366, 748-751, 1993
 A:Title: Potential virulence determinants in terminal regions of variola smallpox virus
 A:Reference number: Z20488; MUID:94088747; PMID:8264798
 A:Accession: T28615
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-574 <MAS>
 A:Cross-references: UNIPROT:P33824; UNIPARC:UPI000013822B; EMBL:L22579; NID:g623595; PID
 A:Experimental source: strain Bangladesh 1975

Query Match 55.6%; Score 5; DB 2; Length 574;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 |||||
 Db 424 DDTFY 428

RESULT 95

C72174
 DBR protein - variola minor virus (strain Garcia-1966)
 C:Species: variola minor virus
 C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004
 C:Accession: C72174
 R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopaz
 submitted to GenBank, March 1998
 A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
 A:Reference number: A72150
 A:Accession: C72174
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-574 <SHC>
 A:Cross-references: UNIPROT:Q89523; UNIPARC:UPI0000061D83; GB:Y16780; NID:g5830555; PIDN
 A:Experimental source: strain Garcia-1966
 C:Genetics:
 A:Gene: DBR

Query Match 55.6%; Score 5; DB 2; Length 574;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 |||||
 Db 424 DDTFY 428

RESULT 96

ERBP29
 DNA-directed DNA polymerase (EC 2.7.7.7) - phage phi-29
 N:Alternate names: early protein gp2
 C:Species: phage phi-29
 A:Note: host Bacillus subtilis
 C:Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 31-Dec-2004
 C:Accession: A04282; B93439; S11668; S11669
 R;Yoshikawa, H.; Ito, J.
 Gene 17, 323-335, 1982

A:Title: Nucleotide sequence of the major early region of bacteriophage phi129.
 A:Reference number: A31493; MUID:82262795; PMID:6809534
 A:Accession: A04282
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-575 <YOS>

A:Cross-references: UNIPROT:P03680; UNIPARC:UPI00001297E1; GB:J02478; NID:g15
 A:Note: the authors report the amino acid composition of the translated protein; the ref
 R;Escarmis, C.; Salas, M.
 Nucleic Acids Res. 10, 5785-5798, 1982

A:Title: Nucleotide sequence of the early genes 3 and 4 of bacteriophage psi129.
 A:Reference number: A93439; MUID:83064518; PMID:6292852
 A:Accession: B93439
 A:Molecule type: DNA

A:Residues: 1-85 <ESC>
 A:Cross-references: UNIPARC:UPI0000174B74
 C:Genetics:

A:Gene: 2
 A:Map position: 16-6
 C:Superfamily: DNA polymerase, Bacillus phage type

C:Keywords: DNA binding; DNA replication; early protein; nucleotidyltransferase
 Query Match 55.6%; Score 5; DB 1; Length 575;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 Db 568 VDDTF 572

RESULT 97

S46210
 3-dehydroquinase dehydratase (EC 4.2.1.10) / shikimate 5-dehydrogenase (EC 1.1.1.25) pre
 N:Contains: 3-dehydroquinase dehydratase (EC 4.2.1.10); shikimate 5-dehydrogenase (EC 1.1.
 C:Species: Nicotiana tabacum (common tobacco)
 C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
 C:Accession: S46210; S77973
 R;Bonner, C.A.; Jensen, R.A.
 Biochem. J. 302, 11-14, 1994

A:Title: Cloning of cDNA encoding the bifunctional dehydroquinase shikimate dehydrogenas
 A:Reference number: S46210; MUID:94347087; PMID:8067995
 A:Accession: S46210
 A:Molecule type: mRNA

A:Residues: 1-579 <BON>
 A:Cross-references: UNIPROT:Q42947; UNIPARC:UPI00000A5896; GB:L32794; NID:g535770; PIDN:

A:Experimental source: strain SR1
 A:Accession: S77973
 A:Molecule type: protein

A:Residues: 24-30 <JEN>
 A:Cross-references: UNIPARC:UPI00000176055
 C:Genetics:

A:Genome: nuclear

C;Superfamily: 3-dehydroquininate dehydratase / shikimate dehydrogenase; 3-dehydroquininate
 C;Keywords: carbon-oxygen lyase; hydro-lyase; oxidoreductase; plastid
 F;1-23/Domain: transit peptide (plastid) (fragment) #status predicted <TNP>
 F;24-579/Product: 3-dehydroquininate dehydratase / shikimate 5-dehydrogenase #status expected
 F;34-245/Domain: 3-dehydroquininate dehydratase homology <QD>
 F;315-520/Domain: shikimate dehydrogenase homology <SKD>

Query Match 55.6%; Score 5; DB 2; Length 579;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
 |||||
 Db 461 KVDDT 465

RESULT 98

JC5721

vacuolar protein sorting protein 33b - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 09-Jul-2004

C;Accession: JC5721

R;Pevsner, J.; Heu, S.C.; Hyde, P.S.; Scheller, R.H.

Gene 183, 7-14, 1996

A;Title: Mammalian homologues of yeast vacuolar protein sorting (vps) genes implicated in
 A;Reference number: JC5720; MUID:97149272; PMID:8996080

A;Accession: JC5721

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-617 <PRV>

A;Cross-references: UNIPROT:Q63616; UNIPARC:UPI00001388FF; GB:U35245; NID:g1477469; PIDN

A;Experimental source: brain

C;Comment: This protein is involved in vasicular trafficking between the Golgi and lysos

Query Match 55.6%; Score 5; DB 2; Length 617;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
 |||||
 Db 251 VDDTF 255

RESULT 99

T45864

probable tyrosine phosphatase - Arabidopsis thaliana

N;Alternate names: protein F3A4.190

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C;Accession: T45864

R;Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May

submitted to the Protein Sequence Database, December 1999

A;Reference number: Z23007

A;Accession: T45864

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-628 <BAR>

A;Cross-references: UNIPROT:Q9SN07; UNIPARC:UPI00000A6AB3; EMBL:AL132978

A;Experimental source: cultivar Columbia; BAC clone F3A4

C;Genetics:

A;Map position: 3

A;Introns: 192/3; 226/3; 245/3; 267/3; 326/3; 355/3; 377/2; 399/1; 414/3; 458/2; 481/3

A;Note: F3A4.190

Query Match 55.6%; Score 5; DB 2; Length 628;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
 |||||
 Db 57 KVDDT 61

RESULT 100

AC0741

oligopeptidase B (EC 3.4.21.83) [imported] - Salmonella enterica subsp. enterica serovar

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AC0741

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
 th, T.; Connerton, P.; Cronin, A.; Davies, R.M.; Dowd, L.; White, N.; Farrar

, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AC0741

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-683 <PAR>

A;Cross-references: UNIPARC:UPI0000059D05; GB:AL513382; PIDN:CAD05630.1; PID:g16503127;

C;Genetics:

A;Gene: STY2085

C;Superfamily: prolyl oligopeptidase

C;Keywords: hydrolase; serine proteinase

Query Match 55.6%; Score 5; DB 2; Length 683;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFY 7
 |||||
 Db 221 DDTFY 225

RESULT 101

AB0217

oligopeptidase B (EC 3.4.21.83) [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C;Accession: AB0217

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AB0217

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-683 <KUR>

A;Cross-references: UNIPROT:Q8ZFD4; UNIPARC:UPI00000CD849; GB:AL590842; PIDN:CAC90598.1

C;Genetics:

A;Gene: ptrB

C;Superfamily: prolyl oligopeptidase

C;Keywords: hydrolase; serine proteinase

Query Match 55.6%; Score 5; DB 2; Length 683;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFY 7
 |||||
 Db 221 DDTFY 225

RESULT 102

C90948

proteinnase II [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: C90948

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C90948
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-686 <HAY>
A;Cross-references: UNIPROT:Q8XCK4; UNIPARC:UPI00000D0477; GB:BA000007; PIDN:BA035978.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC82555
C;Superfamily: prolyl oligopeptidase

Query Match 55.6%; Score 5; DB 2; Length 686;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYYV 9
|||
Db 185 TFYYV 189

RESULT 103
G85796
proteainase II [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: G85796
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85796
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-686 <STO>
A;Cross-references: UNIPROT:Q8XCK4; UNIPARC:UPI00000D0477; GB:AE005174; NID:gl2515898; H
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: pTrB
C;Superfamily: prolyl oligopeptidase

Query Match 55.6%; Score 5; DB 2; Length 686;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYYV 9
|||
Db 185 TFYYV 189

RESULT 104
A12849
GDEF family protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 16-Aug-2004
C;Accession: A12849
R;Wood, D.W.; Scubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: A12849
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-696 <KUR>
A;Cross-references: UNIPROT:Q8UDAI; UNIPARC:UPI00000D1E16; GB:AE008688; PIDN:AAL43215.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu2226

A;Map position: circular chromosome
C;Superfamily: Sensor diguanylate cyclase/c-di-GMP phosphodiesterase with MHTY sensor do

Query Match 55.6%; Score 5; DB 2; Length 696;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 672 VDDTF 676

RESULT 105
G97626
hypothetical protein AGR_C_4046 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 05-Oct-2004
C;Accession: G97626
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorillo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: G97626
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-696 <KUR>
A;Cross-references: UNIPROT:Q8UDAI; UNIPARC:UPI00000D1E16; GB:AE007869; PIDN:AAK87968.1;
C;Genetics:
A;Gene: AGR_C_4046
A;Map position: circular chromosome
C;Superfamily: Sensor diguanylate cyclase/c-di-GMP phosphodiesterase with MHTY sensor do

Query Match 55.6%; Score 5; DB 2; Length 696;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 672 VDDTF 676

RESULT 106
TS1034
hypothetical protein B15120.40 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 31-Dec-2004
C;Accession: TS1034
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, July 2000
A;Reference number: 225286
A;Accession: TS1034
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-705 <SCH>
A;Cross-references: UNIPROT:Q96U83; UNIPARC:UPI0000179F6E; EMBL:AL389900; GSPDB:GNO0116;
A;Experimental source: BAC clone B15120; strain OR74A
C;Genetics:
A;Gene: NCSP:B15120.40
A;Map position: 6
A;Introns: 287/3

Query Match 55.6%; Score 5; DB 2; Length 705;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||
Db 379 DDTFY 383

RESULT 107
B32571

ribosomal protein S6 kinase II (EC 2.7.1.-) alpha chain homolog (clone Mu6A) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: B32571
 R:Alcorta, D.A.; Crews, C.M.; Sweet, L.J.; Bankston, L.; Jones, S.W.; Erikson, R.L.
 Mol. Cell. Biol. 9, 3850-3859, 1989
 A:Title: Sequence and expression of chicken and mouse rsk: homologs of Xenopus laevis r-
 A:Reference number: A93113; MUID:89384612; PMID:2779569
 A:Accession: B32571
 A:Molecule type: mRNA
 A:Residues: 1-724 <ALC>
 A:Cross-references: UNIPROT:P18653; UNIPARC:UPI0000020D74; GB:M23489
 C:Superfamily: ribosomal protein S6 kinase II; protein kinase homology
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:60-321/Domain: protein kinase homology <KIN1>
 F:68-76/Region: protein kinase ATP-binding motif
 F:416-675/Domain: protein kinase homology <KIN2>
 F:405-664/Domain: protein kinase homology <KIN2>

Query Match 55.6%; Score 5; DB 1; Length 724;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 |||||
 Db 335 DDTFY 339

RESULT 108
 I51901
 ribosomal protein S6 kinase 2 (EC 2.7.1.-) 1 - human
 N:Alternate names: MAP kinase-activated PK1; p90 S6 kinase; ribosomal protein S6 kinase
 C:Species: Homo sapiens (man)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I51901
 R:Moller, D.E.; Xia, C.H.; Tang, W.; Zhu, A.X.; Jakubowski, M.
 Am. J. Physiol. 266, 351-359, 1994
 A:Title: Human rsk isoforms: cloning and characterization of tissue-specific expression.
 A:Reference number: I51901
 A:Accession: I51901
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-735 <MOL>
 A:Cross-references: UNIPROT:Q15418; UNIPARC:UPI0000035BE4; GB:I07597; NID:g292456; PIDN:
 C:Comment: Although ribosomal protein S6 (see PIR:R3HU6) is phosphorylated by this enzym
 C:Genetics:
 A:Gene: GDB:RPS6KAL; RSK; HU-1; RSK1
 A:Cross-references: GDB:365638; OMIM:601684
 A:Map position: 3pter-3qter
 C:Superfamily: ribosomal protein S6 kinase II; protein kinase homology
 C:Keywords: ATP; monomer; phosphoprotein; phosphotransferase; serine/threonine-specific
 F:60-321/Domain: protein kinase homology <KIN1>
 F:68-76/Region: protein kinase ATP-binding motif
 F:416-675/Domain: protein kinase homology <KIN2>
 F:424-432/Region: protein kinase ATP-binding motif

Query Match 55.6%; Score 5; DB 2; Length 735;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 |||||
 Db 346 DDTFY 350

RESULT 109
 A53300
 ribosomal protein S6 kinase (EC 2.7.-) II - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: A53300
 R:Grove, J.R.; Price, D.J.; Banerjee, P.; Balasubramanyam, A.; Ahmad, M.F.; Avruch, J.
 Biochemistry 32, 7727-7738, 1993
 A:Title: Regulation of an epitope-tagged recombinant Rsk-1 S6 kinase by phorbol ester an

A:Reference number: A53300; MUID:93349850; PMID:7688567
 A:Accession: A53300
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-735 <RES>
 A:Cross-references: UNIPROT:Q63531; UNIPARC:UPI000012DB2D; GB:M99169; NID:g206771; PIDN:
 C:Genetics:
 A:Gene: Rsk-1
 C:Superfamily: ribosomal protein S6 kinase II; protein kinase homology
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:60-321/Domain: protein kinase homology <KIN1>
 F:68-76/Region: protein kinase ATP-binding motif
 F:416-675/Domain: protein kinase homology <KIN2>
 F:424-432/Region: protein kinase ATP-binding motif #status atypical

Query Match 55.6%; Score 5; DB 2; Length 735;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 |||||
 Db 346 DDTFY 350

RESULT 110
 A81430
 outer membrane protein Cj0129c [imported] - Campylobacter jejuni (strain NCTC 11168)
 C:Species: Campylobacter jejuni
 C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C:Accession: A81430
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilli:
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre
 Nature 403, 665-668, 2000
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy:
 A:Reference number: A81250; MUID:20150912; PMID:10688204
 A:Accession: A81430
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-739 <PAR>
 A:Cross-references: UNIPROT:Q9PI28; UNIPARC:UPI00000C2051; GB:AL1139074; GB:AL111168; NI:
 A:Experimental source: serotype O2, strain NCTC 11168
 C:Genetics:
 A:Gene: Cj0129c

Query Match 55.6%; Score 5; DB 2; Length 739;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 |||||
 Db 400 KVDDT 404

RESULT 111
 A32571
 ribosomal protein S6 kinase II (EC 2.7.1.-) alpha chain homolog - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A32571
 R:Alcorta, D.A.; Crews, C.M.; Sweet, L.J.; Bankston, L.; Jones, S.W.; Erikson, R.L.
 Mol. Cell. Biol. 9, 3850-3859, 1989
 A:Title: Sequence and expression of chicken and mouse rsk: homologs of Xenopus laevis r-
 A:Reference number: A93113; MUID:89384612; PMID:2779569
 A:Accession: A32571
 A:Molecule type: mRNA
 A:Residues: 1-752 <ALC>
 A:Cross-references: UNIPROT:P18652; UNIPARC:UPI000012DB30; GB:M28488; NID:g551555; PIDN:
 C:Superfamily: ribosomal protein S6 kinase II; protein kinase homology
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:78-339/Domain: protein kinase homology <KIN1>
 F:86-94/Region: protein kinase ATP-binding motif
 F:433-692/Domain: protein kinase homology <KIN2>

Query Match 55.6%; Score 5; DB 1; Length 752;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DTFY 7
 |||||
 DB 364 DTFY 368

RESULT 112

T27276
 hypothetical protein Y63D3A.6b - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T27276
 R:White, S.
 submitted to the EMBL Data Library, October 1998
 A:Reference number: Z20335
 A:Accession: T27276
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-752 <WIL>
 A:Cross-references: UNIPROT:Q9UIV9; UNIPARC:UPI000007E517; EMBL:AL032652; PIDN:CAA21710.
 C:Genetics:
 A:Gene: CBSP:Y63D3A.6b
 A:Map position: 1
 A:Introns: 42/1; 80/3; 132/3; 211/3; 248/1; 329/2; 400/3; 564/3; 676/3; 711/3

Query Match 55.6%; Score 5; DB 2; Length 752;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYV 9
 |||||
 DB 14 TFYV 18

RESULT 113

DB7965
 protein Y63D3A.6b [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C:Accession: DB7965
 R:anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
 A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: DB7965
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-778 <STO>
 A:Cross-references: UNIPROT:Q9UIV9; UNIPARC:UPI000017A561; GB:chr_I; PIDN:CAA21710.1; PI
 C:Genetics:
 A:Gene: Y63D3A.6b
 A:Map position: 1

Query Match 55.6%; Score 5; DB 2; Length 778;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYV 9
 |||||
 DB 14 TFYV 18

RESULT 114

T00990
 hypothetical protein At2g26570 [imported] - Arabidopsis thaliana
 N:Alternate names: hypothetical protein T9J22.24
 C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
 C:Accession: T00990; B84662
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau:
 submitted to the EMBL Data Library, April 1998
 A:Description: Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence.
 A:Reference number: Z14161
 A:Accession: T00990
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-807 <ROU>
 A:Cross-references: UNIPROT:O48724; UNIPARC:UPI00000A832E; EMBL:AC002505; NID:g2739359;
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: B84662
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-807 <STO>
 A:Cross-references: UNIPARC:UPI00000A832E; GB:AE002093; NID:g2739382; PIDN:AAC14505.1; C:
 C:Genetics:
 A:Gene: At2g26570; T9J22.24
 A:Map position: 2
 A:Introns: 196/3

Query Match 55.6%; Score 5; DB 2; Length 807;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
 |||||
 DB 80 VDDTF 84

RESULT 115

S69563
 suppressor protein PSp1 - Yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YDR505c
 C:Species: Saccharomyces cerevisiae
 C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 C:Accession: S69563; S59357
 R:Dietrich, F.S.
 submitted to the EMBL Data Library, August 1995
 A:Description: The sequence of S. cerevisiae cosmids 8166, 9787, 9717, and lambda 3073.
 A:Reference number: S69553
 A:Accession: S69563
 A:Molecule type: DNA
 A:Residues: 1-841 <DIE>
 A:Cross-references: UNIPROT:P50896; UNIPARC:UPI00001327E3; EMBL:U33057; NID:g927764; PID
 R:Formosa, T.; Nittis, T.
 submitted to the EMBL Data Library, August 1995
 A:Description: High copy suppressors of the temperature sensitivity of DNA polymerase al
 A:Reference number: S59357
 A:Accession: S59357
 A:Molecule type: DNA
 A:Residues: 1-115, 'C', 117-121, 'KCLRLIQSVP', 134-197, 'RAILLPHTVLAT', 211-731, 'K', 733-841
 A:Cross-references: UNIPARC:UPI0000168A3B; EMBL:U33115; NID:g992653; PID:g992654
 C:Genetics:
 A:Gene: SGD:PSP1; GIN5
 A:Cross-references: SGD:S0002913; MIPS:YDR505c
 A:Map position: 4R
 C:Function:
 A:Description: high copy suppressor of polymerase mutations

Query Match 55.6%; Score 5; DB 2; Length 841;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYV 9
 |||||

Db 734 TFFYV 738

RESULT 116

T01809
hypothetical protein A.TM021B04.3 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01809
R;Dante, M.; Wamaley, P.; Gibson, A.
submitted to the EMBL Data Library, June 1997
A;Description: The sequence of A. thaliana TM021B04.
A;Reference number: Z1440
A;Accession: T01809
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-938 <DAN>
A;Cross-references: UNIPROT:O04660; UNIPARC:UPI00000A24EC; EMBL:AF007271; NID:g2191181;
C;Genetics:
A;Gene: ATSP:A.TM021B04.3
A;Map position: 5
A;Introns: 125/1; 559/3; 664/1; 798/3

Query Match 55.6%; Score 5; DB 2; Length 938;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||||
Db 209 VDDTF 213

RESULT 117

S44622
C50C3.3 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 30-Jun-2001
C;Accession: S44622
R;Favell, A.D.
submitted to the EMBL Data Library, May 1993
A;Description: Sequence of the C. elegans cosmid C50C3.
A;Reference number: S44627
A;Accession: S44622
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-955 <PAV>
A;Cross-references: UNIPARC:UPI000017B6B2; EMBL:L14433; NID:g289649; PID:g289655
C;Genetics:
A;Introns: 203/3; 461/3; 599/3; 702/1

Query Match 55.6%; Score 5; DB 2; Length 955;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||
Db 533 KVDDT 537

RESULT 118

B71468
probable insulinase family/proteinase III - Chlamydia trachomatis (serotype D, strain UM)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 31-Dec-2004
C;Accession: B71468
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: B71468
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-956 <ARN>

A;Cross-references: UNIPROT:O84812; UNIPARC:UPI00000D33B0; GB:AE001353; GB:AE001273; NI;
A;Experimental source: serotype D, strain UW-3/Cx

C;Genetics:
A;Gene: ptr

C;Superfamily: insulin-degrading enzyme (IDE)/zinc protease

Query Match 55.6%; Score 5; DB 2; Length 956;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 491 DDTFY 495

RESULT 119

T39912
conserved hypothetical protein SPBC216.06c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39912
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Oliver, K.; Harris, D.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21890
A;Accession: T39912
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-971 <LYN>
A;Cross-references: UNIPROT:Q9UUM2; UNIPARC:UPI000006C882; EMBL:AL049558; PIDN:CAB40166
A;Experimental source: strain 972h; cosmid c216
C;Genetics:
A;Gene: SPDB:SPBC216.06c
A;Map position: 2
A;Introns: 316/3

Query Match 55.6%; Score 5; DB 2; Length 971;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 8
|||||
Db 670 DTFY 674

RESULT 120

T43656
mating-type switching protein swil - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43656
R;Schmidt, H.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z22605
A;Accession: T43656
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-971 <SCH>
A;Cross-references: UNIPROT:Q9UUM2; UNIPARC:UPI0000169168; EMBL:Y19036; PIDN:CAB44362.1
A;Experimental source: strain L972
C;Genetics:
A;Gene: swil
A;Introns: 316/3

Query Match 55.6%; Score 5; DB 2; Length 971;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 8
|||||
Db 670 DTFY 674

RESULT 121

Db 759 DDTFY 763
|||||
RESULT 126
T14476
pela protein - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T14476
R;Yasukawa, H.; Mohanty, S.; Firtel, R.A.
submitted to the EMBL Data Library, December 1997
A:Reference number: Z18117
A:Accession: T14476
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1269 <YAS>
A:Cross-references: UNIPROT:O43993; UNIPARC:UPI000007CA48; EMBL:AF038919; NID:g2766695;
A:Experimental source: strain Kax3
C:Genetics:
A:Gene: pela
Query Match 55.6%; Score 5; DB 2; Length 1269;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDDT 5
|||||
Db 395 KVDDT 399
RESULT 127
S58307
hypothetical 149.2K protein SPAC1F5.01 c18b11.11 - fission yeast (Schizosaccharomyces po
C:Species: Schizosaccharomyces pombe
C>Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C:Accession: T37903; T38094; S58307
R;Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, August 1995
A:Reference number: Z21753
A:Accession: T37903
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1294 <DE2>
A:Cross-references: UNIPROT:Q09716; UNIPARC:UPI0000139F4B; EMBL:Z50728; NID:g929886; PID
A:Experimental source: strain 972h-; cosmid c18B11
R;Gentles, S.; Odell, C.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z21768
A:Accession: T38094
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1143-1294 <GEN>
A:Cross-references: UNIPARC:UPI0000162011; EMBL:Z68136; PIDN:CAA92229.1; GSPDB:GN000066;
A:Experimental source: strain 972h-; cosmid c1F5
C:Genetics:
A:Gene: SPAC1F5.01; SPAC18B11.11
A:Map position: 1L
Query Match 55.6%; Score 5; DB 2; Length 1294;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TFYVV 9
|||||
Db 560 TFYVV 564
RESULT 128
E71622
probable membrane associated protein PFB0125c - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C>Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004

C:Accession: E71622
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Azavind, L.; Koonin, E.V.
; Perte, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743; PMID:9804551
A:Accession: E71622
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1308 <GAR>
A:Cross-references: UNIPROT:O96129; UNIPARC:UPI000017B62A; GB:AE001374; GB:AE001362; NI
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0125c
Query Match 55.6%; Score 5; DB 2; Length 1308;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 DDTFY 7
|||||
Db 321 DDTFY 325
RESULT 129
T40993
protein kinase cekl - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40993
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
submitted to the EMBL Data Library, March 1999
A:Reference number: Z21962
A:Accession: T40993
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1338 <LYN>
A:Cross-references: UNIPROT:P38938; UNIPARC:UPI00001274D0; EMBL:AL049559; PIDN:CAB40178
A:Experimental source: strain 972h-; cosmid c1450
C:Genetics:
A:Gene: SPDB:SPCC1450.11c
A:Map position: 3
Query Match 55.6%; Score 5; DB 2; Length 1338;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTF 6
|||||
Db 1078 VDDTF 1082
RESULT 130
S50943
hypothetical protein YML049c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YM9827.03c
C:Species: Saccharomyces cerevisiae
C>Date: 10-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S50943
R;Odell, C.; Bowman, S.
submitted to the EMBL Data Library, January 1995
A:Reference number: S50941
A:Accession: S50943
A:Molecule type: DNA
A:Residues: 1-1361 <ODE>
A:Cross-references: UNIPROT:Q04693; UNIPARC:UPI00000530F0; EMBL:Z47816; NID:g642303; PI
C:Genetics:
A:Gene: SGD:RSE1
A:Cross-references: SGD:S0004513; MIPS:YML049c
A:Map position: 13L
Query Match 55.6%; Score 5; DB 2; Length 1361;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 1251 DDTFY 1255

RESULT 131
T22111.2 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: G86344
R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: G86344
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1552 <STO>
A:Cross-references: UNIPROT:Q9LPV0; UNIPARC:UPI00000A17A2; GB:AE005172; NID:g9886986; PI
C:Genetics:
A:Map position: 1

Query Match 55.6%; Score 5; DB 2; Length 1552;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||
Db 465 KVDDT 469

RESULT 132
T29861
hypothetical protein F10G2.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T29861
R:Murray, J.; Wohldmann, P.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid F10G2.
A:Reference number: Z20701
A:Accession: T29861
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1614 <MUR>
A:Cross-references: UNIPARC:UPI000017B8DA; EMBL:U64836; PIDN:AAB04826.1; GSPDB:GN000023;
A:Experimental source: strain Bristol N2; clone F10G2
C:Genetics:
A:Gene: CESP:F10G2.5
A:Map position: 5
A:Introns: 62/2; 738/1; 778/3; 951/3; 1040/3; 1108/2; 1152/2; 1294/3; 1401/3

Query Match 55.6%; Score 5; DB 2; Length 1614;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFIYV 9
|||||
Db 1453 TFIYV 1457

RESULT 133
S48385

hypothetical protein YIL149c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C>Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C:Accession: S48385
R:Churcher, C.
submitted to the EMBL Data Library, September 1994
A:Reference number: S48310
A:Accession: S48385
A:Molecule type: DNA
A:Residues: 1-1679 <CHU>
A:Cross-references: UNIPROT:P40457; UNIPARC:UPI000013B453; GB:Z47047; EMBL:Z38059; NID:g
C:Genetics:
A:Gene: SGD:MLP2; MIPS:YIL149c
A:Cross-references: SGD:S0001411
A:Map position: 9L

Query Match 55.6%; Score 5; DB 2; Length 1679;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||
Db 1084 KVDDT 1088

RESULT 134
T17485
peptide synthetase homolog PCZA363.5 - Amycolatopsis orientalis
C:Species: Amycolatopsis orientalis
C>Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C:Accession: T17485
R:Van Wageningen, A.; Kirkpatrick, P.; Williams, D.; Harris, B.; Kershaw, J.; Lennard, N
Chem. Biol. 3, 155-162, 1998
A:Title: Sequencing and analysis of genes involved in the biosynthesis of a vancomycin g
A:Reference number: Z18804
A:Accession: T17485
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1860 <VAN>
A:Cross-references: UNIPROT:O52821; UNIPARC:UPI0000081899; EMBL:AJ223999; NID:el251240;
C:Keywords: carrier protein
F:512-953/Domain: acetate-CoA ligase homology <ACL>
F:969-1037/Domain: acyl carrier protein homology <ACP>

Query Match 55.6%; Score 5; DB 2; Length 1860;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||||
Db 990 VDDTF 994

RESULT 135
T03884
hypothetical protein F07G11.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T03884
R:Sammons, L.; Wohldmann, P.; Sansone, J.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid F07G11.
A:Reference number: Z15127
A:Accession: T03884
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2025 <SAM>
A:Cross-references: UNIPROT:O16237; UNIPARC:UPI0000077F90; EMBL:AF016419; NID:g22291159;
C:Genetics:
A:Map position: V
A:Introns: 62/2; 703/1; 743/3; 930/3; 1019/3; 1087/2; 1131/2; 1273/3; 1380/3; 1593/2; 19
A:Note: F07G11.9

Query Match 55.6%; Score 5; DB 2; Length 2025;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TFYV 9
 |||||
 Db 1432 TFYV 1436

RESULT 136
 T00327
 polypeptide - infectious flacherie virus
 C;Species: infectious flacherie virus
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T00327
 R;Isawa, H.; Asano, S.; Sahara, K.; Iizuka, T.; Bando, H.
 Arch. Virol. 143, 127-143, 1998
 A;Title: Analysis of genetic information of an insect picorna-like virus, infectious flacherie virus.
 A;Reference number: Z14139; MUID:98166871; PMID:9505971
 A;Accession: T00327
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: genomic RNA
 A;Residues: 1-3085 <ISA>
 A;Cross-references: UNIPROT:O70710; UNIPARC:UPI00000F1097; EMBL:AB000906; NID:G3025414;
 C;Keywords: polyprotein

Query Match 55.6%; Score 5; DB 2; Length 3085;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
 |||||
 Db 1175 VDDTF 1179

RESULT 137
 T22812
 hypothetical protein ZC116.3 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T22812; T27494
 R;Burton, J.
 submitted to the EMBL Data Library, June 1996
 A;Reference number: Z19618
 A;Accession: T22812
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-3871 <WIL>
 A;Cross-references: UNIPROT:Q20911; UNIPARC:UPI00000821EA; EMBL:Z74473; PIDN:CAA98952.1;
 A;Experimental source: clone F56H9
 R;Smye, R.
 submitted to the EMBL Data Library, June 1996
 A;Reference number: Z20376
 A;Accession: T27494
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-3871 <W12>
 A;Cross-references: UNIPARC:UPI00000821EA; EMBL:Z74046; PIDN:CAA98557.1; GSPDB:GN000023;
 A;Experimental source: clone ZC116
 C;Genetics:
 A;Gene: CRSP:ZC116.3
 A;Map position: 5
 A;Introns: 29/3; 66/2; 244/1; 359/3; 422/1; 549/1; 572/1; 728/1; 820/1; 889/3; 1189/1; 1276/1; 2809/1; 2906/3; 3051/3; 3176/1; 3254/1; 3341/2; 3536/1; 3565/2; 3582/3; 3609/1;
 C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology

Query Match 55.6%; Score 5; DB 2; Length 3871;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
 |||||

Db 1380 KVDDT 1384

RESULT 138
 T30192
 probable peptide synthetase - Aureobasidium pullulans
 C;Species: Aureobasidium pullulans
 C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
 C;Accession: T30192
 R;Peery, R.B.; Thornewell, S.J.; Tobin, M.B.; Skatrud, P.L.
 submitted to the EMBL Data Library, January 1997
 A;Description: Discovery of an MDR-like gene adjacent to a peptide synthetase in Aureobasidium pullulans.
 A;Reference number: Z20767
 A;Accession: T30192
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-10797 <PSE>
 A;Cross-references: UNIPROT:O94116; UNIPARC:UPI000017CF3F; EMBL:U85909; NID:G4099310; P
 C;Genetics:
 A;Introns: 2078/3; 4142/3; 6075/3; 7963/3; 7985/2
 C;Keywords: carrier protein
 F;1618-1688/Domain: acyl carrier protein homology <ACP1>
 F;3682-3752/Domain: acyl carrier protein homology <ACP2>
 F;5615-5685/Domain: acyl carrier protein homology <ACP3>
 F;7503-7573/Domain: acyl carrier protein homology <ACP4>
 F;9683-9752/Domain: acyl carrier protein homology <ACP5>

Query Match 55.6%; Score 5; DB 2; Length 10797;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
 |||||
 Db 10462 KVDDT 10466

RESULT 139
 B53415
 lectin chain B - Iris hollandica (Dutch Iris) (fragment)
 C;Species: Iris hollandica (Dutch Iris)
 C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 07-May-1999
 C;Accession: B53415
 R;Mo, H.; Van Damme, E.J.M.; Peumans, W.J.; Goldstein, I.J.
 J. Biol. Chem. 269, 7666-7673, 1994
 A;Title: Isolation and characterization of an N-acetyl-D-galactosamine-binding lectin
 A;Reference number: A53415; MUID:94171801; PMID:8125593
 A;Accession: B53415
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-25 <MOA>
 A;Cross-references: UNIPARC:UPI000017CAD0

Query Match 44.4%; Score 4; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDT 5
 |||||
 Db 1 VDDT 4

RESULT 140
 C64536
 hypothetical protein HP0131 - Helicobacter pylori (strain 26695)
 C;Species: Helicobacter pylori
 C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
 C;Accession: C64536
 R;Tomb, J.F.; White, O.; Kervatage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L
 Nature 388, 539-547, 1997
 A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C
 A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467; PMID:9252185	
A:Accession: C64536	
A>Status: preliminary; nucleic acid sequence not shown; translation not shown	
A:Molecule type: DNA	
A:Residues: 1-33 <TOM>	
A:Cross-references: UNIPROT:O24945; UNIPARC:UPI00000C07A2; GB:AE000535; GB:AE000511; NID	
Query Match 44.4%; Score 4; DB 2; Length 33;	
Best Local Similarity 100.0%; Pred. No. 2.8e+02;	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 5 TFYY 8	
DB 11 TFVY 14	
RESULT 141	
I56058	
C:Species: Mus musculus (house mouse)	
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004	
C:Accession: I56058	
R:Nakayama, K.; Tokito, S.; Jaulin, C.; Delarbre, C.; Kourilsky, P.; Nakauchi, H.; Gache	
J. Immunol. 144, 2400-2408, 1990	
A:Title: Comparative structure of two duplicated T1a class I genes (T10c and 37) of the	
A:Reference number: I56058; MUID:90187889; PMID:1968929	
A:Accession: I56058	
A>Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: DNA	
A:Residues: 1-37 <RES>	
A:Cross-references: UNIPROT:Q31130; UNIPARC:UPI000008A63F; GB:M34072; NID:G623439; PIDN	
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology	
C:Keywords: glycoprotein	
Query Match 44.4%; Score 4; DB 2; Length 37;	
Best Local Similarity 100.0%; Pred. No. 3.1e+02;	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 2 VDDT 5	
DB 18 VDDT 21	
RESULT 142	
S21665	
S:layer protein - Acetogenium kivui	
C:Species: Acetogenium kivui	
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997	
C:Accession: S21665	
R:Peters, J.; Rudolf, S.; Oschkinat, H.; Mengele, R.; Sumper, M.; Kellermann, J.; Lottsp	
Biol. Chem. Hoppe-Seyler 373, 171-176, 1992	
A:Title: Evidence for tyrosine-linked glycosaminoglycan in a bacterial surface protein.	
A:Reference number: S21665; MUID:92281680; PMID:1596358	
A:Accession: S21665	
A>Status: preliminary	
A:Molecule type: protein	
A:Residues: 1-37 <PET>	
A:Cross-references: UNIPARC:UPI000017A8BF	
Query Match 44.4%; Score 4; DB 2; Length 37;	
Best Local Similarity 100.0%; Pred. No. 3.1e+02;	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 KVDD 4	
DB 26 KVDD 29	
RESULT 143	
E72269	
hypothetical protein - Thermotoga maritima (strain MSB8)	
C:Species: Thermotoga maritima	
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004	

C:Accession: E72269	
R:Nelson, K.B.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke	
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.	
C.M.	
Nature 399, 323-329, 1999	
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq	
A:Reference number: A72200; MUID:99287316; PMID:10360571	
A:Accession: E72269	
A>Status: preliminary	
A:Molecule type: DNA	
A:Residues: 1-37 <ARN>	
A:Cross-references: UNIPROT:O9X125; UNIPARC:UPI00000C12B9; GB:AE001785; GB:AE000512; NID	
A:Experimental source: strain MSB8	
C:Genetics:	
A:Gene: TM1299	
Query Match 44.4%; Score 4; DB 2; Length 37;	
Best Local Similarity 100.0%; Pred. No. 3.1e+02;	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 KVDD 4	
DB 5 KVDD 8	
RESULT 144	
S71381	
lebetin 2 isoform alpha - Vipera lebetina	
C:Species: Vipera lebetina	
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004	
A:Accession: S71381; S71382; S71379	
R:Barbouche, R.; Marrakchi, N.; Mansuelle, P.; Krifi, M.; Fenouillet, E.; Rochat, H.; El	
FEBS Lett. 392, 6-10, 1996	
A:Title: Novel anti-platelet aggregation polypeptides from Vipera lebetina venom: isolat	
A:Reference number: S71379; MUID:96354866; PMID:8769304	
A:Accession: S71381	
A:Molecule type: protein	
A:Residues: 1-38 <BA2>	
A:Cross-references: UNIPROT:Q7LZ09; UNIPARC:UPI00000030733	
A:Experimental source: venom	
A:Accession: S71382	
A:Molecule type: protein	
A:Residues: 2-38 <BA2>	
A:Cross-references: UNIPARC:UPI00000030734	
A:Experimental source: venom	
A:Accession: S71379	
A:Molecule type: protein	
A:Residues: 1-13 <BA3>	
A:Cross-references: UNIPARC:UPI0000003072F	
A:Experimental source: venom	
C:Keywords: anticoagulant; venom	
F:14-30/Disulfide bonds: #status predicted	
Query Match 44.4%; Score 4; DB 2; Length 38;	
Best Local Similarity 100.0%; Pred. No. 3.1e+02;	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 KVDD 4	
DB 32 KVDD 35	
RESULT 145	
B81717	
hypothetical protein TC0307 [imported] - Chlamydia muridarum (strain Nigg)	
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn	
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004	
A:Accession: B81717	
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,	
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,	
Nucleic Acids Res. 28, 1397-1406, 2000	
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.	
A:Reference number: A81500; MUID:20150255; PMID:10684935	

A;Accession: B81717
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-46 <TET>
A;Cross-references: UNIPROT:Q9PL01; UNIPARC:UPI0000057893; GB:AE002298; GB:AE002160; NID:10580362;
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0307

Query Match 44.4%; Score 4; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFFY 8
|||
Db 27 TFFY 30

RESULT 146
JH0643
GTP-binding protein rab13 - mouse (fragment)
N;Alternate names: rab protein Rab13
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JH0643
R;Chavrier, P.; Simons, K.; Zerial, M.
Gene 112, 261-264, 1992
A;Title: The complexity of the Rab and Rho GTP-binding protein subfamilies revealed by a
A;Reference number: JH0639; MUID:92210010; PMID:1555775
A;Accession: JH0643
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-49 <CHA>
A;Cross-references: UNIPROT:P35283; UNIPARC:UPI0000027C50; GB:W79303
A;Experimental source: kidney
C;Genetics:
A;Gene: rab13
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; membrane trafficking; P-loop

Query Match 44.4%; Score 4; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTF 6
|||
Db 11 DDTF 14

RESULT 147
A60718
phospholipase A2 homolog, non-pancreatic - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Aug-2004
C;Accession: A60718
R;Seilhamer, J.J.; Randall, T.L.; Johnson, L.K.; Heinzmann, C.; Klisak, I.; Sparkes, R.S.
J. Cell. Biochem. 39, 327-337, 1989
A;Title: Novel gene exon homologous to pancreatic phospholipase A-2: sequence and chromo
A;Reference number: A60718; MUID:89214375; PMID:2708461
A;Accession: A60718
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-50 <SEI>
A;Cross-references: UNIPROT:Q7M4M6; UNIPARC:UPI0000142253
C;Comment: This genomic fragment is homologous to exon 2 of pancreatic phospholipase A2.
C;Genetics:
A;Map position: 1
C;Superfamily: Phospholipase A2

Query Match 44.4%; Score 4; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A;Accession: B81717
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-46 <TET>
A;Cross-references: UNIPROT:Q9PL01; UNIPARC:UPI0000057893; GB:AE002298; GB:AE002160; NID:10580362;
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0307

Query Match 44.4%; Score 4; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFFY 8
|||
Db 27 TFFY 30

RESULT 146
JH0643
GTP-binding protein rab13 - mouse (fragment)
N;Alternate names: rab protein Rab13
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JH0643
R;Chavrier, P.; Simons, K.; Zerial, M.
Gene 112, 261-264, 1992
A;Title: The complexity of the Rab and Rho GTP-binding protein subfamilies revealed by a
A;Reference number: JH0639; MUID:92210010; PMID:1555775
A;Accession: JH0643
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-49 <CHA>
A;Cross-references: UNIPROT:P35283; UNIPARC:UPI0000027C50; GB:W79303
A;Experimental source: kidney
C;Genetics:
A;Gene: rab13
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; membrane trafficking; P-loop

Query Match 44.4%; Score 4; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTF 6
|||
Db 11 DDTF 14

RESULT 147
A60718
phospholipase A2 homolog, non-pancreatic - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Aug-2004
C;Accession: A60718
R;Seilhamer, J.J.; Randall, T.L.; Johnson, L.K.; Heinzmann, C.; Klisak, I.; Sparkes, R.S.
J. Cell. Biochem. 39, 327-337, 1989
A;Title: Novel gene exon homologous to pancreatic phospholipase A-2: sequence and chromo
A;Reference number: A60718; MUID:89214375; PMID:2708461
A;Accession: A60718
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-50 <SEI>
A;Cross-references: UNIPROT:Q7M4M6; UNIPARC:UPI0000142253
C;Comment: This genomic fragment is homologous to exon 2 of pancreatic phospholipase A2.
C;Genetics:
A;Map position: 1
C;Superfamily: Phospholipase A2

Query Match 44.4%; Score 4; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
|||
Db 45 VDDT 48

RESULT 148
B60718
phospholipase A2 homolog, non-pancreatic - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 16-Aug-2004
C;Accession: B60718
R;Seilhamer, J.J.; Randall, T.L.; Johnson, L.K.; Heinzmann, C.; Klisak, I.; Sparkes, R.
J. Cell. Biochem. 39, 327-337, 1989
A;Title: Novel gene exon homologous to pancreatic phospholipase A-2: sequence and chrom
A;Reference number: A60718; MUID:89214375; PMID:2708461
A;Accession: B60718
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <SEI>
A;Cross-references: UNIPROT:Q7M333; UNIPARC:UPI0000175895
C;Superfamily: Phospholipase A2

Query Match 44.4%; Score 4; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
|||
Db 45 VDDT 48

RESULT 149
B84236
hypothetical protein Vng0788h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84236
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,
; Leichauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabb
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: B84236
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-53 <STO>
A;Cross-references: UNIPROT:Q9HRA4; UNIPARC:UPI000006371D; GB:AE004437; NID:10580362;
C;Genetics:
A;Gene: VNG0788H

Query Match 44.4%; Score 4; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
|||
Db 5 VDDT 8

RESULT 150
S05489
alpha-amylase (EC 3.2.1.1) 2.54 precursor - wheat (fragment)
C;Species: Triticum aestivum (common wheat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Dec-2004
C;Accession: S05489
R;Huttly, A.K.; Martienssen, R.A.; Baulcombe, D.C.
Mol. Gen. Genet. 214, 232-240, 1988
A;Title: Sequence heterogeneity and differential expression of the alpha--Amy-2 gene fa
A;Reference number: S05486; MUID:89181522; PMID:2467183
A;Accession: S05489
A;Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-58 <HUT>
A:Cross-references: UNIPROT:P11786; UNIPARC:UPI0000175A39; EMBL:X13580
C:Genetics:
A:Gene: amy2
A:Map position: 7A
A:Introns: 29/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, plant type; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 44.4%; Score 4; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDD 4
Db 49 KVDD 52

Search completed: May 17, 2006, 06:28:04
Job time : 59.5 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2006, 06:28:51 ; Search time 37 Seconds
(without alignments)
21.291 Million cell updates/sec

Title: US-10-764-985-2

Perfect score: 9

Sequence: 1 KVDDTFYV 9

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size : 1

Total number of hits satisfying chosen parameters: 624216

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents_AA.*

1:	/EMC_Celerra SIDS3/ptodata/2/iaa/5 COMB.pcp.*
2:	/EMC_Celerra SIDS3/ptodata/2/iaa/6 COMB.pcp.*
3:	/EMC_Celerra SIDS3/ptodata/2/iaa/7 COMB.pcp.*
4:	/EMC_Celerra SIDS3/ptodata/2/iaa/H COMB.pcp.*
5:	/EMC_Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pcp.*
6:	/EMC_Celerra SIDS3/ptodata/2/iaa/RE COMB.pcp.*
7:	/EMC_Celerra SIDS3/ptodata/2/iaa/baCkfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query #	Score	Match	Length	DB	ID	Description	
1	66.7	6	382	2	US-09-489-039A-10751		Sequence 10751, A	
2	55.6	6	21	2	US-09-962-756-691		Sequence 691, Appl	
3	55.6	27	27	2	US-09-962-756-1425		Sequence 1425, Appl	
4	55.6	78	78	2	US-09-732-210-338		Sequence 338, Appl	
5	55.6	80	80	2	US-09-732-210-346		Sequence 346, Appl	
6	55.6	126	126	2	US-09-740-002-23		Sequence 23, Appl	
7	55.6	128	128	2	US-09-270-767-60895		Sequence 60895, A	
8	55.6	143	143	2	US-09-248-796A-14343		Sequence 14343, A	
9	55.6	157	157	2	US-09-668-262A-2		Sequence 2, Appl	
10	55.6	162	162	2	US-10-427-442-2		Sequence 2, Appl	
11	55.6	162	174	2	US-09-270-767-56930		Sequence 56930, A	
12	55.6	174	174	2	US-09-270-767-57344		Sequence 57344, A	
13	55.6	177	2	US-09-710-273-2532		Sequence 2532, Appl		
14	55.6	202	2	US-09-107-532A-4432		Sequence 4432, Appl		
15	55.6	230	2	US-09-216-393B-31		Sequence 31, Appl		
16	55.6	235	2	US-10-101-464A-787		Sequence 787, Appl		
17	55.6	279	1	US-08-326-286-5		Sequence 5, Appl		
18	55.6	285	2	US-09-252-991A-30991		Sequence 30991, A		
19	55.6	301	2	US-09-328-352-6685		Sequence 6685, Appl		
20	55.6	349	2	US-09-949-016-9786		Sequence 9786, Appl		
21	55.6	370	2	US-09-134-000C-5050		Sequence 5050, Appl		
22	55.6	373	2	US-09-914-098-34		Sequence 34, Appl		
23	55.6	378	2	US-10-414-759-2		Sequence 2, Appl		
24	55.6	378	2	US-10-414-759-4		Sequence 4, Appl		
25	55.6	378	2	US-10-123-058-2		Sequence 2, Appl		
26	55.6	378	2	US-10-123-058-4		Sequence 4, Appl		

100	5	55.6	1912	2	US-09-949-016-10490	Sequence 10490, A	173	4	44.4	21	5	PCT-US93-07545-103	Sequence 103, App
101	4	44.4	6	2	US-09-747-408-22	Sequence 22, Appl	174	4	44.4	22	2	US-09-202-161B-28	Sequence 28, Appl
102	4	44.4	7	2	US-09-996-288-23	Sequence 23, Appl	175	4	44.4	23	1	US-08-293-778-5	Sequence 5, Appl
103	4	44.4	7	2	US-09-996-288-90	Sequence 90, Appl	176	4	44.4	23	1	US-08-480-190-101	Sequence 101, App
104	4	44.4	7	2	US-09-996-288-99	Sequence 99, Appl	177	4	44.4	23	1	US-08-480-190-135	Sequence 195, App
105	4	44.4	7	2	US-09-996-265-23	Sequence 23, Appl	178	4	44.4	23	1	US-08-488-379-101	Sequence 101, App
106	4	44.4	7	2	US-09-996-265-90	Sequence 90, Appl	179	4	44.4	23	1	US-08-488-379-195	Sequence 195, App
107	4	44.4	7	2	US-09-996-265-99	Sequence 99, Appl	180	4	44.4	23	1	US-08-475-399A-101	Sequence 101, App
108	4	44.4	8	2	US-10-092-263-4	Sequence 4, Appl	181	4	44.4	23	2	US-08-475-399A-195	Sequence 195, App
109	4	44.4	10	1	US-08-166-195A-22	Sequence 22, Appl	182	4	44.4	23	2	US-08-077-255A-101	Sequence 101, App
110	4	44.4	10	1	US-08-166-195A-23	Sequence 23, Appl	183	4	44.4	23	2	US-08-077-255A-195	Sequence 195, App
111	4	44.4	10	1	US-08-436-772-22	Sequence 22, Appl	184	4	44.4	23	5	PCT-US93-07545-101	Sequence 101, App
112	4	44.4	10	1	US-08-436-772-23	Sequence 23, Appl	185	4	44.4	23	5	PCT-US93-07545-195	Sequence 195, App
113	4	44.4	10	1	US-08-436-883B-22	Sequence 22, Appl	186	4	44.4	25	2	US-09-200-757-5	Sequence 5, Appl
114	4	44.4	10	1	US-08-436-883B-23	Sequence 23, Appl	187	4	44.4	28	1	US-08-436-772-55	Sequence 55, Appl
115	4	44.4	10	2	US-09-200-757-3	Sequence 3, Appl	188	4	44.4	28	1	US-08-436-883B-55	Sequence 55, Appl
116	4	44.4	14	1	US-09-200-757-4	Sequence 4, Appl	189	4	44.4	34	2	US-09-270-767-59590	Sequence 59590, A
117	4	44.4	14	1	US-07-712-476A-3	Sequence 3, Appl	190	4	44.4	38	1	US-07-712-476A-4	Sequence 4, Appl
118	4	44.4	14	7	5204097-4	Patent No. 5204097	191	4	44.4	38	2	US-08-630-916A-35	Sequence 35, Appl
119	4	44.4	16	1	US-08-480-190-171	Sequence 171, App	192	4	44.4	38	2	US-09-270-767-57102	Sequence 57102, A
120	4	44.4	16	1	US-08-488-379-171	Sequence 171, App	193	4	44.4	38	2	US-09-902-540-13720	Sequence 13720, A
121	4	44.4	16	2	US-08-475-399A-171	Sequence 171, App	194	4	44.4	41	1	US-08-229-280-5	Sequence 5, Appl
122	4	44.4	16	2	US-08-077-255A-171	Sequence 171, App	195	4	44.4	41	2	US-10-318-675-153	Sequence 153, App
123	4	44.4	16	5	PCT-US93-07545-171	Sequence 171, App	196	4	44.4	42	1	US-08-745-254A-2	Sequence 2, Appl
124	4	44.4	17	1	US-08-480-190-97	Sequence 97, App	197	4	44.4	42	2	US-09-383-667-8	Sequence 8, Appl
125	4	44.4	17	1	US-08-480-190-108	Sequence 108, App	198	4	44.4	44	2	US-08-955-636-1	Sequence 1, Appl
126	4	44.4	17	1	US-08-488-379-97	Sequence 97, App	199	4	44.4	44	2	US-08-955-636-19	Sequence 19, Appl
127	4	44.4	17	1	US-08-488-379-108	Sequence 108, App	200	4	44.4	44	2	US-08-955-636-20	Sequence 20, Appl
128	4	44.4	17	1	US-08-672-345C-65	Sequence 65, Appl	201	4	44.4	44	2	US-08-955-636-21	Sequence 21, Appl
129	4	44.4	17	2	US-09-214-095D-65	Sequence 65, Appl	202	4	44.4	44	2	US-08-955-636-22	Sequence 22, Appl
130	4	44.4	17	2	US-08-475-399A-97	Sequence 97, App	203	4	44.4	44	2	US-08-955-636-24	Sequence 24, Appl
131	4	44.4	17	2	US-08-475-399A-108	Sequence 108, App	204	4	44.4	44	2	US-08-955-636-25	Sequence 25, Appl
132	4	44.4	17	2	US-08-077-255A-97	Sequence 97, App	205	4	44.4	44	2	US-08-955-636-35	Sequence 35, Appl
133	4	44.4	17	2	US-08-077-255A-108	Sequence 108, App	206	4	44.4	44	2	US-09-302-239-1	Sequence 1, Appl
134	4	44.4	17	2	US-09-940-727B-65	Sequence 65, Appl	207	4	44.4	44	2	US-09-497-591-1	Sequence 1, Appl
135	4	44.4	17	5	PCT-US93-07545-97	Sequence 97, App	208	4	44.4	45	1	US-08-965-832-2	Sequence 2, Appl
136	4	44.4	18	1	US-08-480-190-106	Sequence 106, App	209	4	44.4	47	2	US-08-930-917A-1	Sequence 1, Appl
137	4	44.4	18	1	US-08-488-379-106	Sequence 106, App	210	4	44.4	47	2	US-08-930-917A-6	Sequence 6, Appl
138	4	44.4	18	2	US-08-475-399A-106	Sequence 106, App	211	4	44.4	47	2	US-10-144-929-121	Sequence 121, App
139	4	44.4	18	2	US-08-077-255A-106	Sequence 106, App	212	4	44.4	47	2	US-09-612-925H-2	Sequence 2, Appl
140	4	44.4	18	2	US-09-612-925H-4	Sequence 4, Appl	213	4	44.4	47	2	US-09-612-925H-10	Sequence 10, Appl
141	4	44.4	18	5	PCT-US93-07545-106	Sequence 106, App	214	4	44.4	48	2	US-08-569-749-9	Sequence 9, Appl
142	4	44.4	19	1	US-08-480-190-94	Sequence 94, App	215	4	44.4	48	2	US-08-569-749-10	Sequence 10, Appl
143	4	44.4	19	1	US-08-480-190-105	Sequence 105, App	216	4	44.4	48	2	US-09-689-366-9	Sequence 9, Appl
144	4	44.4	19	1	US-08-488-379-94	Sequence 94, Appl	217	4	44.4	48	2	US-10-232-286-10	Sequence 10, Appl
145	4	44.4	19	1	US-08-488-379-105	Sequence 105, App	218	4	44.4	48	2	US-10-232-286-9	Sequence 9, Appl
146	4	44.4	19	1	US-08-488-379-105	Sequence 105, App	219	4	44.4	48	2	US-10-232-286-10	Sequence 10, Appl
147	4	44.4	19	2	US-08-475-399A-94	Sequence 94, Appl	220	4	44.4	48	2	US-10-934-717-9	Sequence 9, Appl
148	4	44.4	19	2	US-08-475-399A-105	Sequence 105, App	221	4	44.4	48	2	US-10-934-717-10	Sequence 10, Appl
149	4	44.4	19	2	US-08-077-255A-94	Sequence 94, App	222	4	44.4	48	5	PCT-US96-12860-9	Sequence 9, Appl
150	4	44.4	19	5	PCT-US93-07545-94	Sequence 94, Appl	223	4	44.4	48	5	PCT-US96-12860-10	Sequence 10, Appl
151	4	44.4	19	5	PCT-US93-07545-94	Sequence 94, Appl	224	4	44.4	52	2	US-09-270-767-32185	Sequence 32185, A
152	4	44.4	20	1	US-08-480-190-93	Sequence 93, Appl	225	4	44.4	52	2	US-09-270-767-47402	Sequence 47402, A
153	4	44.4	20	1	US-08-480-190-104	Sequence 104, App	226	4	44.4	52	2	US-09-902-540-13760	Sequence 12760, A
154	4	44.4	20	1	US-08-488-379-93	Sequence 93, App	227	4	44.4	53	2	US-09-513-999C-4527	Sequence 4527, App
155	4	44.4	20	1	US-08-488-379-104	Sequence 104, App	228	4	44.4	56	1	US-07-664-989B-85	Sequence 85, Appl
156	4	44.4	20	2	US-08-475-399A-93	Sequence 93, Appl	229	4	44.4	58	1	US-08-358-160-62	Sequence 62, Appl
157	4	44.4	20	2	US-08-475-399A-104	Sequence 104, App	230	4	44.4	58	1	US-08-086-630C-70	Sequence 70, Appl
158	4	44.4	20	2	US-08-077-255A-104	Sequence 104, App	231	4	44.4	58	1	US-08-086-630C-75	Sequence 75, Appl
159	4	44.4	20	2	US-08-077-255A-93	Sequence 93, App	232	4	44.4	58	1	US-08-086-630C-78	Sequence 78, Appl
160	4	44.4	20	2	US-08-077-255A-104	Sequence 104, App	233	4	44.4	58	1	US-08-086-630C-79	Sequence 79, Appl
161	4	44.4	20	5	PCT-US93-07545-93	Sequence 93, Appl	234	4	44.4	58	1	US-08-086-630C-83	Sequence 83, Appl
162	4	44.4	20	5	PCT-US93-07545-93	Sequence 93, Appl	235	4	44.4	58	1	US-08-086-630C-84	Sequence 84, Appl
163	4	44.4	20	7	5204097-3	Patent No. 5204097	236	4	44.4	58	1	US-08-086-630C-86	Sequence 86, Appl
164	4	44.4	21	1	US-08-480-190-92	Sequence 92, Appl	237	4	44.4	58	1	US-08-086-630C-89	Sequence 89, Appl
165	4	44.4	21	1	US-08-480-190-103	Sequence 103, App	238	4	44.4	58	1	US-08-086-630C-90	Sequence 90, Appl
166	4	44.4	21	1	US-08-488-379-92	Sequence 92, Appl	239	4	44.4	58	1	US-08-086-630C-102	Sequence 102, App
167	4	44.4	21	1	US-08-488-379-103	Sequence 103, App	240	4	44.4	58	1	US-08-086-630C-106	Sequence 106, App
168	4	44.4	21	2	US-08-475-399A-92	Sequence 92, Appl	241	4	44.4	58	1	US-08-086-630C-107	Sequence 107, App
169	4	44.4	21	2	US-08-475-399A-103	Sequence 103, App	242	4	44.4	58	1	US-08-086-630C-127	Sequence 127, App
170	4	44.4	21	2	US-08-077-255A-92	Sequence 92, App	243	4	44.4	58	1	US-08-086-630C-128	Sequence 128, App
171	4	44.4	21	2	US-08-077-255A-103	Sequence 103, App	244	4	44.4	58	1	US-08-086-630C-129	Sequence 129, App
172	4	44.4	21	5	PCT-US93-07545-92	Sequence 92, Appl	245	4	44.4	58	1		

246	4	44.4	58	1	US-08-086-630C-130	Sequence 130, App	319	4	44.4	58	1	US-08-086-328C-268	Sequence 268, App
247	4	44.4	58	1	US-08-086-630C-163	Sequence 163, App	320	4	44.4	58	1	US-08-086-328C-269	Sequence 269, App
248	4	44.4	58	1	US-08-086-630C-164	Sequence 164, App	321	4	44.4	58	1	US-08-086-328C-273	Sequence 273, App
249	4	44.4	58	1	US-08-086-630C-165	Sequence 165, App	322	4	44.4	58	1	US-08-086-328C-276	Sequence 276, App
250	4	44.4	58	1	US-08-086-630C-166	Sequence 166, App	323	4	44.4	58	1	US-08-086-328C-278	Sequence 278, App
251	4	44.4	58	1	US-08-086-630C-246	Sequence 246, App	324	4	44.4	58	1	US-08-086-328C-279	Sequence 279, App
252	4	44.4	58	1	US-08-086-630C-251	Sequence 251, App	325	4	44.4	58	1	US-08-086-328C-282	Sequence 282, App
253	4	44.4	58	1	US-08-086-630C-254	Sequence 254, App	326	4	44.4	58	1	US-08-086-328C-283	Sequence 283, App
254	4	44.4	58	1	US-08-086-630C-255	Sequence 255, App	327	4	44.4	58	1	US-08-086-328C-287	Sequence 287, App
255	4	44.4	58	1	US-08-086-630C-259	Sequence 259, App	328	4	44.4	58	1	US-08-086-328C-288	Sequence 288, App
256	4	44.4	58	1	US-08-086-630C-260	Sequence 260, App	329	4	44.4	58	1	US-08-086-328C-291	Sequence 291, App
257	4	44.4	58	1	US-08-086-630C-262	Sequence 262, App	330	4	44.4	58	1	US-08-086-328C-292	Sequence 292, App
258	4	44.4	58	1	US-08-086-630C-265	Sequence 265, App	331	4	44.4	58	1	US-08-086-328C-293	Sequence 293, App
259	4	44.4	58	1	US-08-086-630C-266	Sequence 266, App	332	4	44.4	58	2	US-09-781-988A-85	Sequence 85, Appl
260	4	44.4	58	1	US-08-086-630C-278	Sequence 278, App	333	4	44.4	60	1	US-08-358-160-128	Sequence 128, App
261	4	44.4	58	1	US-08-086-630C-282	Sequence 282, App	334	4	44.4	60	2	US-09-215-221-13	Sequence 13, Appl
262	4	44.4	58	1	US-08-086-328C-19	Sequence 19, Appl	335	4	44.4	61	2	US-09-270-767-62045	Sequence 62045, A
263	4	44.4	58	1	US-08-086-328C-20	Sequence 20, Appl	336	4	44.4	62	2	US-09-248-796A-24375	Sequence 24375, A
264	4	44.4	58	1	US-08-086-328C-21	Sequence 21, Appl	337	4	44.4	62	2	US-09-248-796A-26706	Sequence 26706, A
265	4	44.4	58	1	US-08-086-328C-22	Sequence 22, Appl	338	4	44.4	63	2	US-09-270-767-60318	Sequence 60318, A
266	4	44.4	58	1	US-08-086-328C-23	Sequence 23, Appl	339	4	44.4	64	2	US-09-513-999C-5256	Sequence 5256, Ap
267	4	44.4	58	1	US-08-086-328C-32	Sequence 32, Appl	340	4	44.4	64	2	US-09-248-796A-25149	Sequence 25149, A
268	4	44.4	58	1	US-08-086-328C-39	Sequence 39, Appl	341	4	44.4	65	2	US-09-270-767-58768	Sequence 58768, A
269	4	44.4	58	1	US-08-086-328C-49	Sequence 49, Appl	342	4	44.4	66	2	US-09-248-796A-25319	Sequence 25319, A
270	4	44.4	58	1	US-08-086-328C-52	Sequence 52, Appl	343	4	44.4	67	2	US-08-511-485-26	Sequence 26, Appl
271	4	44.4	58	1	US-08-086-328C-54	Sequence 54, Appl	344	4	44.4	68	1	US-09-201-932-27	Sequence 27, Appl
272	4	44.4	58	1	US-08-086-328C-55	Sequence 55, Appl	345	4	44.4	68	2	US-09-201-936-26	Sequence 26, Appl
273	4	44.4	58	1	US-08-086-328C-58	Sequence 58, Appl	346	4	44.4	68	2	US-09-011-356-27	Sequence 27, Appl
274	4	44.4	58	1	US-08-086-328C-59	Sequence 59, Appl	347	4	44.4	68	2	US-09-082-514-21	Sequence 21, Appl
275	4	44.4	58	1	US-08-086-328C-73	Sequence 73, Appl	348	4	44.4	68	2	US-09-082-514-21	Sequence 21, Appl
276	4	44.4	58	1	US-08-086-328C-74	Sequence 74, Appl	349	4	44.4	69	1	US-09-583-110-4535	Sequence 4535, Ap
277	4	44.4	58	1	US-08-086-328C-75	Sequence 75, Appl	350	4	44.4	68	2	US-09-270-767-58346	Sequence 58346, A
278	4	44.4	58	1	US-08-086-328C-76	Sequence 76, Appl	351	4	44.4	68	2	US-09-107-433-3140	Sequence 3140, Ap
279	4	44.4	58	1	US-08-086-328C-77	Sequence 77, Appl	352	4	44.4	68	2	US-09-654-743-26	Sequence 26, Appl
280	4	44.4	58	1	US-08-086-328C-87	Sequence 87, Appl	353	4	44.4	68	2	US-09-654-743-27	Sequence 27, Appl
281	4	44.4	58	1	US-08-086-328C-88	Sequence 88, Appl	354	4	44.4	68	2	US-09-654-743-79	Sequence 79, Appl
282	4	44.4	58	1	US-08-086-328C-89	Sequence 89, Appl	355	4	44.4	68	2	US-09-654-743-87	Sequence 87, Appl
283	4	44.4	58	1	US-08-086-328C-90	Sequence 90, Appl	356	4	44.4	69	1	US-09-583-110-4535	Sequence 4535, Ap
284	4	44.4	58	1	US-08-086-328C-94	Sequence 94, Appl	357	4	44.4	69	1	US-09-270-767-58346	Sequence 58346, A
285	4	44.4	58	1	US-08-086-328C-97	Sequence 97, Appl	358	4	44.4	69	1	US-09-107-433-3140	Sequence 3140, Ap
286	4	44.4	58	1	US-08-086-328C-99	Sequence 99, Appl	359	4	44.4	69	1	US-09-654-743-26	Sequence 26, Appl
287	4	44.4	58	1	US-08-086-328C-100	Sequence 100, App	360	4	44.4	69	1	US-09-654-743-87	Sequence 87, Appl
288	4	44.4	58	1	US-08-086-328C-103	Sequence 103, App	361	4	44.4	69	1	US-09-583-110-4535	Sequence 4535, Ap
289	4	44.4	58	1	US-08-086-328C-104	Sequence 104, App	362	4	44.4	69	1	US-09-270-767-58346	Sequence 58346, A
290	4	44.4	58	1	US-08-086-328C-108	Sequence 108, App	363	4	44.4	69	1	US-09-107-433-3140	Sequence 3140, Ap
291	4	44.4	58	1	US-08-086-328C-109	Sequence 109, App	364	4	44.4	69	1	US-09-654-743-26	Sequence 26, Appl
292	4	44.4	58	1	US-08-086-328C-112	Sequence 112, App	365	4	44.4	69	2	US-09-654-743-87	Sequence 87, Appl
293	4	44.4	58	1	US-08-086-328C-113	Sequence 113, App	366	4	44.4	69	2	US-09-583-110-4535	Sequence 4535, Ap
294	4	44.4	58	1	US-08-086-328C-114	Sequence 114, App	367	4	44.4	70	2	US-09-270-767-58346	Sequence 58346, A
295	4	44.4	58	1	US-08-086-328C-150	Sequence 150, App	368	4	44.4	70	2	US-09-107-433-3140	Sequence 3140, Ap
296	4	44.4	58	1	US-08-086-328C-151	Sequence 151, App	369	4	44.4	70	2	US-09-654-743-26	Sequence 26, Appl
297	4	44.4	58	1	US-08-086-328C-154	Sequence 154, App	370	4	44.4	70	2	US-09-654-743-87	Sequence 87, Appl
298	4	44.4	58	1	US-08-086-328C-155	Sequence 155, App	371	4	44.4	70	2	US-09-583-110-4535	Sequence 4535, Ap
299	4	44.4	58	1	US-08-086-328C-156	Sequence 156, App	372	4	44.4	71	2	US-09-270-767-58346	Sequence 58346, A
300	4	44.4	58	1	US-08-086-328C-198	Sequence 198, App	373	4	44.4	71	2	US-09-107-433-3140	Sequence 3140, Ap
301	4	44.4	58	1	US-08-086-328C-199	Sequence 199, App	374	4	44.4	71	2	US-09-654-743-26	Sequence 26, Appl
302	4	44.4	58	1	US-08-086-328C-200	Sequence 200, App	375	4	44.4	71	2	US-09-654-743-87	Sequence 87, Appl
303	4	44.4	58	1	US-08-086-328C-201	Sequence 201, App	376	4	44.4	72	2	US-09-583-110-4535	Sequence 4535, Ap
304	4	44.4	58	1	US-08-086-328C-202	Sequence 202, App	377	4	44.4	72	2	US-09-270-767-58346	Sequence 58346, A
305	4	44.4	58	1	US-08-086-328C-211	Sequence 211, App	378	4	44.4	72	2	US-09-107-433-3140	Sequence 3140, Ap
306	4	44.4	58	1	US-08-086-328C-228	Sequence 228, App	379	4	44.4	72	2	US-09-654-743-26	Sequence 26, Appl
307	4	44.4	58	1	US-08-086-328C-231	Sequence 231, App	380	4	44.4	72	2	US-09-654-743-87	Sequence 87, Appl
308	4	44.4	58	1	US-08-086-328C-233	Sequence 233, App	381	4	44.4	72	2	US-09-583-110-4535	Sequence 4535, Ap
309	4	44.4	58	1	US-08-086-328C-234	Sequence 234, App	382	4	44.4	72	2	US-09-270-767-58346	Sequence 58346, A
310	4	44.4	58	1	US-08-086-328C-237	Sequence 237, App	383	4	44.4	73	2	US-09-107-433-3140	Sequence 3140, Ap
311	4	44.4	58	1	US-08-086-328C-238	Sequence 238, App	384	4	44.4	73	2	US-09-654-743-26	Sequence 26, Appl
312	4	44.4	58	1	US-08-086-328C-252	Sequence 252, App	385	4	44.4	73	2	US-09-654-743-87	Sequence 87, Appl
313	4	44.4	58	1	US-08-086-328C-253	Sequence 253, App	386	4	44.4	73	3	US-09-583-110-4535	Sequence 4535, Ap
314	4	44.4	58	1	US-08-086-328C-254	Sequence 254, App	387	4	44.4	74	2	US-09-270-767-58346	Sequence 58346, A
315	4	44.4	58	1	US-08-086-328C-255	Sequence 255, App	388	4	44.4	75	2	US-09-107-433-3140	Sequence 3140, Ap
316	4	44.4	58	1	US-08-086-328C-256	Sequence 256, App	389	4	44.4	78	2	US-09-654-743-26	Sequence 26, Appl
317	4	44.4	58	1	US-08-086-328C-266	Sequence 266, App	390	4	44.4	79	2	US-09-654-743-87	Sequence 87, Appl
318	4	44.4	58	1	US-08-086-328C-267	Sequence 267, App	391	4	44.4	79	2	US-09-583-110-4535	Sequence 4535, Ap

392	4	44.4	79	2	US-09-732-210-347	Sequence 347, App	465	4	44.4	112	2	US-09-134-001C-2968	Sequence 2968, Ap
393	4	44.4	79	2	US-09-732-210-352	Sequence 352, App	466	4	44.4	112	2	US-09-270-767-38328	Sequence 38328, A
394	4	44.4	79	2	US-09-513-999C-5255	Sequence 5255, App	467	4	44.4	112	2	US-09-270-767-48883	Sequence 48883, A
395	4	44.4	80	2	US-09-134-001C-3508	Sequence 3508, Ap	468	4	44.4	112	2	US-09-270-767-53545	Sequence 53545, A
396	4	44.4	82	2	US-09-134-001C-3874	Sequence 3874, Ap	469	4	44.4	114	2	US-09-344-587-9	Sequence 9, Appli
397	4	44.4	82	2	US-09-621-976-7153	Sequence 7153, Ap	470	4	44.4	114	2	US-10-104-047-3819	Sequence 3819, Ap
398	4	44.4	82	2	US-09-248-796A-26326	Sequence 26326, A	471	4	44.4	115	2	US-09-134-000C-6275	Sequence 6275, Ap
399	4	44.4	84	2	US-09-489-039A-9596	Sequence 9596, Ap	472	4	44.4	115	2	US-09-248-796A-21440	Sequence 21440, A
400	4	44.4	87	2	US-09-381-150A-3	Sequence 3, Appli	473	4	44.4	115	2	US-09-902-540-15352	Sequence 15352, A
401	4	44.4	87	2	US-09-248-796A-23163	Sequence 23163, A	474	4	44.4	116	1	US-07-988-273-5	Sequence 5, Appli
402	4	44.4	89	2	US-08-816-977-4	Sequence 4, Appli	475	4	44.4	116	1	US-08-672-345C-106	Sequence 106, Appl
403	4	44.4	89	2	US-08-816-977-8	Sequence 8, Appli	476	4	44.4	116	2	US-09-270-767-48038	Sequence 48038, A
404	4	44.4	89	2	US-09-334-477-4	Sequence 4, Appli	477	4	44.4	116	2	US-09-726-219A-217	Sequence 217, App
405	4	44.4	89	2	US-09-334-477-8	Sequence 8, Appli	478	4	44.4	116	2	US-09-196-522-217	Sequence 217, App
406	4	44.4	90	2	US-09-673-809-24	Sequence 24, Appl	479	4	44.4	116	5	PCT-US933-12019-5	Sequence 5, Appli
407	4	44.4	90	2	US-09-673-809-103	Sequence 103, App	480	4	44.4	117	2	US-08-936-165A-347	Sequence 347, App
408	4	44.4	90	2	US-09-673-809-105	Sequence 105, App	481	4	44.4	118	1	US-08-524-757-4	Sequence 4, Appli
409	4	44.4	91	2	US-09-248-796A-27490	Sequence 27490, A	482	4	44.4	118	1	US-08-524-757-10	Sequence 10, Appl
410	4	44.4	92	2	US-09-489-039A-11823	Sequence 11823, A	483	4	44.4	118	2	US-09-513-999C-8071	Sequence 8071, Ap
411	4	44.4	92	2	US-09-270-767-31666	Sequence 31666, A	484	4	44.4	118	2	US-09-513-999C-8072	Sequence 8072, Ap
412	4	44.4	93	2	US-09-073-297-12	Sequence 12, Appl	485	4	44.4	118	2	US-09-902-540-14833	Sequence 14833, A
413	4	44.4	93	2	US-09-248-796A-23162	Sequence 23162, A	486	4	44.4	119	2	US-09-732-210-660	Sequence 660, App
414	4	44.4	93	2	US-09-248-796A-24709	Sequence 24709, A	487	4	44.4	119	2	US-10-104-047-2840	Sequence 2840, Ap
415	4	44.4	93	2	US-09-471-276-915	Sequence 915, App	488	4	44.4	120	2	US-09-621-976-7484	Sequence 7484, Ap
416	4	44.4	94	2	US-09-902-540-15017	Sequence 15017, A	489	4	44.4	120	2	US-09-270-767-45419	Sequence 45419, A
417	4	44.4	95	2	US-09-248-796A-21466	Sequence 21466, A	490	4	44.4	120	2	US-09-513-999C-4290	Sequence 4290, Ap
418	4	44.4	95	2	US-09-248-796A-24736	Sequence 24736, A	491	4	44.4	121	2	US-09-187-999-35	Sequence 35, Appl
419	4	44.4	97	2	US-08-816-977-23	Sequence 23, Appl	492	4	44.4	122	1	US-08-276-852-80	Sequence 80, Appl
420	4	44.4	97	2	US-08-816-977-27	Sequence 27, Appl	493	4	44.4	122	1	US-08-899-575-80	Sequence 80, Appl
421	4	44.4	97	2	US-08-818-112-72	Sequence 72, Appl	494	4	44.4	122	1	US-08-899-575-80	Sequence 80, Appl
422	4	44.4	97	2	US-08-818-111-73	Sequence 73, Appl	495	4	44.4	122	1	US-09-134-000C-3427	Sequence 3427, Ap
423	4	44.4	97	2	US-09-056-556-72	Sequence 72, Appl	496	4	44.4	122	5	PCT-US95-08743-80	Sequence 80, Appl
424	4	44.4	97	2	US-09-072-596-73	Sequence 73, Appl	497	4	44.4	123	2	US-09-949-016-6592	Sequence 592, Ap
425	4	44.4	97	2	US-09-072-967-72	Sequence 72, Appl	498	4	44.4	123	2	US-09-550-163-2	Sequence 2, Appli
426	4	44.4	97	2	US-09-334-477-23	Sequence 23, Appl	499	4	44.4	123	2	US-09-550-163-4	Sequence 4, Appli
427	4	44.4	97	2	US-09-334-477-27	Sequence 27, Appl	500	4	44.4	124	2	US-09-513-999C-4287	Sequence 4287, Ap
428	4	44.4	97	2	US-10-193-002-73	Sequence 73, Appl	501	4	44.4	126	2	US-09-240-274-17	Sequence 17, Appl
429	4	44.4	97	2	US-10-084-843-72	Sequence 72, Appl	502	4	44.4	126	2	US-09-848-798-17	Sequence 17, Appl
430	4	44.4	98	2	US-09-248-796A-27698	Sequence 27698, A	503	4	44.4	127	2	US-09-240-274-145	Sequence 145, App
431	4	44.4	98	2	US-09-905-243-45	Sequence 45, Appl	504	4	44.4	127	2	US-09-270-767-48045	Sequence 48045, A
432	4	44.4	99	2	US-09-513-999C-4288	Sequence 4288, Ap	505	4	44.4	127	2	US-09-248-796A-21342	Sequence 21342, A
433	4	44.4	100	2	US-09-248-796A-21520	Sequence 21520, A	506	4	44.4	127	2	US-09-848-798-145	Sequence 145, App
434	4	44.4	100	2	US-10-094-749-2711	Sequence 2711, Ap	507	4	44.4	129	2	US-09-543-681A-7608	Sequence 7608, Ap
435	4	44.4	101	2	US-09-248-796A-25796	Sequence 25796, A	508	4	44.4	130	2	US-08-936-165A-491	Sequence 491, App
436	4	44.4	101	2	US-09-513-999C-6190	Sequence 6190, Ap	509	4	44.4	130	2	US-09-107-433-3668	Sequence 3068, Ap
437	4	44.4	103	2	US-10-094-749-3258	Sequence 3258, Ap	510	4	44.4	130	2	US-09-605-703B-2198	Sequence 2198, Ap
438	4	44.4	104	2	US-08-858-207A-328	Sequence 328, App	511	4	44.4	131	2	US-09-247-155-175	Sequence 175, App
439	4	44.4	104	2	US-09-248-796A-27204	Sequence 27204, A	512	4	44.4	131	2	US-09-839-709-2	Sequence 2, Appli
440	4	44.4	104	2	US-10-014-012-216	Sequence 216, App	513	4	44.4	131	2	US-09-732-210-1340	Sequence 1340, Ap
441	4	44.4	105	2	US-08-899-330-10	Sequence 10, Appl	514	4	44.4	131	2	US-09-732-210-1341	Sequence 1341, Ap
442	4	44.4	105	2	US-09-107-532A-5070	Sequence 5070, Ap	515	4	44.4	131	2	US-09-732-210-1352	Sequence 1352, Ap
443	4	44.4	106	1	US-09-756-541-10	Sequence 10, Appl	516	4	44.4	131	2	US-09-543-681A-5501	Sequence 5501, Ap
444	4	44.4	106	2	US-08-378-939-44	Sequence 44, Appl	517	4	44.4	131	2	US-09-270-767-33577	Sequence 33577, A
445	4	44.4	106	2	US-10-101-464A-657	Sequence 657, App	518	4	44.4	131	2	US-09-270-767-48794	Sequence 48794, A
446	4	44.4	106	2	US-09-996-288-21	Sequence 21, Appl	519	4	44.4	131	2	US-09-513-999C-7397	Sequence 7397, Ap
447	4	44.4	106	2	US-09-996-265-21	Sequence 21, Appl	520	4	44.4	131	2	US-09-991-181-276	Sequence 276, App
448	4	44.4	107	2	US-09-270-767-37624	Sequence 37624, A	521	4	44.4	131	2	US-09-990-444-276	Sequence 276, App
449	4	44.4	107	2	US-09-270-767-52841	Sequence 52841, A	522	4	44.4	131	2	US-09-903-190-175	Sequence 175, App
450	4	44.4	108	1	US-08-245-511-10	Sequence 10, Appl	523	4	44.4	131	2	US-09-997-333-276	Sequence 276, App
451	4	44.4	108	1	US-08-888-366-6	Sequence 6, Appli	524	4	44.4	131	2	US-09-992-598-276	Sequence 276, App
452	4	44.4	108	1	US-09-600-993A-10	Sequence 10, Appl	525	4	44.4	131	2	US-09-989-735-276	Sequence 276, App
453	4	44.4	108	2	US-09-270-767-43418	Sequence 43418, A	526	4	44.4	131	3	US-09-989-726-276	Sequence 276, App
454	4	44.4	109	2	US-09-252-991A-20785	Sequence 20785, A	527	4	44.4	131	3	US-09-997-514-276	Sequence 276, App
455	4	44.4	109	2	US-09-497-997C-29	Sequence 29, Appl	528	4	44.4	131	3	US-09-989-728-276	Sequence 276, App
456	4	44.4	110	2	US-09-214-095D-86	Sequence 86, Appl	529	4	44.4	131	3	US-09-997-349-276	Sequence 276, App
457	4	44.4	110	2	US-09-270-767-34919	Sequence 34919, A	530	4	44.4	131	3	US-09-997-653-276	Sequence 276, App
458	4	44.4	110	2	US-09-270-767-50136	Sequence 50136, A	531	4	44.4	131	3	US-09-989-293A-276	Sequence 276, App
459	4	44.4	110	2	US-09-248-796A-26406	Sequence 26406, A	532	4	44.4	132	2	US-09-673-395A-166	Sequence 166, App
460	4	44.4	110	2	US-09-513-999C-7843	Sequence 7843, Ap	533	4	44.4	133	2	US-09-107-532A-5991	Sequence 5991, Ap
461	4	44.4	110	2	US-09-940-7278-86	Sequence 86, Appl	534	4	44.4	133	2	US-09-270-767-48505	Sequence 48505, A
462	4	44.4	111	1	US-07-754-918A-11	Sequence 11, Appl	535	4	44.4	133	2	US-09-902-540-11050	Sequence 11050, A
463	4	44.4	111	2	US-09-540-236-2670	Sequence 2670, Ap	536	4	44.4	134	2	US-09-134-000C-5312	Sequence 5312, Ap
464	4	44.4	112	2	US-09-134-001C-29933	Sequence 29933, Ap	537	4	44.4	134	2	US-09-540-236-2372	Sequence 2972, Ap

538	4	44.4	134	2	US-09-583-110-4917	Sequence 4917, Ap	611	4	44.4	162	2	US-09-540-236-2231	Sequence 2231, Ap
539	4	44.4	134	2	US-09-270-767-32241	Sequence 32241, A	612	4	44.4	162	2	US-09-270-767-35276	Sequence 35276, A
540	4	44.4	134	2	US-09-270-767-47458	Sequence 47458, A	613	4	44.4	162	2	US-09-270-767-50493	Sequence 50493, A
541	4	44.4	134	2	US-09-270-767-57612	Sequence 57612, A	614	4	44.4	162	2	US-09-248-796A-15063	Sequence 15063, A
542	4	44.4	135	2	US-09-489-039A-13003	Sequence 13003, A	615	4	44.4	162	2	US-09-612-925H-8	Sequence 8, Appl
543	4	44.4	136	2	US-09-513-999C-7844	Sequence 7844, Ap	616	4	44.4	162	2	US-09-612-925H-26	Sequence 26, Appl
544	4	44.4	136	3	US-10-163-315-78	Sequence 78, Appl	617	4	44.4	164	2	US-09-370-838-203	Sequence 203, App
545	4	44.4	137	2	US-09-270-767-33279	Sequence 33279, A	618	4	44.4	164	2	US-09-543-681A-6917	Sequence 6917, Ap
546	4	44.4	137	2	US-09-270-767-48496	Sequence 48496, A	619	4	44.4	164	2	US-09-710-379-2398	Sequence 2398, Ap
547	4	44.4	137	2	US-09-513-999C-4291	Sequence 4291, Ap	620	4	44.4	164	2	US-09-854-113-203	Sequence 203, App
548	4	44.4	138	1	US-08-468-709B-2	Sequence 2, Appl	621	4	44.4	164	2	US-09-902-540-15184	Sequence 15184, A
549	4	44.4	138	1	US-08-468-709B-12	Sequence 12, Appl	622	4	44.4	166	2	US-09-107-532A-4035	Sequence 4035, Ap
550	4	44.4	138	1	US-08-241-664B-2	Sequence 2, Appl	623	4	44.4	166	2	US-09-513-999C-8067	Sequence 8067, Ap
551	4	44.4	138	1	US-08-241-664B-12	Sequence 12, Appl	624	4	44.4	167	2	US-09-489-039A-13896	Sequence 13896, A
552	4	44.4	138	2	US-09-702-705-328	Sequence 328, App	625	4	44.4	167	2	US-09-248-796A-20740	Sequence 20740, A
553	4	44.4	138	2	US-09-736-457-328	Sequence 328, App	626	4	44.4	167	2	US-09-270-767-44166	Sequence 44166, A
554	4	44.4	138	2	US-09-614-124B-328	Sequence 328, App	627	4	44.4	168	2	US-09-248-796A-25866	Sequence 25866, A
555	4	44.4	138	2	US-09-671-325-328	Sequence 328, App	628	4	44.4	168	2	US-09-248-796A-25866	Sequence 24, Appl
556	4	44.4	138	2	US-09-589-184-328	Sequence 328, App	629	4	44.4	169	2	US-09-125-619-24	Sequence 24, Appl
557	4	44.4	138	2	US-09-658-824-328	Sequence 328, App	630	4	44.4	169	2	US-09-583-110-4590	Sequence 4590, Ap
558	4	44.4	138	2	US-09-949-016-11054	Sequence 328, App	631	4	44.4	169	2	US-10-222-566-24	Sequence 24, Appl
559	4	44.4	138	2	US-10-017-754-328	Sequence 11054, A	632	4	44.4	169	2	US-10-143-024A-24	Sequence 24, Appl
560	4	44.4	138	2	US-09-651-563-328	Sequence 328, App	633	4	44.4	169	2	US-09-640-211A-1123	Sequence 1123, Ap
561	4	44.4	138	2	US-09-519-642-328	Sequence 328, App	634	4	44.4	169	2	US-10-222-162-24	Sequence 24, Appl
562	4	44.4	138	5	PCT-US93-03936-2	Sequence 2, Appl	635	4	44.4	170	2	US-09-439-554-18	Sequence 18, Appl
563	4	44.4	139	2	US-09-485-559-12	Sequence 12, Appl	636	4	44.4	170	2	US-09-270-767-45422	Sequence 144, App
564	4	44.4	140	2	US-09-489-039A-10534	Sequence 10534, A	637	4	44.4	170	2	US-09-605-703B-146	Sequence 146, App
565	4	44.4	140	2	US-09-583-110-3229	Sequence 3229, Ap	638	4	44.4	171	2	US-09-605-703B-146	Sequence 18942, A
566	4	44.4	141	2	US-09-328-352-6339	Sequence 6339, Ap	639	4	44.4	172	2	US-09-621-976-4131	Sequence 4131, Ap
567	4	44.4	141	2	US-09-710-279-1718	Sequence 1718, Ap	640	4	44.4	173	2	US-10-094-749-1781	Sequence 1781, Ap
568	4	44.4	142	2	US-09-107-532A-5617	Sequence 5617, Ap	641	4	44.4	175	2	US-09-509-744-4	Sequence 22, Appl
569	4	44.4	142	2	US-09-513-999C-5204	Sequence 5204, Ap	642	4	44.4	176	2	US-09-543-681A-6922	Sequence 398, App
570	4	44.4	143	2	US-09-270-767-41137	Sequence 41137, Ap	643	4	44.4	176	2	US-09-540-236-3395	Sequence 3395, Ap
571	4	44.4	143	2	US-09-270-767-56353	Sequence 56353, A	644	4	44.4	176	2	US-09-605-703B-388	Sequence 388, App
572	4	44.4	144	2	US-08-588-207A-523	Sequence 523, App	645	4	44.4	176	2	US-09-902-540-10996	Sequence 10996, A
573	4	44.4	144	2	US-09-583-110-4496	Sequence 4496, Ap	646	4	44.4	177	2	US-08-770-544-22	Sequence 22, Appl
574	4	44.4	144	2	US-09-270-767-46704	Sequence 46704, A	647	4	44.4	179	2	US-09-579-259-22	Sequence 22, Appl
575	4	44.4	145	1	US-08-166-195A-50	Sequence 50, Appl	648	4	44.4	179	2	US-09-650-324A-22	Sequence 22, Appl
576	4	44.4	145	2	US-09-107-532A-5485	Sequence 5485, Ap	649	4	44.4	179	2	US-09-248-796A-14684	Sequence 56764, A
577	4	44.4	145	2	US-09-513-999C-7009	Sequence 7009, Ap	650	4	44.4	179	2	US-10-039-112A-22	Sequence 22, Appl
578	4	44.4	145	2	US-09-471-276-1287	Sequence 1287, Ap	651	4	44.4	181	2	US-09-013-077A-13	Sequence 13, Appl
579	4	44.4	146	1	US-08-436-772-50	Sequence 50, Appl	652	4	44.4	181	2	US-08-127-954-135	Sequence 135, App
580	4	44.4	146	1	US-08-436-883B-50	Sequence 50, Appl	653	4	44.4	182	1	US-08-127-954-136	Sequence 136, App
581	4	44.4	147	2	US-09-270-767-37475	Sequence 37475, A	654	4	44.4	182	1	US-08-127-954-137	Sequence 137, App
582	4	44.4	147	2	US-09-270-767-52692	Sequence 52692, A	655	4	44.4	182	1	US-08-127-954-141	Sequence 141, App
583	4	44.4	147	2	US-09-902-540-15811	Sequence 15811, A	656	4	44.4	182	1	US-08-127-954-142	Sequence 142, App
584	4	44.4	148	2	US-09-270-767-33466	Sequence 33466, A	657	4	44.4	182	1	US-08-127-954-143	Sequence 143, App
585	4	44.4	148	2	US-09-270-767-35425	Sequence 35425, A	658	4	44.4	182	1	US-08-127-954-144	Sequence 144, App
586	4	44.4	148	2	US-09-270-767-46460	Sequence 46460, A	659	4	44.4	182	1	US-08-127-954-145	Sequence 145, App
587	4	44.4	148	2	US-09-270-767-48683	Sequence 48683, A	660	4	44.4	182	1	US-08-127-954-146	Sequence 146, App
588	4	44.4	148	2	US-09-270-767-50642	Sequence 50642, A	661	4	44.4	182	1	US-08-127-954-147	Sequence 147, App
589	4	44.4	148	7	5180813-2	Patent No. 5180813	662	4	44.4	182	1	US-08-127-954-148	Sequence 148, App
590	4	44.4	149	2	US-09-252-991A-31934	Sequence 31934, A	663	4	44.4	182	1	US-08-127-954-149	Sequence 149, App
591	4	44.4	149	2	US-09-270-767-42544	Sequence 42544, A	664	4	44.4	182	1	US-08-127-954-150	Sequence 150, App
592	4	44.4	149	2	US-09-589-287B-23	Sequence 23, Appl	665	4	44.4	182	1	US-08-127-954-151	Sequence 151, App
593	4	44.4	155	2	US-09-588-947A-23	Sequence 23, Appl	666	4	44.4	182	1	US-08-127-954-152	Sequence 152, App
594	4	44.4	155	2	US-09-589-286A-23	Sequence 23, Appl	667	4	44.4	182	1	US-08-127-954-153	Sequence 153, App
595	4	44.4	155	2	US-09-507-968D-23	Sequence 23, Appl	668	4	44.4	182	1	US-08-127-954-154	Sequence 154, App
596	4	44.4	155	2	US-09-589-285-23	Sequence 23, Appl	669	4	44.4	182	1	US-08-127-954-155	Sequence 155, App
597	4	44.4	156	2	US-09-513-999C-4289	Sequence 4289, Ap	670	4	44.4	182	1	US-08-127-954-156	Sequence 156, App
598	4	44.4	157	2	US-09-489-039A-12693	Sequence 12693, A	671	4	44.4	182	1	US-08-127-954-157	Sequence 157, App
599	4	44.4	157	2	US-09-134-000C-5250	Sequence 5250, Ap	672	4	44.4	182	1	US-08-127-954-158	Sequence 158, App
600	4	44.4	157	5	PCT-US94-01149-34	Sequence 34, Appl	673	4	44.4	182	1	US-08-127-954-159	Sequence 159, App
601	4	44.4	158	2	US-09-107-433-4280	Sequence 4280, Ap	674	4	44.4	182	1	US-08-127-954-160	Sequence 160, App
602	4	44.4	159	1	US-08-606-143-45	Sequence 45, Appl	675	4	44.4	182	1	US-08-127-954-161	Sequence 161, App
603	4	44.4	159	2	US-09-270-767-33621	Sequence 33621, A	676	4	44.4	182	1	US-08-127-954-162	Sequence 162, App
604	4	44.4	159	2	US-09-270-767-48838	Sequence 48838, A	677	4	44.4	182	1	US-08-127-954-163	Sequence 163, App
605	4	44.4	160	2	US-09-543-681A-7581	Sequence 7581, Ap	678	4	44.4	182	1	US-08-127-954-164	Sequence 164, App
606	4	44.4	160	2	US-09-248-796A-15801	Sequence 15801, A	679	4	44.4	182	1		
607	4	44.4	161	2	US-09-605-703B-1830	Sequence 1830, Ap	680	4	44.4	182	1		
608	4	44.4	162	1	US-08-244-557-2	Sequence 2, Appl	681	4	44.4	182	1		
609	4	44.4	162	1	US-08-606-143-44	Sequence 44, Appl	682	4	44.4	182	1		
610	4	44.4	162	2	US-08-930-917A-19	Sequence 19, Appl	683	4	44.4	182	1		

684	4	44.4	1	US-08-127-954-165	Sequence 165, App	757	4	44.4	197	2	US-09-758-759-161	Sequence 161, App
685	4	44.4	1	US-08-127-954-166	Sequence 166, App	758	4	44.4	197	2	US-09-830-230A-620	Sequence 620, App
686	4	44.4	1	US-08-127-954-167	Sequence 167, App	759	4	44.4	199	2	US-09-377-497-69	Sequence 69, Appl
687	4	44.4	1	US-08-127-954-168	Sequence 168, App	760	4	44.4	199	2	US-10-090-365-35	Sequence 35, Appl
688	4	44.4	1	US-08-127-954-169	Sequence 169, App	761	4	44.4	199	2	US-09-728-911-35	Sequence 5989, Ap
689	4	44.4	1	US-08-127-954-170	Sequence 170, App	762	4	44.4	200	2	US-09-134-000C-5989	Sequence 24082, A
690	4	44.4	1	US-08-127-954-171	Sequence 171, App	763	4	44.4	200	2	US-09-248-796A-24082	Sequence 16581, A
691	4	44.4	1	US-08-127-954-172	Sequence 172, App	764	4	44.4	201	2	US-09-902-540-16581	Sequence 1, Appli
692	4	44.4	1	US-08-127-954-173	Sequence 173, App	765	4	44.4	202	1	US-07-807-022A-1	Sequence 20, Appl
693	4	44.4	1	US-09-502-540-14652	Sequence 14652, A	766	4	44.4	202	2	US-08-930-917A-20	Sequence 17985, A
694	4	44.4	1	US-09-270-767-57954	Sequence 57954, A	767	4	44.4	202	2	US-09-252-991A-17985	Sequence 5176, Ap
695	4	44.4	1	US-09-248-796A-21579	Sequence 21579, A	768	4	44.4	202	2	US-09-328-352-5176	Sequence 62, Appl
696	4	44.4	1	US-08-865-336-1	Sequence 1, Appli	769	4	44.4	202	2	US-09-602-777A-62	Sequence 27, Appl
697	4	44.4	1	US-09-153-586-21	Sequence 21, Appl	770	4	44.4	202	2	US-09-612-925H-27	Sequence 32925, A
698	4	44.4	1	US-09-858-580-21	Sequence 21, Appl	771	4	44.4	203	2	US-09-270-767-32925	Sequence 48142, A
699	4	44.4	1	US-08-333-750C-2	Sequence 2, Appli	772	4	44.4	203	2	US-09-270-767-48142	Sequence 318, App
700	4	44.4	1	US-08-965-689A-1	Sequence 2, Appli	773	4	44.4	204	2	US-09-830-230A-318	Sequence 14212, A
701	4	44.4	1	US-09-234-613-2	Sequence 1, Appli	774	4	44.4	206	2	US-09-248-796A-14212	Sequence 7005, Ap
702	4	44.4	1	US-09-359-967-1	Sequence 1, Appli	775	4	44.4	206	2	US-09-949-016-7005	Sequence 4, Appli
703	4	44.4	1	US-09-570-856B-8	Sequence 8, Appli	776	4	44.4	208	2	US-09-094-103-4	Sequence 134, App
704	4	44.4	1	US-09-583-110-5249	Sequence 5249, Ap	777	4	44.4	208	2	US-09-198-452A-134	Sequence 5200, Ap
705	4	44.4	1	US-09-270-767-57496	Sequence 57496, A	778	4	44.4	208	2	US-08-956-171E-5200	Sequence 5200, Ap
706	4	44.4	1	US-09-216-430C-6	Sequence 6, Appli	779	4	44.4	208	2	US-08-781-986A-5200	Sequence 401, App
707	4	44.4	1	US-09-821-726A-13	Sequence 13, Appl	780	4	44.4	209	2	US-09-199-637A-401	Sequence 475, App
708	4	44.4	1	US-09-902-540-15903	Sequence 15903, A	781	4	44.4	209	5	PCU-US94-01149-22	Sequence 22, Appl
709	4	44.4	1	US-09-991-181-211	Sequence 211, App	782	4	44.4	211	2	US-09-134-001C-4194	Sequence 4194, Ap
710	4	44.4	1	US-09-990-444-211	Sequence 211, App	783	4	44.4	211	2	US-09-125-619-40	Sequence 40, Appl
711	4	44.4	1	US-09-997-333-211	Sequence 211, App	784	4	44.4	211	2	US-09-328-352-5256	Sequence 24, Appl
712	4	44.4	1	US-09-992-598-211	Sequence 211, App	785	4	44.4	211	2	US-09-445-774-24	Sequence 44160, A
713	4	44.4	1	US-09-989-735-211	Sequence 211, App	786	4	44.4	211	2	US-10-222-566-40	Sequence 40, Appl
714	4	44.4	1	US-09-989-726-211	Sequence 211, App	787	4	44.4	211	2	US-10-222-162-40	Sequence 32, Appl
715	4	44.4	1	US-09-997-514-211	Sequence 211, App	788	4	44.4	211	2	US-09-125-619-41	Sequence 41, Appl
716	4	44.4	1	US-09-989-728-211	Sequence 211, App	789	4	44.4	212	2	US-09-489-039A-14049	Sequence 6913, Ap
717	4	44.4	1	US-09-997-349-211	Sequence 211, App	790	4	44.4	212	2	US-10-222-566-32	Sequence 32, Appl
718	4	44.4	1	US-09-997-653-211	Sequence 211, App	791	4	44.4	212	2	US-10-222-566-41	Sequence 41, Appl
719	4	44.4	1	US-09-989-293A-211	Sequence 211, App	792	4	44.4	212	2	US-10-222-566-44	Sequence 44, Appl
720	4	44.4	1	US-09-248-796A-28131	Sequence 28131, A	793	4	44.4	212	2	US-10-143-024A-32	Sequence 32, Appl
721	4	44.4	1	US-09-270-767-36772	Sequence 36772, A	794	4	44.4	212	2	US-10-143-024A-41	Sequence 41, Appl
722	4	44.4	1	US-09-270-767-51989	Sequence 51989, A	795	4	44.4	212	2	US-10-143-024A-44	Sequence 44, Appl
723	4	44.4	1	US-09-248-796A-18384	Sequence 18384, A	796	4	44.4	212	2	US-10-222-162-32	Sequence 32, Appl
724	4	44.4	1	US-09-248-796A-20621	Sequence 20621, A	797	4	44.4	212	2	US-10-222-162-44	Sequence 44, Appl
725	4	44.4	1	US-09-080-643-2	Sequence 2, Appli	798	4	44.4	212	2	US-08-874-832-7	Sequence 7, Appli
726	4	44.4	1	US-09-080-643-4	Sequence 4, Appli	799	4	44.4	213	1	US-09-097-233-7	Sequence 34, Appl
727	4	44.4	1	US-09-583-110-4408	Sequence 4408, Ap	800	4	44.4	213	2	US-08-961-083-34	Sequence 39, Appl
728	4	44.4	1	US-09-107-433-5147	Sequence 5147, Ap	801	4	44.4	213	2	US-09-125-619-39	Sequence 34, Appl
729	4	44.4	1	US-09-107-433-4319	Sequence 4319, Ap	802	4	44.4	213	2	US-09-536-784-34	Sequence 34, Appl
730	4	44.4	1	US-09-183-861-82	Sequence 82, Appl	803	4	44.4	213	2	US-09-540-236-3815	Sequence 3815, Ap
731	4	44.4	1	US-09-022-765-82	Sequence 82, Appl	804	4	44.4	213	2	US-10-222-566-39	Sequence 39, Appl
732	4	44.4	1	US-09-551-974A-82	Sequence 82, Appl	805	4	44.4	213	2	US-10-222-566-39	Sequence 39, Appl
733	4	44.4	1	US-09-565-501A-82	Sequence 82, Appl	806	4	44.4	213	2	US-10-143-024A-39	Sequence 19802, A
734	4	44.4	1	US-09-639-206A-82	Sequence 82, Appl	807	4	44.4	213	2	US-09-248-796A-19802	Sequence 719, App
735	4	44.4	1	US-09-874-923-82	Sequence 82, Appl	808	4	44.4	213	2	US-09-538-092-719	Sequence 213, App
736	4	44.4	1	US-09-107-532A-4015	Sequence 4015, Ap	809	4	44.4	213	2	US-09-996-288-213	Sequence 213, App
737	4	44.4	1	US-09-583-110-5295	Sequence 5295, Ap	810	4	44.4	213	2	US-09-996-265-213	Sequence 39, Appl
738	4	44.4	1	US-09-248-796A-20678	Sequence 20678, A	811	4	44.4	213	2	US-10-222-162-39	Sequence 34, Appl
739	4	44.4	1	US-09-107-433-4762	Sequence 4762, Ap	812	4	44.4	213	2	US-09-765-271-34	Sequence 34, Appl
740	4	44.4	1	US-09-393-627B-20	Sequence 20, Appl	813	4	44.4	213	2	US-09-765-272A-34	Sequence 12, Appl
741	4	44.4	1	US-09-393-627B-21	Sequence 21, Appl	814	4	44.4	214	2	US-09-181-183-12	Sequence 12, Appl
742	4	44.4	1	US-09-393-627B-24	Sequence 24, Appl	815	4	44.4	214	2	US-09-280-040-12	Sequence 12, Appl
743	4	44.4	1	US-09-248-796A-24070	Sequence 24070, A	816	4	44.4	214	2	US-09-277-700-12	Sequence 12, Appl
744	4	44.4	1	US-09-107-433-4273	Sequence 4273, Ap	817	4	44.4	214	2	US-09-252-991A-21440	Sequence 21440, A
745	4	44.4	1	US-09-489-039A-11064	Sequence 11064, A	818	4	44.4	214	2	US-09-874-585D-12	Sequence 12, Appl
746	4	44.4	1	US-09-443-067-2	Sequence 2, Appli	819	4	44.4	214	2	US-09-248-796A-14810	Sequence 14810, A
747	4	44.4	1	US-09-377-497-17	Sequence 17, Appl	820	4	44.4	214	2	US-09-902-540-15224	Sequence 15244, A
748	4	44.4	1	US-09-252-991A-21779	Sequence 21779, A	821	4	44.4	215	2	US-09-252-991A-24366	Sequence 24366, A
749	4	44.4	1	US-09-134-000C-6158	Sequence 6158, Ap	822	4	44.4	215	2	US-09-489-039A-8792	Sequence 8792, Ap
750	4	44.4	1	US-09-270-767-41580	Sequence 41580, A	823	4	44.4	215	2	US-09-270-767-44174	Sequence 44174, A
751	4	44.4	1	US-09-270-767-56774	Sequence 56774, A	824	4	44.4	215	2		
752	4	44.4	1	US-09-270-767-56774	Sequence 56774, A	825	4	44.4	215	2		
753	4	44.4	1	US-09-621-976-5041	Sequence 23063, A	826	4	44.4	215	2		
754	4	44.4	1	US-09-270-767-41858	Sequence 5041, Ap	827	4	44.4	215	2		
755	4	44.4	1	US-09-513-999C-4249	Sequence 41858, A	828	4	44.4	215	2		
756	4	44.4	1	US-08-879-561-5	Sequence 5, Appli	829	4	44.4	215	2		

830	4	44.4	216	2	US-09-328-352-6308	Sequence 6308, Ap	903	4	44.4	245	2	US-09-248-796A-18613	Sequence 18613, A
831	4	44.4	216	2	US-09-489-039A-11454	Sequence 11454, A	904	4	44.4	245	2	US-09-949-016-7193	Sequence 7193, Ap
832	4	44.4	217	2	US-09-543-681A-5490	Sequence 5490, A	905	4	44.4	246	2	US-09-248-796A-19220	Sequence 19220, A
833	4	44.4	217	2	US-09-830-230A-317	Sequence 317, App	906	4	44.4	246	2	US-09-902-540-11113	Sequence 11113, A
834	4	44.4	217	2	US-09-605-703B-2470	Sequence 2470, App	907	4	44.4	247	2	US-09-489-039A-11152	Sequence 11152, A
835	4	44.4	218	2	US-09-270-767-42904	Sequence 42904, A	908	4	44.4	248	1	US-08-152-019A-34	Sequence 34, Appl
836	4	44.4	218	2	US-09-270-767-49085	Sequence 49085, A	909	4	44.4	248	2	US-09-107-532A-4568	Sequence 4568, Ap
837	4	44.4	218	2	US-09-248-796A-15695	Sequence 15695, A	910	4	44.4	248	2	US-09-134-000C-5585	Sequence 5585, Ap
838	4	44.4	218	2	US-09-828-080B-4	Sequence 4, Appl	911	4	44.4	248	2	US-09-248-796A-16890	Sequence 16890, A
839	4	44.4	219	2	US-09-648-004-16	Sequence 16, Appl	912	4	44.4	249	1	US-08-152-019A-35	Sequence 35, Appl
840	4	44.4	220	2	US-10-272-419-16	Sequence 16, Appl	913	4	44.4	249	1	US-08-144-121-6	Sequence 6, Appl
841	4	44.4	220	2	US-09-328-352-4134	Sequence 4134, Ap	914	4	44.4	249	1	US-08-460-309-6	Sequence 6, Appl
842	4	44.4	220	2	US-09-538-092-410	Sequence 410, App	915	4	44.4	249	1	US-08-125-077-6	Sequence 6, Appl
843	4	44.4	222	2	US-09-205-258-360	Sequence 360, App	916	4	44.4	249	1	US-08-735-893-6	Sequence 6, Appl
844	4	44.4	222	2	US-09-443-067-16	Sequence 16, Appl	917	4	44.4	249	1	US-09-318-191-34	Sequence 34, Appl
845	4	44.4	222	2	US-09-949-016-8000	Sequence 8000, Ap	918	4	44.4	249	2	US-10-841-139-6	Sequence 6, Appl
846	4	44.4	222	2	US-10-004-860-360	Sequence 360, App	919	4	44.4	251	2	US-08-107-532A-5694	Sequence 5694, Ap
847	4	44.4	222	5	PCT-US94-01149-6	Sequence 6, Appl	920	4	44.4	253	2	US-08-975-762-52	Sequence 52, Appl
848	4	44.4	223	2	US-09-270-767-58723	Sequence 58723, A	921	4	44.4	253	2	US-09-295-028-52	Sequence 52, Appl
849	4	44.4	224	2	US-09-198-452A-683	Sequence 683, App	922	4	44.4	253	2	US-09-106-582-52	Sequence 52, Appl
850	4	44.4	225	5	PCT-US94-01149-30	Sequence 30, Appl	923	4	44.4	253	2	US-09-107-532A-5072	Sequence 5072, Ap
851	4	44.4	226	2	US-09-270-767-36716	Sequence 36716, A	924	4	44.4	253	2	US-09-159-469-52	Sequence 52, Appl
852	4	44.4	226	2	US-09-270-767-51933	Sequence 51933, A	925	4	44.4	253	2	US-09-633-542-52	Sequence 52, Appl
853	4	44.4	226	5	PCT-US94-01149-26	Sequence 26, Appl	926	4	44.4	253	2	US-09-270-767-48906	Sequence 48906, A
854	4	44.4	227	2	US-09-270-767-46812	Sequence 46812, A	927	4	44.4	253	2	US-09-248-796A-27440	Sequence 27440, A
855	4	44.4	227	2	US-09-270-767-61355	Sequence 61355, A	928	4	44.4	253	2	US-09-758-759-19	Sequence 19, Appl
856	4	44.4	227	2	US-09-933-999A-4	Sequence 4, Appl	929	4	44.4	253	5	PCT-US96-01314-53	Sequence 53, Appl
857	4	44.4	229	2	US-09-438-185A-648	Sequence 648, App	930	4	44.4	254	2	US-09-107-532A-4793	Sequence 4793, Ap
858	4	44.4	230	2	US-09-252-991A-20963	Sequence 20963, A	931	4	44.4	254	2	US-09-902-540-12502	Sequence 12502, A
859	4	44.4	230	2	US-09-248-796A-14298	Sequence 14298, A	932	4	44.4	255	2	US-09-543-681A-8065	Sequence 8065, Ap
860	4	44.4	230	2	US-09-830-230A-619	Sequence 619, App	933	4	44.4	255	2	US-09-540-236-2407	Sequence 2407, Ap
861	4	44.4	231	2	US-09-107-532A-5739	Sequence 5739, Ap	934	4	44.4	255	2	US-09-710-279-914	Sequence 914, App
862	4	44.4	231	2	US-09-202-161B-1	Sequence 1, Appl	935	4	44.4	255	2	US-09-902-540-11346	Sequence 11346, A
863	4	44.4	231	5	PCT-US94-01149-29	Sequence 29, Appl	936	4	44.4	255	2	US-09-710-279-2620	Sequence 2620, Ap
864	4	44.4	232	2	US-09-094-103-2	Sequence 2, Appl	937	4	44.4	255	2	US-09-605-703B-2710	Sequence 2710, Ap
865	4	44.4	232	2	US-09-583-110-5010	Sequence 5010, Ap	938	4	44.4	256	2	US-09-902-540-13951	Sequence 13951, A
866	4	44.4	232	2	US-09-270-767-31821	Sequence 31821, A	939	4	44.4	257	2	US-09-107-532A-5440	Sequence 5440, Ap
867	4	44.4	232	2	US-09-911-777-2	Sequence 2, Appl	940	4	44.4	258	2	US-09-396-840-3	Sequence 3, Appl
868	4	44.4	233	2	US-08-871-572B-8	Sequence 8, Appl	941	4	44.4	258	2	US-09-543-681A-6706	Sequence 6706, Ap
869	4	44.4	233	2	US-09-107-532A-5562	Sequence 5562, Ap	942	4	44.4	258	2	US-09-586-106D-103	Sequence 103, App
870	4	44.4	233	2	US-09-902-540-13956	Sequence 13956, A	943	4	44.4	258	2	US-10-799-870-103	Sequence 103, App
871	4	44.4	233	5	PCT-US94-01149-14	Sequence 14, Appl	944	4	44.4	259	2	US-09-134-000C-4642	Sequence 4642, Ap
872	4	44.4	234	2	US-09-134-000C-4928	Sequence 4928, Ap	945	4	44.4	260	2	US-09-993-777-9	Sequence 9, Appl
873	4	44.4	234	2	US-09-134-000C-6200	Sequence 6200, Ap	946	4	44.4	260	2	US-09-993-777-70	Sequence 70, Appl
874	4	44.4	235	2	US-09-949-016-6834	Sequence 6834, Ap	947	4	44.4	260	2	US-09-994-064-9	Sequence 9, Appl
875	4	44.4	237	1	US-08-970-133-5	Sequence 5, Appl	948	4	44.4	260	2	US-09-994-064-70	Sequence 70, Appl
876	4	44.4	237	2	US-09-294-545-5	Sequence 5, Appl	949	4	44.4	260	5	PCT-US96-03916-9	Sequence 9, Appl
877	4	44.4	237	2	US-09-134-000C-6364	Sequence 6364, Ap	950	4	44.4	260	5	PCT-US96-03916-70	Sequence 70, Appl
878	4	44.4	237	2	US-09-902-540-12976	Sequence 12976, A	951	4	44.4	262	2	US-09-489-039A-8063	Sequence 8063, Ap
879	4	44.4	238	1	US-08-452-295-1	Sequence 1, Appl	952	4	44.4	262	2	US-09-252-991A-24153	Sequence 24153, A
880	4	44.4	238	2	US-09-489-039A-7819	Sequence 7819, Ap	953	4	44.4	264	2	US-09-328-352-4654	Sequence 4654, Ap
881	4	44.4	238	5	PCT-US94-01149-24	Sequence 24, Appl	954	4	44.4	264	2	US-09-270-767-41946	Sequence 41946, A
882	4	44.4	239	2	US-09-711-164-367	Sequence 367, App	955	4	44.4	264	2	US-09-543-681A-5709	Sequence 5709, Ap
883	4	44.4	239	2	US-10-169-048-12	Sequence 12, Appl	956	4	44.4	265	2	US-09-248-796A-14892	Sequence 14892, A
884	4	44.4	240	2	US-09-270-767-41540	Sequence 41540, A	957	4	44.4	265	2	US-09-252-991A-27464	Sequence 27464, A
885	4	44.4	242	2	US-08-944-483-29	Sequence 29, Appl	958	4	44.4	266	2	US-09-118-442-17	Sequence 17, Appl
886	4	44.4	242	2	US-09-134-001C-3998	Sequence 3998, Ap	959	4	44.4	267	2	US-09-677-064-17	Sequence 17, Appl
887	4	44.4	242	2	US-09-949-016-9247	Sequence 9247, Ap	960	4	44.4	267	2	US-09-134-000C-5723	Sequence 5723, Ap
888	4	44.4	242	5	PCT-US94-01149-18	Sequence 18, Appl	961	4	44.4	267	2	US-08-993-010-4	Sequence 4, Appl
889	4	44.4	243	2	US-09-134-001C-4239	Sequence 4239, Ap	962	4	44.4	268	5	PCT-US94-01149-20	Sequence 20, Appl
890	4	44.4	243	2	US-09-107-532A-4937	Sequence 4937, App	963	4	44.4	269	2	US-09-634-238-419	Sequence 419, App
891	4	44.4	243	2	US-09-270-767-32768	Sequence 32768, A	964	4	44.4	270	2	US-09-489-039A-10621	Sequence 10621, A
892	4	44.4	243	2	US-09-270-767-47985	Sequence 47985, A	965	4	44.4	270	2	US-09-543-681A-8145	Sequence 8145, Ap
893	4	44.4	243	2	US-09-248-796A-16274	Sequence 16274, A	966	4	44.4	271	2	US-09-134-000C-3651	Sequence 3651, Ap
894	4	44.4	243	2	US-09-248-796A-20638	Sequence 20638, A	967	4	44.4	271	2	US-09-248-796A-19918	Sequence 19918, A
895	4	44.4	243	2	US-09-949-016-9453	Sequence 9453, Ap	968	4	44.4	272	2	US-09-949-016-11056	Sequence 11056, A
896	4	44.4	244	2	US-09-003-287-6	Sequence 6, Appl	969	4	44.4	272	1	US-08-222-851-1	Sequence 1, Appl
897	4	44.4	244	2	US-09-003-287-8	Sequence 8, Appl	970	4	44.4	273	2	US-08-484-905-105	Sequence 105, App
898	4	44.4	244	2	US-09-518-988-2	Sequence 2, Appl	971	4	44.4	273	2		
899	4	44.4	244	2	US-09-248-796A-14680	Sequence 14680, A	972	4	44.4	273	2		
900	4	44.4	244	2	US-09-605-703B-2456	Sequence 2456, Ap	973	4	44.4	273	2		
901	4	44.4	245	2	US-09-252-991A-29983	Sequence 29983, A	974	4	44.4	274	1		
902	4	44.4	245	2	US-09-543-681A-9206	Sequence 9206, Ap	975	4	44.4	274	1		

976 4 44.4 274 1 US-08-484-905-106 Sequence 106, App
977 4 44.4 274 1 US-08-484-905-107 Sequence 107, App
978 4 44.4 274 1 US-08-484-905-108 Sequence 108, App
979 4 44.4 274 2 US-08-481-985B-105 Sequence 105, App
980 4 44.4 274 2 US-08-481-985B-106 Sequence 106, App
981 4 44.4 274 2 US-08-481-985B-107 Sequence 107, App
982 4 44.4 274 2 US-08-481-985B-108 Sequence 108, App
983 4 44.4 274 2 US-08-370-476-105 Sequence 105, App
984 4 44.4 274 2 US-08-370-476-106 Sequence 106, App
985 4 44.4 274 2 US-08-370-476-107 Sequence 107, App
986 4 44.4 274 2 US-08-370-476-108 Sequence 108, App
987 4 44.4 274 2 US-09-595-386-2 Sequence 2, Appli
988 4 44.4 274 2 US-09-593-525-2 Sequence 2, Appli
989 4 44.4 274 2 US-09-248-796A-15791 Sequence 15791, A
990 4 44.4 274 2 US-09-502-540-14541 Sequence 14541, A
991 4 44.4 275 2 US-09-549-016-9056 Sequence 9056, Ap
992 4 44.4 275 2 US-09-902-540-15009 Sequence 15009, A
993 4 44.4 278 2 US-09-710-279-2208 Sequence 2208, Ap
994 4 44.4 280 2 US-09-370-767-32482 Sequence 32482, A
995 4 44.4 281 2 US-09-540-236-2380 Sequence 2380, Ap
996 4 44.4 282 1 US-07-712-476A-5 Sequence 5, Appli
997 4 44.4 282 2 US-09-270-767-39529 Sequence 39529, A
998 4 44.4 282 2 US-09-270-767-54746 Sequence 54746, A
999 4 44.4 283 2 US-09-270-767-45300 Sequence 45300, A
1000 4 44.4 283 2 US-10-211-689-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-489-039A-10751
; Sequence 10751, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10751
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10751

Query Match 66.7%; Score 6; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVV 9
|||||
Db 230 DTFYVV 235

RESULT 2
US-09-962-756-691
; Sequence 691, Application US/09962756
; Patent No. 6875741
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA
; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: SCHAEFFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.
; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ

; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4051US1
; CURRENT APPLICATION NUMBER: US/09/962,756
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 691
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-962-756-691

Query Match 55.6%; Score 5; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 4 DDTFY 8

RESULT 3
US-09-962-756-1425
; Sequence 1425, Application US/09962756
; Patent No. 6875741
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA
; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: SCHAEFFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.
; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4051US1
; CURRENT APPLICATION NUMBER: US/09/962,756
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1425
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-962-756-1425

Query Match 55.6%; Score 5; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 1 DDTFY 5

RESULT 4
US-09-732-210-338
; Sequence 338, Application US/09732210

```

; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 338
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Asparagus officinalis
US-09-732-210-338

Query Match          55.6%; Score 5; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDVT 5
Db 31 KVDVT 35

RESULT 5
US-09-732-210-346
; Sequence 346, Application US/09732210
; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 346
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-09-732-210-346

Query Match          55.6%; Score 5; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDVT 5
Db 31 KVDVT 35

RESULT 6
US-09-740-002-23
; Sequence 23, Application US/09740002
; Patent No. 6537809
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES

```

```

; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-002-23

```

```

Query Match          55.6%; Score 5; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 DDTFY 7
Db 57 DDTFY 61

```

```

RESULT 7
US-09-270-767-60895
; Sequence 60895, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60895
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-60895

```

```

Query Match          55.6%; Score 5; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 5 TFYVY 9
Db 24 TFYVY 28

```

```

RESULT 8
US-09-248-796A-14343
; Sequence 14343, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14343
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Candida albicans

```

US-09-248-796A-14343

Query Match 55.6%; Score 5; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYV 9
|||||
Db 24 TFYV 28

RESULT 9

US-09-668-262A-2
; Sequence 2, Application US/09668262A
; Patent No. 6596926
; GENERAL INFORMATION:
; APPLICANT: Falco, Carl
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Kinney, Tony
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Phosphatidylcholine Biosynthetic Enzyme
; FILE REFERENCE: BB1403 US NA
; CURRENT APPLICATION NUMBER: US/09/668,262A
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155626
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 95
; SEQ ID NO 2
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Zea mays
US-09-668-262A-2

Query Match 55.6%; Score 5; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||
Db 128 KVDDT 132

RESULT 10

US-10-427-442-2
; Sequence 2, Application US/10427442
; Patent No. 6960704
; GENERAL INFORMATION:
; APPLICANT: Falco, Carl
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Kinney, Tony
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Phosphatidylcholine Biosynthetic Enzyme
; FILE REFERENCE: BB1403 US NA
; CURRENT APPLICATION NUMBER: US/10/427,442
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: US/09/668,262A
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155626
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 95
; SEQ ID NO 2
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Zea mays
US-10-427-442-2

Query Match 55.6%; Score 5; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5

Db 128 KVDDT 132

RESULT 11

US-09-270-767-56930
; Sequence 56930, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56930
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-56930

Query Match 55.6%; Score 5; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||
Db 87 KVDDT 91

RESULT 12

US-09-270-767-57344
; Sequence 57344, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57344
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-57344

Query Match 55.6%; Score 5; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 141 DDTFY 145

RESULT 13

US-09-710-279-2532
; Sequence 2532, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2532


```
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-2532

Query Match      55.6%; Score 5; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVDVT 5
Db      18 KVDVT 22

RESULT 14
US-09-107-532A-4432
; Sequence 4432, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4432:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 202 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...202
; SEQUENCE DESCRIPTION: SEQ ID NO: 4432:
US-09-107-532A-4432

Query Match      55.6%; Score 5; DB 2; Length 202;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVDVT 5
```

```
Db      72 KVDVT 76

RESULT 15
US-09-216-393B-31
; Sequence 31, Application US/09216393B
; Patent No. 6514694
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THE
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393B
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,825
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-216-393B-31

Query Match      55.6%; Score 5; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVDVT 5
Db      168 KVDVT 172

RESULT 16
US-10-101-464A-787
; Sequence 787, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 787
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-787

Query Match      55.6%; Score 5; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 DDTFY 7
Db      117 DDTFY 121

RESULT 17
US-08-326-286-5
```

; Sequence 5, Application US/08326286
; Patent No. 5866779
; GENERAL INFORMATION:
; APPLICANT: Sun, Tai-Ping
; APPLICANT: Goodman, Howard M.
; APPLICANT: Ausubel, Frederick M.
; TITLE OF INVENTION: Recombinant Gibberellin DNA and Uses Thereof
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/326,286
; FILING DATE: 20-OCT-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,769
; FILING DATE: 17-JUN-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,996
; FILING DATE: 26-JAN-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/844,300
; FILING DATE: 18-FEB-1992
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence, B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609.2070006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 279 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-326-286-5

Query Match 55.6%; Score 5; DB 1; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 270 VDDTF 274

RESULT 18
US-09-252-991A-30991
; Sequence 30991, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30991
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30991

Query Match 55.6%; Score 5; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 196 KVDDT 200

RESULT 19
US-09-328-352-6685
; Sequence 6685, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6685
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6685

Query Match 55.6%; Score 5; DB 2; Length 301;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 215 KVDDT 219

RESULT 20
US-09-949-016-9786
; Sequence 9786, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9786
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9786

Query Match 55.6%; Score 5; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFY 7
|||||
Db 208 DDTFY 212

RESULT 21
US-09-134-000C-5050
; Sequence 5050, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5050
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (70)..(70)
; OTHER INFORMATION: Amino acid 70 is Xaa wherein Xaa = any amino acid.
US-09-134-000C-5050

Query Match 55.6%; Score 5; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
|||||
Db 145 KVDDT 149

RESULT 22
US-09-914-098-34
; Sequence 34, Application US/09914098
; Patent No. 6855863
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Lysophosphatidic Acid Acetyltransferases
; FILE REFERENCE: BE1332
; CURRENT APPLICATION NUMBER: US/09/914,098
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/121,119
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 34
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Glycine max
US-09-914-098-34

Query Match 55.6%; Score 5; DB 2; Length 373;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
|||||
Db 56 VDDTF 60

RESULT 23
US-10-414-759-2
; Sequence 2, Application US/10414759

; Patent No. 6723329
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: MCGUIRE, MICHAEL J.
; TITLE OF INVENTION: Use of Parapox B2L Protein to Modify Immune Responses to Antigens
; FILE REFERENCE: UTSD:664-1US
; CURRENT APPLICATION NUMBER: US/10/414,759
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/336,694
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 378
; TYPE: PRT
; ORGANISM: PARAPOX
US-10-414-759-2

Query Match 55.6%; Score 5; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
|||||
Db 325 VDDTF 329

RESULT 24
US-10-414-759-4
; Sequence 4, Application US/10414759
; Patent No. 6723329
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: MCGUIRE, MICHAEL J.
; TITLE OF INVENTION: Use of Parapox B2L Protein to Modify Immune Responses to Antigens
; FILE REFERENCE: UTSD:664-1US
; CURRENT APPLICATION NUMBER: US/10/414,759
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/336,694
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 378
; TYPE: PRT
; ORGANISM: PARAPOX
US-10-414-759-4

Query Match 55.6%; Score 5; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
|||||
Db 325 VDDTF 329

RESULT 25
US-10-123-058-2
; Sequence 2, Application US/10123058
; Patent No. 6752995
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: MCGUIRE, MICHAEL J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES USEFUL AS
; FILE REFERENCE: UTSD:664US
; CURRENT APPLICATION NUMBER: US/10/123,058
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2
; LENGTH: 378
; TYPE: PRT
; ORGANISM: PARAPOX
US-10-123-058-2

Query Match 55.6%; Score 5; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 325 VDDTF 329

RESULT 26
US-10-123-058-4
; Sequence 4, Application US/10123058
; Patent No. 6752995
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: MCGUIRE, MICHAEL J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES USEFUL AS
; TITLE OF INVENTION: ADJUVANTS
; FILE REFERENCE: UTSD:664US
; CURRENT APPLICATION NUMBER: US/10/123,058
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 378
; TYPE: PRT
; ORGANISM: PARAPOX
US-10-123-058-4

Query Match 55.6%; Score 5; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 325 VDDTF 329

RESULT 27
US-10-414-609-2
; Sequence 2, Application US/10414609
; Patent No. 6752996
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: MCGUIRE, MICHAEL J.
; TITLE OF INVENTION: Use of Parapox B2L Protein to Modify Immune Responses to Administ
; TITLE OF INVENTION: Antigens
; FILE REFERENCE: UTSD:664-2US
; CURRENT APPLICATION NUMBER: US/10/414,609
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 10/123,058
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/336,694
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 378
; TYPE: PRT
; ORGANISM: PARAPOX
US-10-414-609-2

Query Match 55.6%; Score 5; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6

Db 325 VDDTF 329

RESULT 28
US-10-414-609-4
; Sequence 4, Application US/10414609
; Patent No. 6752996
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: MCGUIRE, MICHAEL J.
; TITLE OF INVENTION: Use of Parapox B2L Protein to Modify Immune Responses to Administ
; TITLE OF INVENTION: Antigens
; FILE REFERENCE: UTSD:664-2US
; CURRENT APPLICATION NUMBER: US/10/414,609
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 10/123,058
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/336,694
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 378
; TYPE: PRT
; ORGANISM: PARAPOX
US-10-414-609-4

Query Match 55.6%; Score 5; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 325 VDDTF 329

RESULT 29
US-10-313-332-1
; Sequence 1, Application US/10313332
; Patent No. 6844000
; GENERAL INFORMATION:
; APPLICANT: Dubois-Stringfellow, Natalie
; TITLE OF INVENTION: Use of PARAPOX B2L Protein to Treat Cancer
; TITLE OF INVENTION: and Modify Immune Responses
; FILE REFERENCE: 002973.00092
; CURRENT APPLICATION NUMBER: US/10/313,332
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/336,694
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Parapox ovis strain NZ2
US-10-313-332-1

Query Match 55.6%; Score 5; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 325 VDDTF 329

RESULT 30
US-10-313-332-3
; Sequence 3, Application US/10313332
; Patent No. 6844000
; GENERAL INFORMATION:
; APPLICANT: Dubois-Stringfellow, Natalie

;; TITLE OF INVENTION: Use of PARAPOX B2L Protein to Treat Cancer
;; TITLE OF INVENTION: and Modify Immune Responses
;; FILE REFERENCE: 002973.00092
;; CURRENT APPLICATION NUMBER: US/10/313,332
;; CURRENT FILING DATE: 2002-12-06
;; PRIOR APPLICATION NUMBER: US 60/336,694
;; PRIOR FILING DATE: 2001-12-07
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 378
;; TYPE: PRT
;; ORGANISM: Parapox ovis strain D1701
US-10-313-332-3

Query Match 55.6%; Score 5; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
| | | | |
DB 325 VDDTF 329

RESULT 31
US-09-198-452A-720
;; Sequence 720, Application US/09198452A
;; Patent No. 6559294
;; GENERAL INFORMATION:
;; APPLICANT: Griffais, R.
;; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
;; TITLE OF INVENTION: and treatment of infection
;; FILE REFERENCE: 9710-003-999
;; CURRENT APPLICATION NUMBER: US/09/198,452A
;; CURRENT FILING DATE: 1998-11-24
;; NUMBER OF SEQ ID NOS: 6849
;; SEQ ID NO 720
;; LENGTH: 428
;; TYPE: PRT
;; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-720

Query Match 55.6%; Score 5; DB 2; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYVV 9
| | | | |
DB 225 TFYVV 229

RESULT 32
US-09-248-796A-17801
;; Sequence 17801, Application US/09248796A
;; Patent No. 6747137
;; GENERAL INFORMATION:
;; APPLICANT: Keith Weinstock et al
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
;; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: 107196.132
;; CURRENT APPLICATION NUMBER: US/09/248,796A
;; CURRENT FILING DATE: 1999-02-12
;; PRIOR APPLICATION NUMBER: US 60/074,725
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: US 60/096,409
;; PRIOR FILING DATE: 1998-08-13
;; NUMBER OF SEQ ID NOS: 28208
;; SEQ ID NO 17801
;; LENGTH: 428
;; TYPE: PRT
;; ORGANISM: Candida albicans
US-09-248-796A-17801

Query Match 55.6%; Score 5; DB 2; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
| | | | |
DB 297 VDDTF 301

RESULT 33
US-09-438-185A-682
;; Sequence 682, Application US/09438185A
;; Patent No. 6822071
;; GENERAL INFORMATION:
;; APPLICANT: Stephens, Richard
;; APPLICANT: Mitchell, Wayne
;; APPLICANT: Kalman, Sue
;; APPLICANT: Davis, Ronald
;; APPLICANT: The Regents of the University of California
;; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
;; FILE REFERENCE: 018941-000411US
;; CURRENT APPLICATION NUMBER: US/09/438,185A
;; CURRENT FILING DATE: 2002-03-13
;; PRIOR APPLICATION NUMBER: US 60/108,279
;; PRIOR FILING DATE: 1998-11-12
;; PRIOR APPLICATION NUMBER: US 60/128,606
;; PRIOR FILING DATE: 1999-04-08
;; NUMBER OF SEQ ID NOS: 1074
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 682
;; LENGTH: 428
;; TYPE: PRT
;; ORGANISM: Chlamydia pneumoniae
;; FEATURE:
;; OTHER INFORMATION: CPn0680
US-09-438-185A-682

Query Match 55.6%; Score 5; DB 2; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFYVV 9
| | | | |
DB 225 TFYVV 229

RESULT 34
US-09-889-738-21
;; Sequence 21, Application US/09889738
;; Patent No. 6734343
;; GENERAL INFORMATION:
;; APPLICANT: Gressel, Jonathan
;; APPLICANT: Eyal, Yoram
;; APPLICANT: Fluhr, Robert
;; TITLE OF INVENTION: RHAMNOSYL-TRANSFERASE GENE AND USES THEREOF
;; FILE REFERENCE: 01/22289
;; CURRENT APPLICATION NUMBER: US/09/889,738
;; CURRENT FILING DATE: 2000-01-20
;; PRIOR APPLICATION NUMBER: IL 128193
;; PRIOR FILING DATE: 1999-01-20
;; PRIOR APPLICATION NUMBER: PCT/IL00/00038
;; PRIOR FILING DATE: 2000-01-20
;; NUMBER OF SEQ ID NOS: 21
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 21
;; LENGTH: 452
;; TYPE: PRT
;; ORGANISM: Citrus X paradisi
US-09-889-738-21

Query Match 55.6%; Score 5; DB 2; Length 452;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5

Db 243 KVDDT 247

RESULT 35

US-09-740-002-27

; Sequence 27, Application US/09740002

; Patent No. 6537809

; GENERAL INFORMATION:

; APPLICANT: BRAMS, PETER

; APPLICANT: MORROW, PHILLIP

; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES

; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR

; FILE REFERENCE: 037003-0275759

; CURRENT APPLICATION NUMBER: US/09/740,002

; CURRENT FILING DATE: 2000-12-20

; PRIOR APPLICATION NUMBER: 09/335,697

; PRIOR FILING DATE: 1999-06-18

; PRIOR APPLICATION NUMBER: 08/488,376

; PRIOR FILING DATE: 1995-06-07

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 27

; LENGTH: 475

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-740-002-27

Query Match

Best Local Similarity 55.6%; Score 5; DB 2; Length 475;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7

Db 76 DDTFY 80

RESULT 36

US-09-134-001C-4435

; Sequence 4435, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 4435

; LENGTH: 479

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-4435

Query Match

Best Local Similarity 55.6%; Score 5; DB 2; Length 479;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5

Db 45 KVDDT 49

RESULT 37

US-10-033-109-12

; Sequence 12, Application US/10033109

; Patent No. 6833492

; GENERAL INFORMATION:

; APPLICANT: Allen, Stephen M.

; APPLICANT: Rafalski, J. Antoni

; APPLICANT: Sakai, Hajime

; TITLE OF INVENTION: Nitrogen Transport Metabolism

; FILE REFERENCE: BB-1210

; CURRENT APPLICATION NUMBER: US/10/033,109

; CURRENT FILING DATE: 2001-12-28

; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 09/384,625

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248

; PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 12

; LENGTH: 486

; TYPE: PRT

; ORGANISM: Glycine max

US-10-033-109-12

Query Match

Best Local Similarity 55.6%; Score 5; DB 2; Length 486;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5

Db 344 KVDDT 348

RESULT 38

US-08-942-012B-27

; Sequence 27, Application US/08942012B

; Patent No. 6235278

; GENERAL INFORMATION:

; APPLICANT: Miller, Lois K.

; APPLICANT: Lu, Albert

; APPLICANT: Dierks, Peter

; APPLICANT: Black, Bruce

; TITLE OF INVENTION: Biological Insect Control Agents Expressing

; FILE REFERENCE: 28-96a

; CURRENT APPLICATION NUMBER: US/08/942,012B

; CURRENT FILING DATE: 1997-10-01

; PRIOR APPLICATION NUMBER: 08/729,606

; PRIOR FILING DATE: 2000-10-01

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 27

; LENGTH: 491

; TYPE: PRT

; ORGANISM: Choristoneura fumiferana nucleopolyhedrovirus

US-08-942-012B-27

Query Match

Best Local Similarity 55.6%; Score 5; DB 2; Length 491;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5

Db 328 KVDDT 332

RESULT 39

US-10-033-109-10

; Sequence 10, Application US/10033109

; Patent No. 6833492

; GENERAL INFORMATION:

; APPLICANT: Allen, Stephen M.

; APPLICANT: Rafalski, J. Antoni

; APPLICANT: Sakai, Hajime

; TITLE OF INVENTION: Nitrogen Transport Metabolism
; FILE REFERENCE: BB-1210
; CURRENT APPLICATION NUMBER: US/10/033.109
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
; PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 10
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-033-109-10

Query Match 55.6%; Score 5; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDVT 5
DB 347 KVDVT 351

RESULT 40
US-09-252-991A-17363
; Sequence 17363, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17363
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17363

Query Match 55.6%; Score 5; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
DB 133 VDDTF 137

RESULT 41
US-09-398-395A-2
; Sequence 2, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22

; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-398-395A-2

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
DB 300 VDDTF 304

RESULT 42
US-09-398-395A-4
; Sequence 4, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-398-395A-4

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
DB 300 VDDTF 304

RESULT 43
US-09-398-395A-6
; Sequence 6, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262

; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-398-395A-6

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 300 VDDTF 304

RESULT 44
US-09-398-395A-8
; Sequence 8, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-398-395A-8

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 300 VDDTF 304

RESULT 45
US-09-398-395A-10
; Sequence 10, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23

; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-398-395A-10

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 300 VDDTF 304

RESULT 46
US-09-398-395A-12
; Sequence 12, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; NAME/KEY: VARIANT
; LOCATION: (1)...(548)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-398-395A-12

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 300 VDDTF 304

RESULT 47
US-09-887-586A-2
; Sequence 2, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628


```

; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-887-586A-2

```

```

Query Match      55.6%  Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 VDDTF 6
      |||||
Db      300 VDDTF 304

```

RESULT 48

```

US-09-887-586A-4
; Sequence 4, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-887-586A-4

```

```

Query Match      55.6%  Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 VDDTF 6
      |||||
Db      300 VDDTF 304

```

RESULT 49

```

US-09-887-586A-6
; Sequence 6, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22

```

```

; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-887-586A-6

```

```

Query Match      55.6%  Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 VDDTF 6
      |||||
Db      300 VDDTF 304

```

RESULT 50

```

US-09-887-586A-8
; Sequence 8, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-887-586A-8

```

```

Query Match      55.6%  Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 VDDTF 6
      |||||
Db      300 VDDTF 304

```

RESULT 51

```

US-09-887-586A-10
; Sequence 10, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262

```

; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-887-586A-10

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 300 VDDTF 304

RESULT 52
US-09-887-586A-12
; Sequence 12, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; NAME/KEY: VARIANT
; LOCATION: (1)...(548)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-887-586A-12

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 300 VDDTF 304

RESULT 53
US-09-895-752-2
; Sequence 2, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65592971, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17

; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-895-752-2

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 300 VDDTF 304

RESULT 54
US-09-895-752-4
; Sequence 4, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65592971, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-895-752-4

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 300 VDDTF 304

RESULT 55
US-09-895-752-6
; Sequence 6, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65592971, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752

; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-895-752-6

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred.No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
| | | | |
Db 300 VDDTF 304

RESULT 56
US-09-895-752-8
; Sequence 8, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65592971, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-895-752-8

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred.No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
| | | | |
Db 300 VDDTF 304

RESULT 57
US-09-895-752-10
; Sequence 10, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65592971, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.

; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-895-752-10

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred.No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
| | | | |
Db 300 VDDTF 304

RESULT 58
US-09-895-752-12
; Sequence 12, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65592971, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(548)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-895-752-12

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred.No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
| | | | |
Db 300 VDDTF 304

RESULT 59
US-09-903-012B-2

; Sequence 2, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-903-012B-2

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 2 VDDTF 6
Db 300 VDDTF 304

RESULT 60
US-09-903-012B-4
; Sequence 4, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-903-012B-4

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 2 VDDTF 6
Db 300 VDDTF 304

RESULT 61
US-09-903-012B-6
; Sequence 6, Application US/09903012B

; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-903-012B-6

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 2 VDDTF 6
Db 300 VDDTF 304

RESULT 62
US-09-903-012B-8
; Sequence 8, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-903-012B-8

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 2 VDDTF 6
Db 300 VDDTF 304

RESULT 63
US-09-903-012B-10
; Sequence 10, Application US/09903012B
; Patent No. 6569656

US-09-903-012B-10
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 300 VDDTF 304

RESULT 64
US-09-903-012B-12
; Sequence 12, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(548)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-903-012B-12

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 300 VDDTF 304

RESULT 65

US-09-900-797-2
; Sequence 2, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 66457621, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-900-797-2

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 300 VDDTF 304

RESULT 66
US-09-900-797-4
; Sequence 4, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 66457621, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-900-797-4

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
Db 300 VDDTF 304

RESULT 67
US-09-900-797-6

RESULT 69
US-09-900-797-10
; Sequence 10. Application US/09900797

RESULT 71

US-09-893-820-2
; Sequence 2, Application US/09893820
; Patent No. 6890752
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6890752L, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893,820
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR FILING DATE: 1998-09-18
; PRIOR FILING DATE: 1999-04-22
; PRIOR FILING DATE: 1999-04-22
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-893-820-2

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||||
Db 300 VDDTF 304

RESULT 72

US-09-893-820-4
; Sequence 4, Application US/09893820
; Patent No. 6890752
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6890752L, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893,820
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-893-820-4

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||||

Db 300 VDDTF 304

RESULT 73

US-09-893-820-6
; Sequence 6, Application US/09893820
; Patent No. 6890752
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6890752L, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893,820
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR FILING DATE: 1998-09-18
; PRIOR FILING DATE: 1999-04-22
; PRIOR FILING DATE: 1999-04-22
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-893-820-6

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||||
Db 300 VDDTF 304

RESULT 74

US-09-893-820-8
; Sequence 8, Application US/09893820
; Patent No. 6890752
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6890752L, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893,820
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-893-820-8

Query Match 55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      2 VDDTF 6
Db      300 VDDTF 304

US-09-893-820-10
; Sequence 10, Application US/09893820
; Patent No. 6890752
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 68907521, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893,820
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-893-820-10

Query Match      55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VDDTF 6
Db      300 VDDTF 304

US-09-893-820-12
; LOCATION: (1)....(548)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-893-820-12

Query Match      55.6%; Score 5; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VDDTF 6
Db      300 VDDTF 304

US-08-443-639-8
; Sequence 8, Application US/08443639
; Patent No. 5981843
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: Yin, Shaohui
; APPLICANT: Cornett, Catherine A.G.
; TITLE OF INVENTION: Transcriptional Control Sequences and
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,639
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33878
; REFERENCE/DOCKET NUMBER: 69-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 550 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-443-639-8

Query Match      55.6%; Score 5; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VDDTF 6
Db      302 VDDTF 306

US-08-577-483-8
; Sequence 8, Application US/08577483
; Patent No. 6100451
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: Yin, Shaohui
; APPLICANT: Cornett, Catherine A.G.
; TITLE OF INVENTION: Transcriptional Control Sequences and
```


;; TITLE OF INVENTION: Methods
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson, P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: US
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/577,483
;; FILING DATE: 22-DEC-1995
;; CLASSIFICATION: 800
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Paul T. Clark
;; REGISTRATION NUMBER: 32,164
;; REFERENCE/DOCKET NUMBER: 07678/003001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 542-5070
;; TELEFAX: (617) 542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 550 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-577-483-8

Query Match 55.6%; Score 5; DB 2; Length 550;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

Qy 2 VDDTF 6
Db 302 VDDTF 306

RESULT 79
US-09-435-380-8
; Sequence 8, Application US/09435380
; Patent No. 6605764
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: Yin, Shaohui
; APPLICANT: Cornett, Catherine A.G.
; TITLE OF INVENTION: Transcriptional Control Sequences and
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/435,380
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,639
; FILING DATE: 18-MAY-1995

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ferber, Donna M.
;; REGISTRATION NUMBER: 33878
;; REFERENCE/DOCKET NUMBER: 69-94
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (303) 499-8080
;; TELEFAX: (303) 499-8089
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 550 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-435-380-8

Query Match 55.6%; Score 5; DB 2; Length 550;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

Qy 2 VDDTF 6
Db 302 VDDTF 306

RESULT 80
US-09-398-395A-32
; Sequence 32, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 556
; TYPE: PRI
; ORGANISM: Solanum tuberosum
; US-09-398-395A-32

Query Match 55.6%; Score 5; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

Qy 2 VDDTF 6
Db 308 VDDTF 312

RESULT 81
US-09-887-586A-32
; Sequence 32, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22

```

; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-09-887-586A-32

```

```

Query Match          55.6%; Score 5; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 VDDTF 6
        |||||
Db      308 VDDTF 312

```

```

RESULT 82
US-09-895-752-32
; Sequence 32, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6559297, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-09-895-752-32

```

```

Query Match          55.6%; Score 5; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 VDDTF 6
        |||||
Db      308 VDDTF 312

```

```

RESULT 83
US-09-903-012B-32
; Sequence 32, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6569656, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B

```

```

; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-09-903-012B-32

```

```

Query Match          55.6%; Score 5; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 VDDTF 6
        |||||
Db      308 VDDTF 312

```

```

RESULT 84
US-09-900-797-32
; Sequence 32, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6645762, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-09-900-797-32

```

```

Query Match          55.6%; Score 5; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 VDDTF 6
        |||||
Db      308 VDDTF 312

```

```

RESULT 85
US-09-893-820-32
; Sequence 32, Application US/09893820
; Patent No. 6890752
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6890752, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893,820
; CURRENT FILING DATE: 2001-06-28

```

;; PRIOR APPLICATION NUMBER: US/09/398,395A
;; PRIOR FILING DATE: 1999-09-17
;; PRIOR APPLICATION NUMBER: 60/100,993
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/130,628
;; PRIOR FILING DATE: 1999-04-22
;; PRIOR APPLICATION NUMBER: 60/150,262
;; PRIOR FILING DATE: 1999-08-23
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 32
;; LENGTH: 556
;; TYPE: PRT
;; ORGANISM: Solanum tuberosum
US-09-893-820-32

Query Match 55.6%; Score 5; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
|||
Db 308 VDDTF 312

RESULT 86
US-10-094-749-2545
;; Sequence 2545, Application US/10094749
;; Patent No. 6979557
;; GENERAL INFORMATION:
;; APPLICANT: ISOGAI, TAKAO
;; APPLICANT: SUGIYAMA, TOMOYASU
;; APPLICANT: OTSUKI, TETSUJI
;; APPLICANT: WAKAMATSU, AI
;; APPLICANT: SATO, HIROYUKI
;; APPLICANT: ISHII, SHIZUKO
;; APPLICANT: YAMAMOTO, JUN-ICHI
;; APPLICANT: ISONO, YUUKO
;; APPLICANT: HIO, YURI
;; APPLICANT: OTSUKA, KAORU
;; APPLICANT: NAGAI, KEIICHI
;; APPLICANT: IRIE, RYOTARO
;; APPLICANT: TAMECHIKA, ICHIRO
;; APPLICANT: SEKI, NAOHICO
;; APPLICANT: YOSHIKAWA, TSUTOMU
;; APPLICANT: OTSUKA, MOTOKYU
;; APPLICANT: NAGAHARI, KENJI
;; APPLICANT: MASUHO, YASUHIKO
;; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
;; FILE REFERENCE: 084335/0160
;; CURRENT APPLICATION NUMBER: US/10/094,749
;; CURRENT FILING DATE: 2002-03-12
;; PRIOR APPLICATION NUMBER: 60/350,435
;; PRIOR FILING DATE: 2002-01-24
;; PRIOR APPLICATION NUMBER: JP 2001-328381
;; PRIOR FILING DATE: 2001-09-14
;; NUMBER OF SEQ ID NOS: 3381
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2545
;; LENGTH: 566
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-094-749-2545

Query Match 55.6%; Score 5; DB 2; Length 566;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDST 5
|||
Db 178 KVDST 182

RESULT 87
US-09-902-540-11767
;; Sequence 11767, Application US/09902540
;; Patent No. 6833447
;; GENERAL INFORMATION:
;; APPLICANT: Goldman, Barry S.
;; APPLICANT: Hinkle, Gregory J.
;; APPLICANT: Slater, Steven C.
;; APPLICANT: Wiegand, Roger C.
;; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;; FILE REFERENCE: 38-10(15849)B
;; CURRENT APPLICATION NUMBER: US/09/902,540
;; CURRENT FILING DATE: 2001-07-10
;; PRIOR APPLICATION NUMBER: 60/217,883
;; PRIOR FILING DATE: 2000-07-10
;; NUMBER OF SEQ ID NOS: 16825
;; SEQ ID NO 11767
;; LENGTH: 567
;; TYPE: PRT
;; ORGANISM: Myxococcus xanthus
US-09-902-540-11767

Query Match 55.6%; Score 5; DB 2; Length 567;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
|||
Db 379 VDDTF 383

RESULT 88
US-09-902-540-12279
;; Sequence 12279, Application US/09902540
;; Patent No. 6833447
;; GENERAL INFORMATION:
;; APPLICANT: Goldman, Barry S.
;; APPLICANT: Hinkle, Gregory J.
;; APPLICANT: Slater, Steven C.
;; APPLICANT: Wiegand, Roger C.
;; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;; FILE REFERENCE: 38-10(15849)B
;; CURRENT APPLICATION NUMBER: US/09/902,540
;; CURRENT FILING DATE: 2001-07-10
;; PRIOR APPLICATION NUMBER: 60/217,883
;; PRIOR FILING DATE: 2000-07-10
;; NUMBER OF SEQ ID NOS: 16825
;; SEQ ID NO 12279
;; LENGTH: 581
;; TYPE: PRT
;; ORGANISM: Myxococcus xanthus
US-09-902-540-12279

Query Match 55.6%; Score 5; DB 2; Length 581;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
|||
Db 307 VDDTF 311

RESULT 89
US-09-248-796A-16044
;; Sequence 16044, Application US/09248796A
;; Patent No. 6747137
;; GENERAL INFORMATION:
;; APPLICANT: Keith Weinstock et al
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
;; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: 107196.132
;; CURRENT APPLICATION NUMBER: US/09/248,796A
;; CURRENT FILING DATE: 1999-02-12

;
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16044
; LENGTH: 584
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16044

Query Match 55.6%; Score 5; DB 2; Length 584;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
DB 80 VDDTF 84

RESULT 90
US-09-248-796A-17444
; Sequence 17444, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17444
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17444

Query Match 55.6%; Score 5; DB 2; Length 651;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||
DB 445 KVDDT 449

RESULT 91
US-09-540-236-2284
; Sequence 2284, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2284
; LENGTH: 783
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2284

Query Match 55.6%; Score 5; DB 2; Length 783;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||
DB 16 KVDDT 20

RESULT 92
US-09-248-796A-20875
; Sequence 20875, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20875
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20875

Query Match 55.6%; Score 5; DB 2; Length 812;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
DB 159 VDDTF 163

RESULT 93
US-09-489-039A-8469
; Sequence 8469, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8469
; LENGTH: 825
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8469

Query Match 55.6%; Score 5; DB 2; Length 825;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||
DB 14 VDDTF 18

RESULT 94
US-09-248-796A-18967
; Sequence 18967, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18967
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18967

```
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18967
; LENGTH: 832
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18967

Query Match      55.6%; Score 5; DB 2; Length 832;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVDVT 5
      |||||
Db      508 KVDVT 512

RESULT 95
US-09-134-000C-5052
; Sequence 5052, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5052
; LENGTH: 869
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (9)..(9)
; OTHER INFORMATION: Amino acid 9 is Xaa wherein Xaa = any amino acid.
US-09-134-000C-5052

Query Match      55.6%; Score 5; DB 2; Length 869;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVDVT 5
      |||||
Db      670 KVDVT 674

RESULT 96
US-09-134-000C-4697
; Sequence 4697, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4697
```

```
; LENGTH: 899
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4697

Query Match      55.6%; Score 5; DB 2; Length 899;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 DDTFY 7
      |||||
Db      399 DDTFY 403

RESULT 97
US-09-270-767-42083
; Sequence 42083, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42083
; LENGTH: 910
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42083

Query Match      55.6%; Score 5; DB 2; Length 910;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 DDTFY 7
      |||||
Db      528 DDTFY 532

RESULT 98
US-09-252-991A-27976
; Sequence 27976, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27976
; LENGTH: 1123
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27976

Query Match      55.6%; Score 5; DB 2; Length 1123;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVDVT 5
      |||||
Db      239 KVDVT 243
```

```
RESULT 99
US-09-862-027-82
; Sequence 82, Application US/09862027
; Patent No. 6858418
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: No. 6858418el Kinases and Uses Thereof
; FILE REFERENCE: 35800/234862
; CURRENT APPLICATION NUMBER: US/09/862,027
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/345,473
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 1309
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1309)
; OTHER INFORMATION: xaa = Any Amino Acid
US-09-862-027-82

Query Match          55.6%; Score 5; DB 2; Length 1309;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VDDTF 6
Db      1078 VDDTF 1082

RESULT 100
US-09-949-016-10490
; Sequence 10490, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10490
; LENGTH: 1912
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10490

Query Match          55.6%; Score 5; DB 2; Length 1912;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VDDTF 6
Db      1710 VDDTF 1714

RESULT 101
US-09-747-408-22
; Sequence 22, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
```

```
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: Cerebral Amyloid Angiopathy
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-22

Query Match          44.4%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVDD 4
Db      1 KVDD 4

RESULT 102
US-09-996-288-23
; Sequence 23, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxi
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-23

Query Match          44.4%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 DTFY 7
Db      1 DTFY 4

RESULT 103
US-09-996-288-90
; Sequence 90, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxi
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 7
```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-90

Query Match 44.4%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFY 7
|
|
|
Db 1 DTFY 4

RESULT 104

US-09-996-288-99
; Sequence 99, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-99

Query Match 44.4%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFY 7
|
|
|
Db 1 DTFY 4

RESULT 105

US-09-996-265-23
; Sequence 23, Application US/09996265
; Patent No. 6855493
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-23

Query Match 44.4%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFY 7
|
|
|
Db 1 DTFY 4

RESULT 106

US-09-996-265-90
; Sequence 90, Application US/09996265
; Patent No. 6855493
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-90

Query Match 44.4%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFY 7
|
|
|
Db 1 DTFY 4

RESULT 107

US-09-996-265-99
; Sequence 99, Application US/09996265
; Patent No. 6855493
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-99

Query Match 44.4%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFY 7
|
|
|
Db 1 DTFY 4

RESULT 108

US-10-092-263-4
; Sequence 4, Application US/10092263
; Patent No. 6800477
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: STEREoselective REDUCTION OF SUBSTITUTED ACETOPHENONE
; FILE REFERENCE: CT-2657NP
; CURRENT APPLICATION NUMBER: US/10/092,263
; CURRENT FILING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4

```
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Pichia methanolica
US-10-092-263-4

Query Match      44.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVDD 4
Db      1 KVDD 4

RESULT 109
US-08-166-195A-22
; Sequence 22, Application US/08166195A
; Patent No. 5480799
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Lea, Isabel
; APPLICANT: Richardson, Richard T.
; TITLE OF INVENTION: Sperm Antigen Corresponding to a
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5480799th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/166,195A
; FILING DATE: 10 DEC 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470/73
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-166-195A-23

Query Match      44.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVDD 4
Db      3 KVDD 6

RESULT 111
US-08-436-772-22
; Sequence 22, Application US/08436772
; Patent No. 5814456
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 581456th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,772
```


;; FILING DATE: 08-MAY-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sibley, Kenneth D.
;; REGISTRATION NUMBER: 31,665
;; REFERENCE/DOCKET NUMBER: 5470-73B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 919-881-3140
;; TELEFAX: 919-881-3175
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-436-772-22

Query Match 44.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDD 4
|||
Db 6 KVDD 9

RESULT 112
US-08-436-772-23
; Sequence 23 Application US/08436772
; Patent No. 5814456
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5814456th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/436,772
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-73B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-436-772-23

Query Match 44.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDD 4
|||
Db 3 KVDD 6

RESULT 113
US-08-436-883B-22
; Sequence 22 Application US/08436883B
; Patent No. 5820861
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5820861th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/436,883B
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-73C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-436-883B-22

Query Match 44.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDD 4
|||
Db 6 KVDD 9

RESULT 114
US-08-436-883B-23
; Sequence 23 Application US/08436883B
; Patent No. 5820861
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Kenneth D. Sibley
STREET: P.O. Box 34009
CITY: Charlotte
STATE: No. 5820861th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,883B
FILING DATE: 08-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-73C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-436-883B-23

Query Match 44.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDD 4
Db 3 KVDD 6

RESULT 115
US-09-200-757-3
; Sequence 3, Application US/09200757
; Patent No. 6277958
; GENERAL INFORMATION:
; APPLICANT: Aimoto, Saburho
; TITLE OF INVENTION: METHOD FOR PREPARING PEPTIDE THIOL ESTER
; FILE REFERENCE: 31763-138092
; CURRENT APPLICATION NUMBER: US/09/200,757
; CURRENT FILING DATE: 1998-11-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Asp(OBUT)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (2)
; OTHER INFORMATION: Asp(OBUT)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (3)
; OTHER INFORMATION: Asp(OBUT)
; FEATURE:
; NAME/KEY: MOD_RES

LOCATION: (4)
; OTHER INFORMATION: Thr(But)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: Thr(But)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)
; OTHER INFORMATION: Lys(Boc)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)
; OTHER INFORMATION: Gly(S-C(CH3)2CH2-CO)
; FEATURE:
; OTHER INFORMATION: this peptide has an amidated C-terminus
US-09-200-757-3

Query Match 44.4%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTF 6
Db 2 DDTF 5

RESULT 116
US-09-200-757-4
; Sequence 4, Application US/09200757
; Patent No. 6277958
; GENERAL INFORMATION:
; APPLICANT: Aimoto, Saburho
; TITLE OF INVENTION: METHOD FOR PREPARING PEPTIDE THIOL ESTER
; FILE REFERENCE: 31763-138092
; CURRENT APPLICATION NUMBER: US/09/200,757
; CURRENT FILING DATE: 1998-11-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)
; OTHER INFORMATION: Gly(S-C(CH3)2CH2-CO)
; FEATURE:
; OTHER INFORMATION: this peptide has an amidated C-terminus
US-09-200-757-4

Query Match 44.4%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTF 6
Db 2 DDTF 5

RESULT 117
US-07-712-476A-3
; Sequence 3, Application US/07712476A
; Patent No. 5304496
; GENERAL INFORMATION:
; APPLICANT: Hoyer et al.
; TITLE OF INVENTION: Biological Regulation of
; TITLE OF INVENTION: Mineralization
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5304496ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC DOS
; SOFTWARE: WORDPERFECT 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/712,476A
; FILING DATE: 19910610
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Suzanne E. Miller
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN 0473
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568 3100
; TELEFAX: (215) 568 3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; US-07-712-476A-3

```

```

Query Match 44.4%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 VDDT 5
Db 6 VDDT 9

```

```

RESULT 118
5204097-4
; Patent No. 5204097
; APPLICANT: ARNON, RUTH; HARARI, ILANA; KEUSCH, GERALD T.
; DONOHUE-ROLFE, ARTHUR
; TITLE OF INVENTION: SHIGA TOXIN B CHAIN POLYPEPTIDES AND
; VACCINE THEREOF
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/364,506
; FILING DATE: 09-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 70,243
; FILING DATE: 06-JUL-1987
; SEQ ID NO: 4:
; LENGTH: 14
5204097-4

```

```

Query Match 44.4%; Score 4; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 DDTF 6
Db 5 DDTF 8

```

```

RESULT 119
US-08-480-190-171
; Sequence 171, Application US/08480190
; Patent No. 5827516

```

```

; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 171:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-480-190-171

```

```

Query Match 44.4%; Score 4; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 VDDT 5
Db 1 VDDT 4

```

```

RESULT 120
US-08-488-379-171
; Sequence 171, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts

```

```
/
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ COMPUTER: IBM PS/2 Model 502 or 55SX
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: WordPerfect (Version 5.1)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/488,379
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/077,255
/ FILING DATE: June 15, 1993
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 171:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ US-08-488-379-171

Query Match 44.4%; Score 4; DB 1; Length 16;
Best Local Similarity 100.0%; Pred.No.1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 121
US-08-475-399A-171
/ Sequence 171, Application US/08475399A
/ Patent No. 6509033
/ GENERAL INFORMATION:
/ APPLICANT: Urban, Robert G.
/ APPLICANT: Chiciz, Roman M.
/ APPLICANT: Vignali, Dario A.A.
/ APPLICANT: Hedley, Mary L.
/ APPLICANT: Stern, Lawrence J.
/ APPLICANT: Strominger, Jack L.
/ TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
/ NUMBER OF SEQUENCES: 276
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson, P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: US
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows95
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/475,399A
/ FILING DATE: 07-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/077,255
/ FILING DATE: 15-JUN-1993
/ APPLICATION NUMBER: 07/925,460
```

```
/
/ FILING DATE: 11-AUG-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fraser, Janis K.
/ REGISTRATION NUMBER: 34,819
/ REFERENCE/DOCKET NUMBER: 00246/168003
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617/542-507
/ TELEFAX: 617/542-890
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 171:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-475-399A-171

Query Match 44.4%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred.No.1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 122
US-08-077-255A-171
/ Sequence 171, Application US/08077255A
/ Patent No. 6696061
/ GENERAL INFORMATION:
/ APPLICANT: Robert G. Urban
/ APPLICANT: Roman M. Chiciz
/ APPLICANT: Dario A. A. Vignali
/ APPLICANT: Mary L. Hedley
/ APPLICANT: Lawrence J. Stern
/ APPLICANT: Jack L. Strominger
/ TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
/ NUMBER OF SEQUENCES: 274
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ COMPUTER: IBM PS/2 Model 502 or 55SX
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: WordPerfect (Version 5.1)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/077,255A
/ FILING DATE: June 15, 1993
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 171:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ US-08-077-255A-171
```

Query Match 44.4%; Score 4; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDT 5
 ||||
 Db 1 VDDT 4

RESULT 123

PCT-US93-07545-171
 ; Sequence 171, Application PC/TUS9307545
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Urban
 ; APPLICANT: Roman M. Chicz
 ; APPLICANT: Dario A. A. Vignali
 ; APPLICANT: Mary L. Hedley
 ; APPLICANT: Lawrence J. Stern
 ; APPLICANT: Jack L. Strominger
 ; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
 ; NUMBER OF SEQUENCES: 273
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 50Z or 55SX
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/07545
 ; FILING DATE: 19930811
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/925,460
 ; FILING DATE: August 11, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 00246/168001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 171:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; PCT-US93-07545-171

Query Match 44.4%; Score 4; DB 5; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDT 5
 ||||
 Db 1 VDDT 4

RESULT 124

US-08-480-190-97
 ; Sequence 97, Application US/08480190
 ; Patent No. 5827516
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Urban
 ; APPLICANT: Roman M. Chicz
 ; APPLICANT: Dario A. A. Vignali

; APPLICANT: Mary L. Hedley
 ; APPLICANT: Lawrence J. Stern
 ; APPLICANT: Jack L. Strominger
 ; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
 ; NUMBER OF SEQUENCES: 274
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 50Z or 55SX
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/480,190
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/077,255
 ; FILING DATE: June 15, 1993
 ; APPLICATION NUMBER: 07/925,460
 ; FILING DATE: August 11, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 00246/168001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 97:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-08-480-190-97

Query Match 44.4%; Score 4; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDT 5
 ||||
 Db 1 VDDT 4

RESULT 125

US-08-480-190-108
 ; Sequence 108, Application US/08480190
 ; Patent No. 5827516
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Urban
 ; APPLICANT: Roman M. Chicz
 ; APPLICANT: Dario A. A. Vignali
 ; APPLICANT: Mary L. Hedley
 ; APPLICANT: Lawrence J. Stern
 ; APPLICANT: Jack L. Strominger
 ; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
 ; NUMBER OF SEQUENCES: 274
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

;
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-480-190-108

Query Match 44.4%; Score 4; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 VDDT 5
Db 1 VDDT 4

RESULT 126
US-08-488-379-97
; Sequence 97, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.

;
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-488-379-97

Query Match 44.4%; Score 4; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 VDDT 5
Db 1 VDDT 4

RESULT 127
US-08-488-379-108
; Sequence 108, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-488-379-108

Query Match 44.4%; Score 4; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 128
US-08-672-345C-65
; Sequence 65, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-65

Query Match 44.4%; Score 4; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 7
Db 8 DTFY 11

RESULT 129
US-09-214-095D-65
; Sequence 65, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 17
; TYPE: PRT

; ORGANISM: Murinae gen. sp.
US-09-214-095D-65

Query Match 44.4%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 7
Db 8 DTFY 11

RESULT 130
US-08-475-399A-97
; Sequence 97, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,399A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00246/168003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-507
; TELEFAX: 617/542-890
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-475-399A-97

Query Match 44.4%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 131
US-08-475-399A-108
; Sequence 108, Application US/08475399A
; Patent No. 6509033

```

; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,399A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00246/168003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-507
; TELEFAX: 617/542-890
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-475-399A-108

Query Match 44.4%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 132
US-08-077-255A-97
; Sequence 97, Application US/08077255A
; Patent No. 6696061
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chiciz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/077,255A
; FILING DATE: June 15, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/077,255A
; FILING DATE: June 15, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-077-255A-97

Query Match 44.4%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 133
US-08-077-255A-108
; Sequence 108, Application US/08077255A
; Patent No. 6696061
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chiciz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/077,255A
; FILING DATE: June 15, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001

```



```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-077-255A-108

```

```

Query Match 44.4%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 VDDT 5
Db 1 VDDT 4

```

RESULT 134

```

US-09-940-727B-65
; Sequence 65, Application US/09940727B
; Patent No. 6913917
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 17
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-65

```

```

Query Match 44.4%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 DTFY 7
Db 8 DTFY 11

```

RESULT 135

```

PCT-US93-07545-97
; Sequence 97, Application PC/TUS9307545
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07545
; FILING DATE: 19930811
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US93-07545-97

```

```

Query Match 44.4%; Score 4; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 VDDT 5
Db 1 VDDT 4

```

RESULT 136

```

PCT-US93-07545-108
; Sequence 108, Application PC/TUS9307545
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07545
; FILING DATE: 19930811
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 17
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-07545-108

Query Match 44.4%; Score 4; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 137
US-08-480-190-106
Sequence 106, Application US/08480190
Patent No. 5827516
GENERAL INFORMATION:

APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-106

Query Match 44.4%; Score 4; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 138
US-08-488-379-106
Sequence 106, Application US/08488379
Patent No. 5880103
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,379
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-488-379-106

Query Match 44.4%; Score 4; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 139
US-08-475-399A-106
Sequence 106, Application US/08475399A
Patent No. 6509033
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Vignali, Dario A.A.

```
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,399A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00246/168003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-507
; TELEFAX: 617/542-890
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-475-399A-106

Query Match 44.4%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 140
US-08-077-255A-106
; Sequence 106, Application US/08077255A
; Patent No. 6696061
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
```

```
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/077,255A
; FILING DATE: June 15, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-077-255A-106
```

Query Match 44.4%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

```
RESULT 141
US-09-612-925H-4
; Sequence 4, Application US/09612925H
; Patent No. 6921809
; GENERAL INFORMATION:
; APPLICANT: Cano, Carlos Antonio Durante
; APPLICANT: Nieto, Enrique Gerardo Guillen
; APPLICANT: Acosta, Anabel Alvarez
; APPLICANT: Munoz, Luis Emilio Carpio
; APPLICANT: Vazquez, Diogenes Quintana
; APPLICANT: Rodriguez, Carmen Elena Gomez
; APPLICANT: Rodriguez, Recardo de la Caridad Siva
; APPLICANT: Galvez, Consuelo Nazabal
; APPLICANT: Angulo, Maria de Jesus Leal
; APPLICANT: Dunn, Alejandro Miguel Martin
; TITLE OF INVENTION: Expression System of Heterologous Antigens as Fusion Proteins
; FILE REFERENCE: LEXSA P-13DIV2
; CURRENT APPLICATION NUMBER: US/09/612,925H
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 08/930,917
; PRIOR FILING DATE: 1997-09-16
; PRIOR APPLICATION NUMBER: PCT/CU97/00001
; PRIOR FILING DATE: 1997-01-17
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Neisseria meningitidis (group B)
; US-09-612-925H-4
```

Query Match 44.4%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 9 VDDT 12

RESULT 142
PCT-US93-07545-106
; Sequence 106, Application PC/TUS9307545
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07545
; FILING DATE: 19930811
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US93-07545-106
Query Match 44.4%; Score 4; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDT 5
Db 1 VDDT 4
RESULT 143
US-08-480-190-94
; Sequence 94, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston

; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-480-190-94
Query Match 44.4%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDT 5
Db 1 VDDT 4
RESULT 144
US-08-480-190-105
; Sequence 105, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255

```
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-480-190-105

Query Match 44.4%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 145
US-08-488-379-94
; Sequence 94, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-488-379-105

Query Match 44.4%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4

RESULT 146
US-08-488-379-105
; Sequence 105, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-488-379-105

Query Match 44.4%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDT 5
Db 1 VDDT 4
```

RESULT 147
US-08-475-399A-94
; Sequence 94, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,399A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00246/168003
; TELEPHONE: 617/542-507
; TELEFAX: 617/542-890
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-475-399A-94
Query Match 44.4%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDT 5
Db 1 VDDT 4
RESULT 148
US-08-475-399A-105
; Sequence 105, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street

; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,399A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00246/168003
; TELEPHONE: 617/542-507
; TELEFAX: 617/542-890
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-475-399A-105
Query Match 44.4%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDT 5
Db 1 VDDT 4
RESULT 149
US-08-077-255A-94
; Sequence 94, Application US/08077255A
; Patent No. 6696061
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chiciz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/077,255A
; FILING DATE: June 15, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-077-255A-94

Query Match 44.4%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDT 5
Db 1 VDDT 4

RESULT 150

US-08-077-255A-105
Sequence 105, Application US/08077255A
Patent No. 6696061
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,255A
FILING DATE: June 15, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-077-255A-105

Query Match 44.4%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDT 5
Db 1 VDDT 4

Search completed: May 17, 2006, 06:30:27
Job time : 52 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2006, 06:12:05 ; Search time 199 Seconds
(without alignments)
41.835 Million cell updates/sec

Title: US-10-764-985-2

Perfect score: 9

Sequence: 1 KVDDTFYV 9

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	150	1 VHR2_CAMPM	P68643 camelpox vi
2	9	100.0	150	1 VHR2_CAMPS	P68642 camelpox vi
3	9	100.0	150	1 VHR2_VACCA	P68598 vaccinia vi
4	9	100.0	150	1 VHR2_VACCC	P68599 vaccinia vi
5	9	100.0	150	1 VHR2_VACCV	P68600 vaccinia vi
6	9	100.0	150	1 VHR2_VACV	P33860 variola vir
7	9	100.0	150	2 Q49QR1_9POXV	Q49qr1 vaccinia vi
8	9	100.0	150	2 Q6RZS8_9POXV	Q6rzs8 rabbitpox v
9	9	100.0	150	2 Q76Q66_VAVR	Q76q66 variola min
10	9	100.0	150	2 Q76QL6_COWPX	Q76ql6 cowpox viru
11	9	100.0	150	2 Q77TN9_VACCT	Q77tn9 vaccinia vi
12	9	100.0	150	2 Q8JLI7_9POXV	Q8jli7 ectromelia
13	9	100.0	150	2 Q8QN33_COWPX	Q8qn33 cowpox viru
14	7	77.8	512	2 Q4WIR3_ASPFU	Q4wir3 aspergillus
15	7	77.8	515	2 Q2U7D1_ASPOR	Q2u7d1 aspergillus
16	7	77.8	770	2 P73845_SYNV3	P73845 synechocyst
17	6	66.7	103	2 Q8VUM8_STAHO	Q8vum8 staphylococ
18	6	66.7	126	2 Q38248_9CAUD	Q38248 lactococcus
19	6	66.7	176	2 Q5A2T5_CANAL	Q5a2t5 candida alb
20	6	66.7	205	1 RAS3_RHRA	P22280 rhizomucor
21	6	66.7	231	2 Q8T5E9_RICFL	Q8t5e9 ricordea fl
22	6	66.7	232	2 Q5TOR6_ANOGA	Q5tor6 anopheles g
23	6	66.7	261	2 Q9CAE4_ARATH	Q9cae4 arabidopsis
24	6	66.7	298	2 Q2NEH9_9EURY	Q2neh9 methanospira
25	6	66.7	311	2 Q4K6A8_PSEF5	Q4k6a8 pseudomonas
26	6	66.7	330	2 Q6DB07_ERWCT	Q6db07 erwinia car
27	6	66.7	376	2 Q5WC87_BACSK	Q5wc87 legionella
28	6	66.7	399	2 Q5WX32_LEGFL	Q5wx32 legionella
29	6	66.7	399	2 Q5X5Q2_LEGPA	Q5x5q2 legionella
30	6	66.7	399	2 Q5ZYV4_LEGPH	Q5zyv4 legionella
31	6	66.7	400	1 TRPB_NEIGO	Q849j9 neisseria g

32	6	66.7	400	1 TRPB_NEIMA	Q9jvc0 neisseria m
33	6	66.7	400	1 TRPB_NEIMB	Q9kb05 neisseria m
34	6	66.7	400	2 Q5F9W3_NEIG1	Q5f9w3 neisseria g
35	6	66.7	401	2 Q31HH4_THICR	Q31hh4 thiomicrosp
36	6	66.7	404	2 Q44BZ8_CHRSL	Q44bz8 chromohalob
37	6	66.7	405	2 Q604P3_METCA	Q604p3 methylococc
38	6	66.7	406	2 Q36T45_MARHY	Q36t45 marinobacte
39	6	66.7	409	1 TRPB_PSESH	Q849p2 pseudomonas
40	6	66.7	409	1 TRPB_PSESM	Q88b61 pseudomonas
41	6	66.7	409	2 Q48QG6_PSE14	Q48qg6 pseudomonas
42	6	66.7	409	2 Q500R4_PSEU2	Q500r4 pseudomonas
43	6	66.7	410	2 Q2SJD1_9GAMM	Q2sjd1 hahella che
44	6	66.7	411	2 Q35ZW5_9GAMM	Q35zw5 alkalilimn
45	6	66.7	416	2 Q3MWU8_9DELT	Q3mwu8 syntrophoba
46	6	66.7	474	2 Q3EM85_BACTI	Q3em85 bacillus th
47	6	66.7	482	2 Q60051_THREUV	Q60051 thermoactin
48	6	66.7	485	2 Q8L9B9_ARATH	Q8l9b9 arabidopsis
49	6	66.7	485	2 Q9LNJ3_ARATH	Q9lnj3 arabidopsis
50	6	66.7	499	2 Q2V3N3_ARATH	Q2v3n3 arabidopsis
51	6	66.7	500	2 Q8RX11_ARATH	Q8rx11 arabidopsis
52	6	66.7	500	2 Q9LS40_ARATH	Q9ls40 arabidopsis
53	6	66.7	512	2 Q63GZ3_BACCZ	Q63gz3 bacillus ce
54	6	66.7	512	2 Q6HPG6_BACHK	Q6hpg6 bacillus th
55	6	66.7	514	2 Q6Z6Q8_ORYSA	Q6z6q8 oryza sativ
56	6	66.7	535	2 Q9LYS8_ARATH	Q9lys8 arabidopsis
57	6	66.7	567	2 Q50EJ4_LACRE	Q50ej4 lactobacill
58	6	66.7	671	2 Q70Q68_PERMR	Q70q68 perla margi
59	6	66.7	678	2 Q8FLC6_ECOL6	Q8flc6 escherichia
60	6	66.7	731	2 Q7XJX7_ORYSA	Q7xjx7 oryza sativ
61	6	66.7	870	2 Q2Z173_9CAUD	Q2z173 pseudomonas
62	6	66.7	892	2 Q9S9U5_ARATH	Q9s9u5 arabidopsis
63	6	66.7	894	2 Q8T043_DROME	Q8t043 drosophila
64	6	66.7	900	2 Q9VPH1_DROME	Q9vph1 drosophila
65	6	66.7	1080	2 Q4I709_GIBZE	Q4i709 gibberella
66	6	66.7	1111	1 SEC8_NEUCR	Q9hse8 neurospora
67	6	66.7	1256	2 Q9XVH4_CABEL	Q9xvh4 caenorhabdi
68	6	66.7	1284	2 Q61VN1_CABEL	Q61vn1 caenorhabdi
69	6	66.7	1286	2 Q21025_CABEL	Q21025 caenorhabdi
70	5	55.6	51	2 Q73C85_BACCI	Q73c85 bacillus ce
71	5	55.6	56	2 Q838E6_ENTFA	Q838e6 enterococcu
72	5	55.6	60	2 Q514Y7_ENTHI	Q514y7 entamoeba h
73	5	55.6	70	2 Q81GV6_BACCR	Q81gv6 bacillus ce
74	5	55.6	78	1 RS27A_ASPOF	P31753 asparagus o
75	5	55.6	80	1 RS27A_LYCES	P62380 lycopersico
76	5	55.6	80	1 RS27A_SOLTU	P62981 solanum tub
77	5	55.6	80	2 Q3GRU5_9GAMM	Q3gru9 psychrobact
78	5	55.6	81	2 Q48Q06_STRPM	Q48qg6 streptococc
79	5	55.6	87	2 Q4FQ61_PSTAR	Q4fq61 psychrobact
80	5	55.6	90	1 Y3711_CLOAB	Q04353 clostridium
81	5	55.6	91	2 Q8JM27_9NUCL	Q8j277 mamestra co
82	5	55.6	92	2 Q63CD4_BACCZ	Q63cd4 bacillus ce
83	5	55.6	92	2 Q81RL2_BACAN	Q81rl2 bacillus an
84	5	55.6	92	2 Q2Z0L6_9ADEN	Q2z0l6 human adeno
85	5	55.6	94	2 Q2WLY5_CLOBE	Q2wly5 clostridium
86	5	55.6	100	2 Q4DFB0_TRYCR	Q4dfb0 trypanosoma
87	5	55.6	104	2 Q2J0A0_RHOPA	Q2j0a0 rhodopseudo
88	5	55.6	106	2 Q6SG18_BACLD	Q6sg18 bacillus li
89	5	55.6	108	2 Q5WEA4_BACSK	Q5wea4 bacillus cl
90	5	55.6	109	2 Q4XCY7_PLACH	Q4xcy7 plasmodium
91	5	55.6	116	2 Q6Y8R4_MYCHO	Q6y8r4 mycoplasma
92	5	55.6	119	2 Q63BU1_BACCZ	Q63bu1 bacillus ce
93	5	55.6	119	2 Q6HJB1_BACHK	Q6hjb1 bacillus th
94	5	55.6	119	2 Q81D21_BACCR	Q81dz1 bacillus ce
95	5	55.6	119	2 Q81R08_BACAN	Q81r08 bacillus an
96	5	55.6	119	2 Q738W2_BACCI	Q738w2 bacillus ce
97	5	55.6	120	2 Q8U332_PYRFU	Q8u332 pyrococcus
98	5	55.6	120	2 Q4MNT5_BACCZ	Q4mte5 bacillus ce
99	5	55.6	126	2 Q5DHT7_SCHJA	Q5dht7 schistosoma
100	5	55.6	128	2 Q33XT4_9GAMM	Q33xt4 shewanella
101	5	55.6	128	2 Q8X3T8_ECO57	Q8x3t8 escherichia
102	5	55.6	130	2 Q7NF95_GLOVI	Q7nf95 gloebacter
103	5	55.6	134	1 PA2_APTCC	Q9bmk4 apis cerana
104	5	55.6	134	2 Q8Z174_YERPE	Q8z174 yersinia pe

105 Q2NCA0_9SPHN 137 5 55.6
 106 RABP2_RAT 138 5 55.6
 107 Q315F6_DESDG 138 5 55.6
 108 Q4U9J7_THEAN 139 5 55.6
 109 SKB5_SCHPO 140 5 55.6
 110 Q4N291_THEHPA 141 5 55.6
 111 Q586G7_9TRYR 142 5 55.6
 112 Q60DU6_ORYSA 147 5 55.6
 113 Q72QW4_LEPIC 148 5 55.6
 114 Q8F4Y0_LEPIN 148 5 55.6
 115 Q5IFZ7_9PROT 149 5 55.6
 116 Q93AM5_9BACT 150 5 55.6
 117 Q9AF59_9PROT 151 5 55.6
 118 Q665U0_YERPS 151 5 55.6
 119 Q8CKF9_YERPE 153 5 55.6
 120 Q41753_MAIZE 155 5 55.6
 121 Q7WKG7_PORGI 155 5 55.6
 122 Q6Q131_RAT 155 5 55.6
 123 Q9VJR2_DROME 157 5 55.6
 124 Q7QZ72_CANFA 159 5 55.6
 125 Q4UID3_THEAN 161 5 55.6
 126 Q43W25_SOLUS 162 5 55.6
 127 Q4N780_THEPA 162 5 55.6
 128 Q4ZPM6_PSEU2 163 5 55.6
 129 Q5SVM6_HUMAN 166 5 55.6
 130 Q5IY06_MONPV 167 5 55.6
 131 Q5C0Z6_SCHJA 170 5 55.6
 132 Q5K255_GUTH 170 5 55.6
 133 Q6LVZ2_HELPH 171 5 55.6
 134 Q7VIT4_THEHP 171 5 55.6
 135 Q6WHR4_BPKV4 175 5 55.6
 136 Q9DHU6_YLDV 176 5 55.6
 137 Q5GSE5_WOLTR 179 5 55.6
 138 Q4D000_TYCR 180 5 55.6
 139 Q3ZEE6_SHIDS 180 5 55.6
 140 Q5FJR3_LACAC 182 5 55.6
 141 Q64LE1_9ADEN 183 5 55.6
 142 Q5CNC5_CRYHO 186 5 55.6
 143 Q7YFE2_CRYPV 186 5 55.6
 144 Q47L35_THEPY 188 5 55.6
 145 Q3YI44_ENTFC 189 5 55.6
 146 Q5MJW8_TOBAC 191 5 55.6
 147 Q6C1Q6_YARLI 192 5 55.6
 148 Q36C04_MARHY 194 5 55.6
 149 Q9RBX9_PSEIN 195 5 55.6
 150 Q3FPC2_9BURK 196 5 55.6
 151 Q76XPS_9CAUD 196 5 55.6
 152 Q4MN44_BACCE 199 5 55.6
 153 Q3ZLB4_OREMO 199 5 55.6
 154 Q3AU66_CHLCH 200 5 55.6
 155 Q6L009_PICTO 202 5 55.6
 156 Q3QW04_9RHO 202 5 55.6
 157 Q3B2E2_COXHU 202 5 55.6
 158 Q3VVD4_PROAE 208 5 55.6
 159 Q3H6V1_TRIER 210 5 55.6
 160 Q97A41_THEVO 211 5 55.6
 161 Q9V162_PVRAB 211 5 55.6
 162 Q6W6S8_CANFA 211 5 55.6
 163 Q4KED7_PSEF5 211 5 55.6
 164 Q3SD18_PARTE 212 5 55.6
 165 Q3IMT7_NATPD 213 5 55.6
 166 Q63F37_BACCZ 213 5 55.6
 167 Q73CJ5_BACC1 213 5 55.6
 168 Q4UH05_THEAN 215 5 55.6
 169 Q3YB22_SARSH 216 5 55.6
 170 Q2T8L4_BURTH 216 5 55.6
 171 Q6C580_YARLI 217 5 55.6
 172 Q341U2_RHOPI 219 5 55.6
 173 Q41UB2_BACAN 220 5 55.6
 174 Q47FJ7_DECAR 221 5 55.6
 175 Q6N1B3_RHOPI 221 5 55.6
 176 Q8KU99_ENTFA 221 5 55.6
 177 Q371X9_RHOPI 222 5 55.6

Q2NCA0 erythrobaact
 P51673 rattus norv
 Q315f6 desulfobr
 Q4u9j7 theileria a
 Q9u859 schizosacch
 Q4n291 theileria p
 Q586g7 trypanosoma
 Q60du6 oryza sativ
 Q72qw4 leptospira
 Q8f4y0 leptospira
 Q5ifz7 uncultured
 Q93am5 uncultured
 Q9af59 uncultured
 Q665u0 yersinia ps
 Q8ckf9 yersinia pe
 Q41753 zea mays (m
 Q7mxg7 porphyromon
 Q6q131 rattus norv
 Q9vjr2 drosophila
 Q7qz72 canis famil
 Q4uid3 theileria a
 Q43w25 solibacter
 Q4n780 theileria p
 Q4zpm6 pseudomonas
 Q5svm6 homo sapien
 Q5iy06 monkeypox v
 Q5c0z6 schistosoma
 Q5k255 guillardia
 Q6lvz2 photobacter
 Q7vit4 helicobacte
 Q6whr4 bacterioph
 Q9dhue yaba-like d
 Q5gae5 wolbachia s
 Q4d000 trypanosoma
 Q3zee6 shigella dy
 Q5fjr3 lactobacill
 Q64le1 human adeno
 Q5cnc5 cryptospori
 Q7yfe2 cryptospori
 Q47l35 thermobifid
 Q3yl44 enterococcu
 Q5mjw8 nicotiana t
 Q6c1q6 yarrowia li
 Q36c04 marinobacte
 Q9rbx9 pseudomonas
 Q3fpc2 rhodofera
 Q76xf5 enterobacte
 Q4mn44 bacillus ce
 Q3zlb4 oreochromis
 Q3au66 chlorobium
 Q6l009 picrophilus
 Q3qw04 silicibacte
 Q83e29 coxiella bu
 Q3vvd4 prosthecoch
 Q3h6v1 trichodesmi
 Q97a41 thermoplas
 Q9v162 pyrococcus
 Q6w6s8 canis famil
 Q4ked7 pseudomonas
 Q3sd18 paramycium
 Q3imt7 natronomona
 Q6c580 yarrowia li
 Q341u2 rhodopseudo
 Q41ub2 bacillus an
 Q47fj7 dechloromon
 Q6n1b3 rhodopseudo
 Q8ku99 enterococcu
 Q371x9 rhodopseudo

2 Q4HKS1_CAMLA
 1 TRMD_MYCPPE
 2 Q6NPS9_ARATH
 2 Q6CST8_YARLI
 2 Q5AQJ7_EMENI
 2 SNF7_KLULA
 2 Q626V0_CABBR
 1 D8OD_PSEHT
 2 Q3ORV9_THIDN
 2 Q3I797_9METZ
 2 Q3I798_9METZ
 2 Q3I799_9METZ
 2 Q5TT21_AMOGA
 2 Q4V5S8_PLACH
 2 Q37EQ9_RHOPI
 2 Q6LN97_PHOPR
 2 Q58MZ0_9CAUD
 2 Q5YV13_NOCFA
 2 Q3V3D7_MOUSE
 2 Q4N8M1_THEPA
 2 Q9XYH3_BABBI
 2 Q5BX52_SCHJA
 2 Q3CGG4_THET
 2 Q2Q0D5_9ZZZZ
 2 Q46E39_METBA
 2 Q2UQV7_ASPOR
 1 TRUA_HELPHP
 2 Q3GLG1_9GAMM
 2 Q4UM49_RICFE
 2 Q8VEB8_MOUSE
 2 Q5COA1_CRYPV
 2 Q67PC4_SYMTH
 2 Q8H469_ORYSA
 2 Q65NZ3_BACLD
 2 Q5KX41_GOKA
 2 Q8Y2A0_RALSO
 2 Q3CLA2_ALTAT
 2 Q36A47_9GAMM
 2 Q8XMG6_CLOPE
 2 Q684R0_MOUSE
 2 Q83Z90_ENTFA
 2 Q9KA41_BACHD
 2 Q9FVSO_ARATH
 2 Q4HA89_9DEIO
 2 Q5WFR4_BACSK
 2 Q4XG96_PLACH
 2 Q2NFZ6_9EURY
 2 Q3IGU6_PSEHT
 2 Q2WRY1_CLOBE
 2 Q4YPD8_PLABE
 2 Q3FK89_9BURK
 2 Q3J7B1_NITOC
 2 Q3M1M6_ANAVT
 2 Q9YI68_BUFMA
 2 Q4J9I7_SULAC
 2 Q4E0D4_TYCR
 2 Q4GZF2_9TRYP
 2 Q2XEX9_PSEPU
 2 Q51386_PSEAE
 2 Q8RSQ3_PSEPU
 2 Q88KT1_PSEPK
 2 Q91433_PSEAK
 2 Q88L11_PSEBP
 2 Q7VWH8_BORPE
 2 Q7WL48_BORBR
 1 TRMD_DEIRA
 2 Q2NFC1_9EURY
 2 Q9HJV3_THRAC
 2 Q2L1W2_BORAV
 2 Q4L3B6_STAHH
 2 Q5LXJ4_STRT1
 2 Q5M244_STRT2

Q4hks1 campylobact
 Q8cxq6 mycoplasma
 Q6nps9 arabidopsis
 Q6cst8 yarrowia li
 Q5aqj7 aspergillus
 Q6cjl0 kluyveromyc
 Q626v0 caenorhabdi
 Q3icuh pseudosalter
 Q30rv9 thimicrosp
 Q3i797 trichoplax
 Q3i798 trichoplax
 Q3i799 trichoplax
 Q5tt21 anophelles g
 Q4v5s8 plasmodium
 Q37eq9 rhodopseudo
 Q6ln97 photobacter
 Q58mz0 cyanophage
 Q5yv13 nocardia fa
 Q3v3d7 mus musculu
 Q4n8m1 theileria p
 Q9xyh3 babesia big
 Q5bx52 schistosoma
 Q3cgg4 thermaanaer
 Q2q0d5 uncultured
 Q46e39 methanogarc
 Q2ugy7 aspergillus
 Q7u328 helicobacte
 Q3glg1 psychrobact
 Q4um49 rickettsia
 Q8vee8 mus musculu
 Q5co11 cryptospori
 Q67pc4 symbiobacte
 Q8h469 oryza sativ
 Q65nz3 bacillus li
 Q5kx41 geobacillus
 Q8y2a0 ralstonia s
 Q3cl12 pseudosalter
 Q36a47 shewanella
 Q8xmg6 clostridium
 Q684r0 mus musculu
 Q83z90 enterococcu
 Q9ka41 bacillus ha
 Q9fvs0 arabidopsis
 Q4ha89 deinococcus
 Q5wfr4 bacillus cl
 Q4xg96 plasmodium
 Q2nfz6 methanosphe
 Q3igu6 pseudosalter
 Q2wry1 clostridium
 Q4ypd8 plasmodium
 Q3fk89 rhodofera
 Q3j7b1 nitrosococc
 Q3m1m6 anabaena va
 Q9yi68 bufo marinu
 Q4j9i7 sulfolobus
 Q4e0d4 trypanosoma
 Q4gzf2 trypanosoma
 Q2xek9 pseudomonas
 Q51386 pseudomonas
 Q8rsq3 pseudomonas
 Q88kt1 pseudomonas
 Q91433 pseudomonas
 Q88l11 pseudomonas
 Q7vwh8 bordetella
 Q7wl48 bordetella
 Q9hfv3 thermoplas
 Q2nfc1 methanosphe
 Q2l1w2 thermoplas
 Q4l3b6 staphylococ
 Q5lxj4 streptococc
 Q5m244 streptococc

251	5	55.6	284	2	Q20180_CABEL	Q20180	caenorhabdi	324	5	55.6	314	2	Q36LS9_MARRY	Q36LS9	marinobacte
252	5	55.6	284	2	Q579D9_BRUSU	Q579D9	brucella ab	325	5	55.6	314	2	Q7TN47_RAT	Q7TN47	rattus norv
253	5	55.6	284	2	Q8FVC3_BRUSU	Q8FVC3	brucella ab	326	5	55.6	315	2	Q37K10_RHOPA	Q37K10	rhodopseudo
254	5	55.6	284	2	Q8YD01_BRUME	Q8YD01	brucella me	327	5	55.6	315	2	Q39I10_BURS3	Q39I10	burkholderi
255	5	55.6	284	2	Q2YI06_BRUA2	Q2YI06	brucella ab	328	5	55.6	315	2	Q2J387_RHOPA	Q2J387	rhodopseudo
256	5	55.6	287	2	Q2UK29_ASPOR	Q2UK29	aspergillus	329	5	55.6	315	2	Q57TP1_SALCH	Q57TP1	salmonella
257	5	55.6	287	2	Q5DBK4_SCHJA	Q5DBK4	schistosoma	330	5	55.6	315	2	Q5PDJ3_SALPA	Q5PDJ3	salmonella
258	5	55.6	288	2	Q7PWN1_ANOGA	Q7PWN1	anopheles g	331	5	55.6	315	2	Q89X49_BRAJA	Q89X49	bradyrhizob
259	5	55.6	291	2	Q2W9S3_MAGSA	Q2W9S3	magnetospir	332	5	55.6	315	2	Q8ZS13_SALTY	Q8ZS13	salmonella
260	5	55.6	291	2	Q46TN4_RALEJ	Q46TN4	raletstonia e	333	5	55.6	315	2	Q8Z9R0_SALTI	Q8Z9R0	salmonella
261	5	55.6	292	2	Q6MD42_PARUW	Q6MD42	parachlamyid	334	5	55.6	316	2	Q8LF62_ARATH	Q8LF62	arabidopsis
262	5	55.6	292	2	Q2SV19_BURTH	Q2SV19	burkholderi	335	5	55.6	316	2	Q8RWV5_ARATH	Q8RWV5	arabidopsis
263	5	55.6	293	2	Q888V3_PSESM	Q888V3	pseudomonas	336	5	55.6	316	2	Q3Z0H1_SHIGS	Q3Z0H1	shigella so
264	5	55.6	294	1	NUCG_MOUSE	Q88600	mus musculus	337	5	55.6	316	2	Q8X4U0_EC057	Q8X4U0	escherichia
265	5	55.6	294	2	Q2SRH4_SGAMM	Q2SRH4	hahella che	338	5	55.6	316	2	Q8FG54_EC057	Q8FG54	escherichia
266	5	55.6	294	2	Q3R961_XYLFA	Q3R961	xyella fas	339	5	55.6	317	2	Q21395_CABEL	Q21395	caenorhabdi
267	5	55.6	294	2	Q4JLE9_LACRE	Q4JLE9	lactobacilli	340	5	55.6	317	2	Q9VLN1_DROME	Q9VLN1	drosophila
268	5	55.6	294	2	Q3UN47_MOUSE	Q3UN47	mus musculus	341	5	55.6	317	2	Q2KUQ1_BORAV	Q2KUQ1	bordetella
269	5	55.6	294	2	Q3V5X8_RAT	Q3V5X8	rattus norv	342	5	55.6	318	2	Q4CK93_TRYCR	Q4CK93	trypanosoma
270	5	55.6	296	2	Q6D8P9_ERWCT	Q6D8P9	erwinia car	343	5	55.6	319	2	Q650W8_ORYSA	Q650W8	oryza sativ
271	5	55.6	297	1	NUCG_HUMAN	Q14249	homo sapien	344	5	55.6	319	2	Q31PT7_SYN7P	Q31PT7	synecococc
272	5	55.6	297	2	Q5T281_HUMAN	Q5T281	homo sapien	345	5	55.6	319	2	Q5N4E1_SYN6P	Q5N4E1	synecococc
273	5	55.6	297	2	Q69L70_ORYSA	Q69L70	oryza sativ	346	5	55.6	322	2	Q9VEP0_DROME	Q9VEP0	drosophila
274	5	55.6	297	2	Q2ZIE1_CALSA	Q2ZIE1	caldicellul	347	5	55.6	323	2	Q6LY02_METWP	Q6LY02	methanococc
275	5	55.6	297	2	Q7VCD9_PROMA	Q7VCD9	prochloroco	348	5	55.6	323	2	Q3IU00_NATPD	Q3IU00	natronomona
276	5	55.6	298	2	Q84PD3_ORYSA	Q84PD3	oryza sativ	349	5	55.6	327	2	Q4UI51_THEAN	Q4UI51	theileria a
277	5	55.6	298	2	Q91LM3_WSSV	Q91LM3	white spot	350	5	55.6	327	2	Q5FPT9_GLUOX	Q5FPT9	gluconobact
278	5	55.6	299	1	NUCG_BOVIN	F38447	bos taurus	351	5	55.6	327	2	Q62K80_BURMA	Q62K80	burkholderi
279	5	55.6	299	2	Q62K14_BURMA	Q62K14	burkholderi	352	5	55.6	327	2	Q63TX8_BURPS	Q63TX8	burkholderi
280	5	55.6	299	2	Q63TS0_BURPS	Q63TS0	burkholderi	353	5	55.6	327	2	Q83R08_SHIFL	Q83R08	shigella fl
281	5	55.6	299	2	Q65KZ1_BACLD	Q65KZ1	bacillus l1	354	5	55.6	329	1	NUC1_YEAST	NUC1	saccharomyc
282	5	55.6	300	2	Q39979_HYOMU	Q39979	hyoscyamus	355	5	55.6	330	2	Q41KF3_GIBZE	Q41KF3	gibberella
283	5	55.6	302	2	Q5B412_EMENI	Q5B412	aspergillus	356	5	55.6	330	2	Q625V8_CABEL	Q625V8	caenorhabdi
284	5	55.6	303	2	Q2WML8_CLOBE	Q2WML8	clostridium	357	5	55.6	330	2	Q9UAT6_CABEL	Q9UAT6	caenorhabdi
285	5	55.6	304	2	Q7MS6_SALCH	Q7MS6	salmonella	358	5	55.6	330	2	Q663X7_YEPPS	Q663X7	yersinia ps
286	5	55.6	304	2	Q5PDQ0_SALPA	Q5PDQ0	salmonella	359	5	55.6	330	2	Q829Y6_YEAPB	Q829Y6	yersinia pe
287	5	55.6	304	2	Q7CQB0_SALTY	Q7CQB0	salmonella	360	5	55.6	331	1	YIAH_ECOLI	YIAH	escherichia
288	5	55.6	304	2	Q8XET1_SALTI	Q8XET1	salmonella	361	5	55.6	331	2	Q86KC3_DICDI	Q86KC3	dictyosteli
289	5	55.6	306	2	Q3RR04_RALME	Q3RR04	ralstonia m	362	5	55.6	331	2	Q31JC0_THICR	Q31JC0	thiomicrosp
290	5	55.6	306	2	Q9L973_9LACT	Q9L973	lactococcus	363	5	55.6	331	2	Q31V57_SHIBS	Q31V57	shigella bo
291	5	55.6	306	2	Q97HX0_CLOAB	Q97HX0	clostridium	364	5	55.6	331	2	Q3YVU3_SHISS	Q3YVU3	shigella so
292	5	55.6	306	2	Q8K2G5_MOUSE	Q8K2G5	mus musculus	365	5	55.6	331	2	Q2W7M4_ECOLI	Q2W7M4	escherichia
293	5	55.6	307	2	Q9L741_ARATH	Q9L741	arabidopsis	366	5	55.6	331	2	Q57IG3_SALCH	Q57IG3	salmonella
294	5	55.6	308	2	Q38LN0_5TRYP	Q38LN0	trypanosoma	367	5	55.6	331	2	Q8XDM7_ECO57	Q8XDM7	escherichia
295	5	55.6	308	2	Q81P99_DROME	Q81P99	drosophila	368	5	55.6	331	2	Q8XDM7_ECO57	Q8XDM7	escherichia
296	5	55.6	308	2	Q81PA1_DROME	Q81PA1	drosophila	369	5	55.6	331	2	Q8ZL93_SALTY	Q8ZL93	salmonella
297	5	55.6	308	2	Q88XV4_LACPL	Q88XV4	lactobacilli	370	5	55.6	331	2	Q8FCE7_ECOL6	Q8FCE7	escherichia
298	5	55.6	308	2	Q80ZV0_MOUSE	Q80ZV0	mus musculus	371	5	55.6	331	2	Q83J36_SHIFL	Q83J36	shigella fl
299	5	55.6	308	2	Q9DD14_MOUSE	Q9DD14	mus musculus	372	5	55.6	332	2	Q41TW8_FERPL	Q41TW8	ferroplasma
300	5	55.6	309	1	YEEY_ECOLI	P76369	escherichia	373	5	55.6	332	2	Q6CSJ8_KLUJA	Q6CSJ8	kluyveromyc
301	5	55.6	309	2	Q323J7_SHIBS	Q323J7	shigella bo	374	5	55.6	332	2	Q7RY75_NEUCR	Q7RY75	neurospora
302	5	55.6	310	2	Q5R6M3_PONPY	Q5R6M3	pongo pygma	375	5	55.6	332	2	Q328M4_SHIDS	Q328M4	shigella dy
303	5	55.6	311	2	Q2UJN5_ASPOR	Q2UJN5	aspergillus	376	5	55.6	332	2	Q49ZV4_STAS1	Q49ZV4	staphylococ
304	5	55.6	311	2	Q9LXU1_ARATH	Q9LXU1	arabidopsis	377	5	55.6	333	2	Q4MMI0_BACEE	Q4MMI0	bacillus ce
305	5	55.6	312	2	Q8GHF1_PSEPU	Q8GHF1	pseudomonas	378	5	55.6	333	2	Q63CL9_BACCK	Q63CL9	bacillus ce
306	5	55.6	313	2	Q5YQF3_NOCPA	Q5YQF3	nocardia fa	379	5	55.6	333	2	Q6HK24_BACHK	Q6HK24	bacillus th
307	5	55.6	313	2	Q6UXN9_HUMAN	Q6UXN9	homo sapien	380	5	55.6	333	2	Q81EN7_BACRC	Q81EN7	bacillus ce
308	5	55.6	313	2	Q4EPR6_LISMO	Q4EPR6	listeria mo	381	5	55.6	333	2	Q739X3_BACC1	Q739X3	bacillus ce
309	5	55.6	313	2	Q4ENB4_LISMO	Q4ENB4	listeria mo	382	5	55.6	335	2	Q4QHT9_LETMA	Q4QHT9	leishmania
310	5	55.6	313	2	Q71VY3_LISMF	Q71VY3	listeria mo	383	5	55.6	336	2	Q5CHR4_CRYHO	Q5CHR4	cryptospori
311	5	55.6	313	2	Q8Y6K0_LISMO	Q8Y6K0	listeria mo	384	5	55.6	336	2	Q8MR15_DROME	Q8MR15	drosophila
312	5	55.6	313	2	Q92AX6_LISIN	Q92AX6	listeria in	385	5	55.6	337	2	Q6BN78_DEBHA	Q6BN78	debaromyce
313	5	55.6	313	2	Q8BFO4_MOUSE	Q8BFO4	m 12 days e	386	5	55.6	337	2	Q4PIT0_CABEL	Q4PIT0	caenorhabdi
314	5	55.6	313	2	Q5QJN5_9REOV	Q5QJN5	human rotav	387	5	55.6	339	2	Q8IGUL_DROME	Q8IGUL	drosophila
315	5	55.6	313	2	Q82052_9REOV	Q82052	human rotav	388	5	55.6	339	2	Q9BLB5_CABEL	Q9BLB5	caenorhabdi
316	5	55.6	313	2	Q58E77_XENLA	Q58E77	xenopus lae	389	5	55.6	339	2	Q482C4_COLP3	Q482C4	colwellia p
317	5	55.6	313	2	Q5ZMV7_CHICK	Q5ZMV7	gallus gall	390	5	55.6	340	2	Q7QY86_GIALA	Q7QY86	giardia lam
318	5	55.6	313	2	Q640J6_XENLA	Q640J6	xenopus lae	391	5	55.6	340	2	Q3EWR2_BACTI	Q3EWR2	bacillus th
319	5	55.6	313	2	Q6GL39_XENTR	Q6GL39	xenopus tro	392	5	55.6	341	2	Q7XLD1_ORYSA	Q7XLD1	oryza sativ
320	5	55.6	313	2	Q6NV31_BRARE	Q6NV31	brachydanio	393	5	55.6	341	2	Q3M183_ANAVT	Q3M183	anabaena va
321	5	55.6	313	2	Q803V6_BRARE	Q803V6	brachydanio	394	5	55.6	343	2	Q41QJ0_GIBZE	Q41QJ0	gibberella
322	5	55.6	314	2	Q5DH19_SCHJA	Q5DH19	schistosoma	395	5	55.6	344	2	Q63646_BABBO	Q63646	babesia bov
323	5	55.6	314	2	Q7QJN9_ANOGA	Q7QJN9	anopheles g	396	5	55.6	345	2	Q2SVP8_BURTH	Q2SVP8	burkholderi

397	5	55.6	345	2	Q3FB19_9BURK	Q3fb19 burkholderi	470	5	55.6	385	2	Q8X058_NEUCR	Q8x058 neurospora
398	5	55.6	345	2	Q452G9_9BURK	Q452g9 burkholderi	471	5	55.6	385	2	Q7N3I2_PHOLL	Q7n3i2 photorhabdu
399	5	55.6	345	2	Q4LRC6_9BURK	Q4lrc6 burkholderi	472	5	55.6	387	2	Q6YXZ5_ORYSA	Q6yxz5 oryza sativ
400	5	55.6	345	2	Q39GT2_BURS3	Q39gt2 burkholderi	473	5	55.6	387	2	Q21XS4_9DELT	Q21xs4 anaeromyxob
401	5	55.6	345	2	Q3USP5_BURP1	Q3usp5 burkholderi	474	5	55.6	389	2	Q76XG1_9CAUD	Q76xg1 enterobacte
402	5	55.6	346	2	Q4BCG5_BURP1	Q4bcg5 burkholderi	475	5	55.6	389	2	Q6NX00_BRARE	Q6nx00 brachydanio
403	5	55.6	348	2	Q9MCCB6_9VIRU	Q9mccb6 lactococcus	476	5	55.6	391	2	Q8IU02_CABEL	Q8iu02 caenorhabdi
404	5	55.6	348	2	Q9MCCB7_9VIRU	Q9mccb7 lactococcus	477	5	55.6	395	2	Q8I3K3_PLAF7	Q8i3k3 plasmodium
405	5	55.6	348	2	Q3JSM4_BURP1	Q3jsw4 burkholderi	478	5	55.6	396	2	Q2ZLK5_SHEPU	Q2zlk5 shewanella
406	5	55.6	350	2	Q58H09_9NEOP	Q58h09 nephelodes	479	5	55.6	396	2	Q82A13_STRAW	Q82a13 streptomyce
407	5	55.6	350	2	Q61PM4_CABER	Q61pm4 caenorhabdi	480	5	55.6	397	2	Q5QX66_IDILO	Q5qx66 idiomarina
408	5	55.6	350	2	Q9MCCB8_9VIRU	Q9mccb8 lactococcus	481	5	55.6	399	1	TRPB_BACHD	Q9kcb0 lactobacill
409	5	55.6	350	2	Q39980_HYOMU	Q39980 hyoscyamus	482	5	55.6	399	2	Q38WL3_LACSS	Q38wl3 lactobacill
410	5	55.6	351	2	Q5M3F7_STRT2	Q5m3f7 streptococ	483	5	55.6	399	2	Q5WGS1_BACSK	Q5wgs1 bacillus cl
411	5	55.6	352	2	Q6NEE5_CORDI	Q6nee5 corynebacte	484	5	55.6	399	2	Q6D6V7_ERWCT	Q6d6v7 erwinia car
412	5	55.6	353	1	VP10_RDVA	Q85447 rice dwarf	485	5	55.6	402	2	Q2W9V3_MAGSA	Q2w9v3 magnetospi
413	5	55.6	353	1	VP10_RDVF	Q85434 rice dwarf	486	5	55.6	402	2	Q9JFR8_RAHAB	Q9jfr8 wheat roset
414	5	55.6	353	1	VP10_RDVF	P16594 rice dwarf	487	5	55.6	404	2	Q470V9_RALEJ	Q470v9 ralestonia e
415	5	55.6	353	2	Q33JP6_METHU	Q33jp6 methanospir	488	5	55.6	406	1	TRPB_LACCA	P17167 lactobacill
416	5	55.6	353	2	Q86150_DICDI	Q86150 dictyosteli	489	5	55.6	406	2	Q2SLZ3_9SPHI	Q2slz3 salinibacte
417	5	55.6	354	2	Q54198_DICDI	Q54198 dictyosteli	490	5	55.6	406	2	Q5LS43_SIIPO	Q5ls43 silicibacte
418	5	55.6	354	2	Q895Z7_CLOTE	Q895z7 clostridium	491	5	55.6	407	2	Q33YL7_SOLUS	Q33yl7 solibacter
419	5	55.6	355	2	Q97AJ9_THEVO	Q97aj9 thermoplasm	492	5	55.6	408	2	Q3WJ20_9ACTO	Q3wj20 frankia sp.
420	5	55.6	356	2	Q55Y83_CRYNE	Q55y83 cryptococcu	493	5	55.6	408	2	Q9S3U3_ZYMMP	Q9s3u3 zymomonas m
421	5	55.6	356	2	Q5K1Q5_CRYNE	Q5k1q5 cryptococcu	494	5	55.6	408	2	Q5NPZ6_ZYMMP	Q5npz6 zymomonas m
422	5	55.6	358	2	Q33ZC3_RHOPA	Q33zc3 rhodopseudo	495	5	55.6	409	2	Q4DVU4_TRYCR	Q4dvu4 trypanosoma
423	5	55.6	358	2	Q3W7S3_ANAVT	Q3w7s3 anabaena va	496	5	55.6	411	2	Q8FNP9_COREF	Q8fnp9 corynebacte
424	5	55.6	358	2	Q8YNS0_ANASP	Q8yns0 anabaena sp	497	5	55.6	412	1	PHOA_PENCH	P37274 penicillium
425	5	55.6	359	2	Q3EBK4_ARATH	Q3ebk4 arabidopsis	498	5	55.6	412	2	Q4B8T9_BURVI	Q4b8t9 burkholderi
426	5	55.6	360	2	Q7X786_ORYSA	Q7x786 oryza sativ	499	5	55.6	417	1	PHOA_ASPNG	P34724 aspergillus
427	5	55.6	360	2	Q37FH9_RHOPA	Q37fh9 rhodopseudo	500	5	55.6	417	2	Q5B3F0_EMENI	Q5b3f0 aspergillus
428	5	55.6	360	2	Q3SRN4_NITWN	Q3srn4 nitrobacter	501	5	55.6	418	2	Q2U0U6_ASPOR	Q2u0u6 aspergillus
429	5	55.6	362	2	Q94BT8_ARATH	Q94bt8 arabidopsis	502	5	55.6	421	1	PHOX_KIULA	P05440 kluyveromyc
430	5	55.6	363	1	TAGH_LACPL	Q88zh4 lactobacill	503	5	55.6	421	2	Q7PS87_ANOGA	Q7ps87 aspergillus g
431	5	55.6	364	1	OPSG_SCICA	Q35478 sciurus car	504	5	55.6	421	2	Q72DX6_DESVH	Q72dx6 desulfovib
432	5	55.6	364	2	Q3FFG6_9BURK	Q3ffg6 burkholderi	505	5	55.6	423	2	Q3SQ87_NITWN	Q3sq87 nitrobacter
433	5	55.6	364	2	Q4NGG3_9MICC	Q4ngg3 arthrobacte	506	5	55.6	425	2	Q9X8T4_STRCO	Q9x8t4 streptomyc
434	5	55.6	364	2	Q2NUW2_SODGL	Q2nuw2 sodalig glo	507	5	55.6	426	1	Y680_CHLPN	Q927m4 chlamydia p
435	5	55.6	364	2	Q51R82_SPETR	Q51r82 spermophili	508	5	55.6	428	2	Q3MPN0_CANAL	Q3mpn0 candida alb
436	5	55.6	367	2	Q4BXS8_CROWT	Q4bxs8 crocospaer	509	5	55.6	428	2	Q59S52_CANAL	Q59s52 candida alb
437	5	55.6	370	2	Q9APJ9_9RHIZ	Q9apj9 hyphomicrob	510	5	55.6	428	2	Q35Y70_9GAMM	Q35y70 shewanella
438	5	55.6	370	2	Q8A2F1_BACTN	Q8a2f1 bacteroides	511	5	55.6	428	2	Q3QF16_9GAMM	Q3qf16 shewanella
439	5	55.6	371	2	Q6C101_YARLI	Q6c101 yarrowia li	512	5	55.6	428	2	Q9RDL4_STRCO	Q9rdl4 streptomyc
440	5	55.6	371	2	Q553Y1_DICDI	Q553y1 dictyosteli	513	5	55.6	429	2	Q5AX38_EMENI	Q5ax38 aspergillus
441	5	55.6	371	2	Q6PHL8_XANAC	Q6phl8 xanthomonas	514	5	55.6	429	2	Q4DZ83_TRYCR	Q4dz83 trypanosoma
442	5	55.6	371	2	Q6NRP1_XENLA	Q6nrl1 xenopus lae	515	5	55.6	429	2	Q3VBH9_9SPHN	Q3vbh9 spHINGOPYXI
443	5	55.6	372	2	Q6C7K3_YARLI	Q6c7k3 yarrowia li	516	5	55.6	431	2	Q4BS69_BURVI	Q4bs69 burkholderi
444	5	55.6	372	2	Q2LW90_9DELT	Q2lw90 syntrophus	517	5	55.6	431	2	Q5X8G1_LEGPA	Q5x8g1 legionella
445	5	55.6	372	2	Q9KEC2_BACHD	Q9kec2 bacillus ha	518	5	55.6	432	2	Q37NA2_RHOPA	Q37na2 rhodopseudo
446	5	55.6	373	2	Q417X2_GIBZE	Q417x2 gibberella	519	5	55.6	433	2	Q5CIH8_CRYHO	Q5cih8 cryptospori
447	5	55.6	373	2	Q6VYD8_ONYPE	Q6vyd8 onion yello	520	5	55.6	435	2	Q3AAB4_CAUCR	Q3aab4 caulobacter
448	5	55.6	374	2	Q61139_CABBR	Q61i39 caenorhabdi	521	5	55.6	438	2	Q54LN6_DICDI	Q54ln6 dictyosteli
449	5	55.6	376	1	CENAZ2_RAT	Q93k15 rattus norv	522	5	55.6	438	2	Q8FU11_COREF	Q8fui1 corynebacte
450	5	55.6	378	2	Q3VQB4_9CHLB	Q3vqb4 pelodictyon	523	5	55.6	439	2	Q2DH09_YLDV	Q2dhq9 yaba-like d
451	5	55.6	378	2	Q6TBP6_9POXV	Q6tbp6 bovine papu	524	5	55.6	441	1	COAT_SOCNV	P15627 soybean chl
452	5	55.6	378	2	Q6TBP7_9POXV	Q6tbp7 pseudocowpo	525	5	55.6	441	2	Q3FU78_TOBAC	Q3fuy8 nicotiana t
453	5	55.6	378	2	Q6TBP8_9POXV	Q6tbp8 orf virus.	526	5	55.6	441	2	Q604K6_METCA	Q604k6 methylococc
454	5	55.6	378	2	Q6TBP9_9POXV	Q6tbp9 orf virus.	527	5	55.6	444	2	Q2U0U6_ASPOR	Q2uuu6 aspergillus
455	5	55.6	378	2	Q6TBPQ_9POXV	Q6tbpq orf virus.	528	5	55.6	445	2	Q6Z412_ORYSA	Q6z412 oryza sativ
456	5	55.6	378	2	Q6TVH7_9POXV	Q6tvh7 bovine papu	529	5	55.6	445	2	Q35LZ9_9BRAD	Q35lzt9 bradyrhizob
457	5	55.6	378	2	Q6TVV9_9POXV	Q6tvv9 orf virus.	530	5	55.6	445	2	Q37DJ9_RHOPA	Q37dj9 rhodopseudo
458	5	55.6	378	2	Q6TW89_9POXV	Q6tw89 orf virus.	531	5	55.6	447	2	Q8X176_ASPFU	Q8x176 aspergillus
459	5	55.6	378	2	Q7T6C4_9POXV	Q7t6c4 orf virus.	532	5	55.6	447	2	Q7Q943_ANOGA	Q7q943 anopheles g
460	5	55.6	378	2	Q7T6C5_9POXV	Q7t6c5 orf virus.	533	5	55.6	447	2	Q5CXR2_CRYPV	Q5cxr2 cryptospori
461	5	55.6	378	2	Q84145_9POXV	Q84145 orf virus.	534	5	55.6	448	2	Q4WK63_ASPFU	Q4wk63 aspergillus
462	5	55.6	379	2	Q4TG93_TETNG	Q4tg93 tetraodon n	535	5	55.6	448	2	Q3WBA1_9ACTO	Q3wba1 frankia sp.
463	5	55.6	380	2	Q5TNC6_ANOGA	Q5tnc6 anopheles g	536	5	55.6	449	2	Q3PPD3_NITWA	Q3ppd3 nitrobacter
464	5	55.6	380	2	Q21ZR4_RHOPA	Q21zr4 rhodopseudo	537	5	55.6	450	2	Q869J7_9MYRI	Q869j7 glomeris ma
465	5	55.6	382	2	Q41BJ2_GIBZE	Q41bj2 gibberella	538	5	55.6	450	2	Q449P1_SOLUS	Q449p1 solibacter
466	5	55.6	382	2	Q4BEG3_BURVI	Q4beg3 burkholderi	539	5	55.6	451	2	Q6M8V4_CORGL	Q6m8v4 corynebacte
467	5	55.6	383	2	Q94M47_9CAUD	Q94m47 streptococc	540	5	55.6	451	2	Q8NU94_CORGL	Q8nu94 corynebacte
468	5	55.6	384	2	Q4WY68_ASPFU	Q4wy68 aspergillus	541	5	55.6	452	2	Q5TMD5_9CHOR	Q5tmd5 asymmetron
469	5	55.6	384	2	Q4BCU2_BURVI	Q4bcu2 burkholderi	542	5	55.6	452	2	Q8GVB3_CITWA	Q8gve3 citrus maxi

543	5	55.6	452	2	Q9LI73_ARATH	Q9LI73	arabidopsis	616	5	55.6	500	2	Q94D20_ORYSA	Q94D20	oryza sativ
544	5	55.6	452	2	Q5F6L2_NEIGL	Q5f6l2	neisseria g	617	5	55.6	501	2	Q5WRQ8_CAEEL	Q5wrq8	caenorhabdi
545	5	55.6	452	2	Q9J5Z1_NEIMA	Q9j5z1	neisseria m	618	5	55.6	501	2	Q73EX0_BAC11	Q73ex0	bacillus ce
546	5	55.6	452	2	Q8CN35_STAES	Q8cn35	staphylococ	619	5	55.6	501	2	Q68F54_XENLA	Q68f54	xenopus lae
547	5	55.6	452	2	Q5HLC7_STAEO	Q5hlc7	staphylococ	620	5	55.6	503	2	Q5AWQ5_EMENI	Q5awq5	aspergillus
548	5	55.6	453	2	Q67U29_ORYSA	Q67u29	oryza sativ	621	5	55.6	503	2	Q37MX6_RHOPA	Q37mx6	rhodopsuendo
549	5	55.6	453	2	Q9FVL2_LYCSG	Q9fv12	lycopersico	622	5	55.6	503	2	Q7NST0_CHRVO	Q7nst0	chromobacte
550	5	55.6	454	2	Q3QXN0_XYLFA	Q3qxn0	xyella fas	623	5	55.6	504	2	Q9AWT3_ORYSA	Q9awt3	oryza sativ
551	5	55.6	454	2	Q4BM51_BURVI	Q4bm51	burkholderi	624	5	55.6	506	2	Q97VP1_SULSO	Q97vp1	sulfolobus
552	5	55.6	455	2	Q9K0Y8_NEIMB	Q9k0y8	neisseria m	625	5	55.6	506	2	Q4CYO9_TRYCR	Q4cyo9	trypanosoma
553	5	55.6	457	2	Q6C3F9_YARLI	Q6c3f9	yarrowia li	626	5	55.6	506	2	Q4DZV5_TRYCR	Q4dzv5	trypanosoma
554	5	55.6	457	2	Q2UI97_ASPOR	Q2ui97	aspergillus	627	5	55.6	509	2	Q2O930_CAEEL	Q2o930	caenorhabdi
555	5	55.6	458	2	Q2QV19_ORYSA	Q2qv19	oryza sativ	628	5	55.6	510	2	Q5WRQ7_CAEEL	Q5wrq7	caenorhabdi
556	5	55.6	460	2	Q4IUC0_GIBZE	Q4iuc0	gibberella	629	5	55.6	511	2	Q6PKS3_CANGA	Q6pks3	candida gla
557	5	55.6	462	2	Q3CTE3_ALTAT	Q3cte3	pseudoealter	630	5	55.6	511	2	Q4MZP7_THEPA	Q4mzp7	theileria p
558	5	55.6	463	2	Q58LR6_9CAUD	Q58lr6	cyanophage	631	5	55.6	513	2	Q5CIR4_CRYHO	Q5cir4	cryptospori
559	5	55.6	463	2	Q6YZC7_ORYSA	Q6yzc7	oryza sativ	632	5	55.6	513	2	Q5CXK6_CRYPV	Q5cxk6	cryptospori
560	5	55.6	464	2	Q82866_RHOSU	Q82866	rhodovulum	633	5	55.6	514	2	Q4N3N3_THEPA	Q4n3n3	theileria p
561	5	55.6	465	2	Q840X0_STRMU	Q840x0	streptococc	634	5	55.6	514	2	Q8KZ28_9PROT	Q8kz28	uncultured
562	5	55.6	465	2	Q82877_STRMU	Q82877	streptococc	635	5	55.6	515	2	Q3JKV0_BURP1	Q3jkv0	burkholderi
563	5	55.6	465	2	Q8DUS2_STRMU	Q8dus2	streptococc	636	5	55.6	517	2	Q4ED79_9RICK	Q4ed79	wolbachia e
564	5	55.6	469	2	Q91256_CAEEL	Q91256	caenorhabdi	637	5	55.6	518	1	CRTI_RHOS4	P54980	rhodobacter
565	5	55.6	469	2	Q82G55_STRAW	Q82g55	streptomyce	638	5	55.6	518	2	Q69XG4_ORYSA	Q69xg4	sulfolobus
566	5	55.6	471	2	Q2NG96_9EURY	Q2ng96	methanosphe	639	5	55.6	519	2	Q5FHQ9_LACAC	Q5fhq9	lactobacill
567	5	55.6	472	2	Q7PEV2_ANOGA	Q7pev2	anopheles g	640	5	55.6	519	2	Q39978_HYOMU	Q39978	hyoscyamus
568	5	55.6	474	1	KPKY_CORBF	Q8fp04	corynebacte	641	5	55.6	520	2	CRTI_RHOCA	P17054	rhodobacter
569	5	55.6	474	2	Q2WYA3_9GAMM	Q2wya3	shewanella	642	5	55.6	524	1	GSHI_PSEPK	Q88r90	pseudomonas
570	5	55.6	474	2	Q73GB9_WOLPM	Q73gb9	wolbachia p	643	5	55.6	525	1	Q8MXR4_CAEEL	Q8mxr4	caenorhabdi
571	5	55.6	475	1	AWT2_AEATH	Q9m6n7	arabidopsis	644	5	55.6	526	2	Q4HSJ1_CAMUP	Q4hsj1	campylobact
572	5	55.6	475	2	Q6L558_ORYSA	Q6l558	oryza sativ	645	5	55.6	527	2	Q6ML54_BDEBA	Q6ml54	belliobvibri
573	5	55.6	477	2	Q6MSH0_MYCMS	Q6msh0	mycoplasma	646	5	55.6	527	2	Q757C1_ASHGO	Q757c1	ashleya goss
574	5	55.6	478	2	Q7PVC3_ANOGA	Q7pvc3	anopheles g	647	5	55.6	528	2	Q7F9L3_ORYSA	Q7f9l3	oryza sativ
575	5	55.6	478	2	Q2WKW1_CLOBE	Q2kw1	clostridium	648	5	55.6	530	2	Q2XBY1_PSRPU	Q2xbv1	pseudomonas
576	5	55.6	478	2	Q3Y079_ENTFC	Q3y079	enterococcu	649	5	55.6	530	2	Q4IEC4_GIBZE	Q4iec4	gibberella
577	5	55.6	479	2	Q3XB09_METEL	Q3xb09	methylobaci	650	5	55.6	531	2	Q6IKS4_CAEER	Q6iks4	caenorhabdi
578	5	55.6	479	2	Q7PFB6_FUSNV	Q7pfb6	fusobacteri	651	5	55.6	531	2	Q8SD85_9CAUD	Q8sd85	pseudomonas
579	5	55.6	479	2	Q7NVE1_CHRVN	Q7nve1	chromobacte	652	5	55.6	533	2	Q64MV8_BACFR	Q64mv8	bacteroides
580	5	55.6	479	2	Q82Q54_STRAW	Q82q54	streptomyce	653	5	55.6	533	2	Q97VY5_SULSO	Q97vy5	sulfolobus
581	5	55.6	480	2	Q38300_BPLC2	Q38300	lactococcusc	654	5	55.6	535	2	Q6L086_PICTO	Q6l086	picophilus
582	5	55.6	481	2	Q62319_9CAUD	Q62319	lactococcusc	655	5	55.6	537	2	ACR7_CAEEL	Q45963	caenorhabdi
583	5	55.6	481	2	Q615E1_ORYSA	Q615e1	oryza sativ	656	5	55.6	538	1	Q7UKP3_RHOBA	Q7ukp3	rhodopirell
584	5	55.6	483	2	Q8TWF0_METKA	Q8twf0	methanopyru	657	5	55.6	538	2	Q61Z18_CAEER	Q61z18	caenorhabdi
585	5	55.6	483	2	Q7MAU8_KLUWA	Q7mau8	kluyveromyc	658	5	55.6	539	2	YMBM_YEAST	Q03263	saccharomyc
586	5	55.6	483	2	Q9CGM0_ARATH	Q9cgm0	arabidopsis	659	5	55.6	540	1	Q41TF8_FERAC	Q41tf8	ferroplasma
587	5	55.6	483	2	Q9M356_ARATH	Q9m356	arabidopsis	660	5	55.6	540	2	Q93GZ4_STRAW	Q93gz4	streptomyce
588	5	55.6	483	2	Q3RUL1_XYLFA	Q3rfu1	xyella fas	661	5	55.6	543	2	Q974R6_SULTO	Q974r6	sulfolobus
589	5	55.6	484	1	GLGA_BAGSU	P39125	bacillus su	662	5	55.6	544	2	Q7SAQ4_NEUCR	Q7saq4	neutrospora
590	5	55.6	484	2	Q87CP1_XYLFT	Q87cp1	xyella fas	663	5	55.6	545	2	Q65917_LYCES	Q65917	lycopersico
591	5	55.6	486	2	Q84K95_ORYSA	Q84k95	oryza sativ	664	5	55.6	545	2	GSPA_AERHY	P45754	aeromonas h
592	5	55.6	486	2	Q84KJ7_ORYSA	Q84kj7	oryza sativ	665	5	55.6	547	1	Q3GFL7_9GAMM	Q3gfl7	psychrobact
593	5	55.6	486	2	Q93X02_LOTJA	Q93x02	lotus japon	666	5	55.6	547	2	Q4FS25_PSYAR	Q4fs25	psychrobact
594	5	55.6	486	2	Q92CG1_LISIN	Q92cg1	listeria in	667	5	55.6	548	1	SEAS_TOBAC	Q40577	nicotiana t
595	5	55.6	489	2	Q2K5Q1_MAGGR	Q2ked1	magnaporthe	668	5	55.6	548	2	Q7X9A3_TOBAR	Q7x9a3	nicotiana t
596	5	55.6	490	2	Q5WRQ6_CAEEL	Q5wrq6	caenorhabdi	669	5	55.6	548	2	Q84LF0_9SOLA	Q84lf0	nicotiana a
597	5	55.6	491	2	Q6MSI4_MYCMS	Q6msi4	mycoplasma	670	5	55.6	548	2	Q84LF1_9SOLA	Q84lf1	nicotiana a
598	5	55.6	491	1	UDPE_NPVCF	Q90157	choristoneu	671	5	55.6	548	2	Q84LF2_9SOLA	Q84lf2	nicotiana a
599	5	55.6	492	2	Q7Q4I4_ANOGA	Q7q4i4	anopheles g	672	5	55.6	548	2	Q84LG0_9SOLA	Q84lg0	nicotiana a
600	5	55.6	492	2	Q48SF2_STRPM	Q48sf2	streptococc	673	5	55.6	549	2	Q9XJZ0_SULTU	Q9xjz0	solanum tub
601	5	55.6	492	2	Q938L1_9CAUD	Q938l1	temperate p	674	5	55.6	549	2	Q9XJZ5_SULTU	Q9xjz5	solanum tub
602	5	55.6	492	2	Q79XU4_STRP3	Q79xu4	streptococc	675	5	55.6	550	2	Q9SBJ0_SULTU	Q9sbj0	solanum tub
603	5	55.6	492	2	Q9PCD7_XYLFA	Q9pcd7	xyella fas	676	5	55.6	550	2	Q9ZTQ6_SULTU	Q9ztq6	solanum tub
604	5	55.6	493	1	AMPA_XANCP	Q8pcr4	xanthomonas	677	5	55.6	551	2	Q46VS9_RALEB	Q46vs9	ralesconia e
605	5	55.6	493	2	Q4UOP6_XANCB	Q4uop6	xanthomonas	678	5	55.6	552	2	Q40GE0_9RHEJ	Q40ge0	jannaschia
606	5	55.6	494	2	Q8H251_MEDTR	Q8h251	medicago tr	679	5	55.6	552	2	Q8FGS2_ECOL6	Q8fgs2	escherichia
607	5	55.6	495	2	Q3QDW7_9GAMM	Q3qdw7	shewanella	680	5	55.6	554	2	Q9ATN5_CAPAN	Q9atn5	capasicum an
608	5	55.6	496	2	Q89ZQ7_BACTN	Q89zq7	bacteroides	681	5	55.6	556	2	Q9FVL3_LYCES	Q9fv13	lycopersico
609	5	55.6	497	2	Q8S230_ORYSA	Q8s230	oryza sativ	682	5	55.6	556	2	Q9XJ32_SULTU	Q9xj32	solanum tub
610	5	55.6	497	2	Q8S233_ORYSA	Q8s233	oryza sativ	683	5	55.6	556	2	Q9ZTQ7_SULTU	Q9ztq7	solanum tub
611	5	55.6	497	2	Q3V9X0_9SPHN	Q3v9x0	sphingopyxi	684	5	55.6	557	2	Q9ZTQ8_SULTU	Q9ztq8	solanum tub
612	5	55.6	497	2	Q5XAR5_STRP6	Q5xar5	streptococc	685	5	55.6	558	2	Q3WTR7_9RHIZ	Q3wtr7	mesorhizobi
613	5	55.6	497	2	Q8NZR7_STRP8	Q8nzz7	streptococc	686	5	55.6					
614	5	55.6	497	2	Q9AOP2_STRP1	Q9aop2	streptococc	687	5	55.6					
615	5	55.6	498	2	Q3NQ88_SHEPR	Q3ng88	shewanella	688	5	55.6					

689	5	55.6	559	2	Q4WB27_ASPFU	Q4wb27 aspergillus	762	5	55.6	2	Q9SN07_ARATH	Q9sn07 arabidopsis
690	5	55.6	559	2	Q6ATB2_ORYSA	Q6atb2 oryza sativ	763	5	55.6	2	Q4CMJ1_TRYCR	Q4cmj1 trypanosoma
691	5	55.6	560	2	Q9SDN9_CAPAN	Q9sdn9 capsicum an	764	5	55.6	2	Q5QYD8_IDILO	Q5qyd8 idiomarina
692	5	55.6	561	2	Q580M8_9TRYP	Q580m8 trypanosoma	765	5	55.6	2	Q6CSY9_YARLI	Q6csy9 yarrowia li
693	5	55.6	562	2	Q4MZf8_THSPTA	Q4mzf8 theileria p	766	5	55.6	2	Q8H106_ARATH	Q8h106 arabidopsis
694	5	55.6	565	2	Q31BG3_PSEHT	Q3ieg3 pseudoalter	767	5	55.6	2	Q6ET07_ORYSA	Q6et07 oryza sativ
695	5	55.6	566	2	Q972D3_SULSO	Q97xd3 sulfolobus	768	5	55.6	2	Q7PY63_ANOGA	Q7py63 anopheles g
696	5	55.6	566	2	Q4KMX2_HUMAN	Q4kxm2 homo sapien	769	5	55.6	2	Q811L8_PLAF7	Q811l8 plasmodium
697	5	55.6	566	2	Q5VTB9_HUMAN	Q5vib9 homo sapien	770	5	55.6	2	Q3ZLT0_BURCE	Q3zlt0 burkholderi
698	5	55.6	566	2	Q8HXD5_MACFA	Q8hxd5 macca fasc	771	5	55.6	2	Q416M5_GIBZE	Q416m5 gibberella
699	5	55.6	566	2	Q6PDX6_MOUSE	Q6pdx6 mus musculu	772	5	55.6	2	Q4L530_STAHE	Q4l530 staphylococ
700	5	55.6	567	2	Q9HG9 ASPOR	Q9hgh9 aspergillus	773	5	55.6	2	HTPG_FREDE	P61188 treponema d
701	5	55.6	569	2	Q6PUF9_TOBAC	Q6puf9 nicotiana t	774	5	55.6	2	Q87RQ5_VIBPA	Q87rq5 vibrio para
702	5	55.6	571	1	DPOL_BPZA	Q8mxr5 caenorhabdi	775	5	55.6	2	Q61L64_CAEBR	Q61l64 caenorhabdi
703	5	55.6	572	1	DPOL_BPZA	Q6950 bacterioph	776	5	55.6	2	Q7RLK4_NEURC	Q7rlk4 neurospora
704	5	55.6	573	2	Q4V9N6_BRARE	Q4v9n6 brachydanio	777	5	55.6	2	Q61L64_CAEBR	Q61l64 caenorhabdi
705	5	55.6	574	1	VB18_VACCA	Q57263 vaccinia vi	778	5	55.6	2	Q9FVW8_XENTR	Q9fvw8 xenopus tro
706	5	55.6	574	1	VB18_VACCC	P21076 vaccinia vi	779	5	55.6	2	Q9VLK1_DROME	Q9vllk1 drosophila
707	5	55.6	574	1	VB18_VACCV	Q01222 vaccinia vi	780	5	55.6	2	Q4WJTA_ASPFU	Q4wtj4 aspergillus
708	5	55.6	574	1	VB18_VACV	P33824 variola vir	781	5	55.6	2	Q5AHK7_CANAL	Q5ahk7 candida alb
709	5	55.6	574	2	Q41R24_GIBZE	Q4i224 gibberella	782	5	55.6	2	Q5AHX7_CANAL	Q5ahx7 candida alb
710	5	55.6	574	2	Q72753_COMPE	Q72753 compox viru	783	5	55.6	2	Q3SR82_NITWN	Q3sr82 nitrobacter
711	5	55.6	574	2	Q6RZB3_9POXV	Q6rzb3 rabbitpox v	784	5	55.6	2	Q4LSC5_FERAC	Q4lsc5 ferroplasma
712	5	55.6	574	2	Q76PT5_VARV	Q76pt5 variola min	785	5	55.6	2	Q5JLP9_ORYSA	Q5jlp9 oryza sativ
713	5	55.6	574	2	Q89114_VARV	Q89114 variola vir	786	5	55.6	2	Q5V0F1_HALMA	Q5v0f1 haloarcula
714	5	55.6	574	2	Q89523_VARV	Q89523 variola vir	787	5	55.6	2	Q54PF9_DICDI	Q54pf9 dictyosteli
715	5	55.6	574	2	Q8QMN6_COMPX	Q8qmn6 compox viru	788	5	55.6	2	Q6NUC4_XENLA	Q6nuc4 xenopus lae
716	5	55.6	574	2	Q9JF35_VACCT	Q9jf35 vaccinia vi	789	5	55.6	2	Q34BQ7_RHOPA	Q34bq7 rhodopseuo
717	5	55.6	575	1	DPOL_BPPH2	P03680 bacterioph	790	5	55.6	2	Q8XSL2_RALSO	Q8xsl2 ralstonia a
718	5	55.6	575	2	Q38545_BPPH2	Q38545 bacterioph	791	5	55.6	2	Q3ZVL7_SPTCI	Q3zvl7 spirosinia pe
719	5	55.6	577	2	Q6C526_YARLI	Q6c526 yarrowia li	792	5	55.6	2	Q8D097_YERPE	Q8d097 yersinia pe
720	5	55.6	577	2	Q2SS55_MYCCA	Q2ss55 mycoplasma	793	5	55.6	2	Q9L6C8_SALET	Q9l6c8 salmonella
721	5	55.6	578	2	Q5SVMS_HUMAN	Q5svms homo sapien	794	5	55.6	2	Q57NC1_SALCH	Q57nc1 salmonella
722	5	55.6	578	2	Q2W5C6_MAGSA	Q2w5c6 oryza sativ	795	5	55.6	2	Q5PHK7_SALPA	Q5phk7 salmonella
723	5	55.6	578	2	Q2W5C6_MAGSA	Q2w5c6 magnetospir	796	5	55.6	2	Q66BW0_YERPS	Q66bw0 yersinia ps
724	5	55.6	579	2	Q9U1W0_CAEEL	Q9u1w0 caenorhabdi	797	5	55.6	2	Q8ZFD4_YERPE	Q8zfd4 yersinia pe
725	5	55.6	579	2	Q54FY7_DICDI	Q54fy7 dictyosteli	798	5	55.6	2	Q8ZFN3_SALTY	Q8zfn3 salmonella
726	5	55.6	579	2	Q42947_TOBAC	Q42947 nicotiana t	799	5	55.6	2	Q8Z5X7_SALTI	Q8z5x7 salmonella
727	5	55.6	580	2	Q4D3V2_TRYCR	Q4d3v2 trypanosoma	800	5	55.6	2	Q75CQ8_ASHGO	Q75cq8 ashbya gos
728	5	55.6	580	2	Q4D7V3_TRYCR	Q4d7v3 trypanosoma	801	5	55.6	2	Q3Z2J6_SHISS	Q3z2j6 shigella so
729	5	55.6	585	2	Q97918_THRVO	Q97918 thermoplasm	802	5	55.6	2	Q32HB7_SHIDS	Q32hb7 shigella dy
730	5	55.6	585	2	Q7UZ29_RHOBA	Q7uz29 rhodopirell	803	5	55.6	2	Q8XCK4_ECO57	Q8xck4 escherichia
731	5	55.6	587	2	Q6D3Z9_ERWCT	Q6d3z9 erwinia car	804	5	55.6	2	Q83R69_SHIFL	Q83r69 shigella fl
732	5	55.6	588	2	Q61BC2_CAEER	Q61bc2 caenorhabdi	805	5	55.6	2	Q4YX27_PLABE	Q4yx27 plasmodium
733	5	55.6	588	2	Q3RTQ2_RALME	Q3rtq2 ralstonia m	806	5	55.6	2	Q2JUV15_9CYAN	Q2jv15 cyanobacter
734	5	55.6	592	2	Q81LM1_PLAF7	Q81lm1 plasmodium	807	5	55.6	2	Q95YGI_PENJP	Q95ygi penaeus jap
735	5	55.6	594	2	Q9JFS6_9POXV	Q9jfs6 ectromelia	808	5	55.6	2	Q96U83_NEURC	Q96u83 neurospora
736	5	55.6	600	2	Q41I86_GIBZE	Q41i86 gibberella	809	5	55.6	2	Q474V0_RALEJ	Q474v0 ralstonia e
737	5	55.6	600	2	Q49B63_WOLPI	Q49b63 wolbachia p	810	5	55.6	2	Q2NTH7_SODGL	Q2nth7 sodalis glo
738	5	55.6	600	2	Q6TEM7_BRARE	Q6tem7 brachydanio	811	5	55.6	2	Q381Q3_9TRYP	Q381q3 trypanosoma
739	5	55.6	606	1	Y6D9_ENCCU	Q8evf3 encephalito	812	5	55.6	2	Q2UKD4_ASPOR	Q2ukd4 aspergillus
740	5	55.6	608	2	Q2ZA86_9GAMM	Q2za86 shewanella	813	5	55.6	2	Q3SOP0_RALME	Q3sop0 ralstonia m
741	5	55.6	609	2	Q2ZNY0_SHEPU	Q2zny0 shewanella	814	5	55.6	2	Q7MTR1_PORGI	Q7mtr1 porphyromon
742	5	55.6	610	2	Q2X645_9GAMM	Q2x645 shewanella	815	5	55.6	2	Q8UDAI_AGR5	Q8udai agrobacteri
743	5	55.6	610	2	Q8EPW1_SHEON	Q8epw1 shewanella	816	5	55.6	2	Q50Y29_ENTHI	Q50y29 entamoeba h
744	5	55.6	611	2	Q4XFQ2_PLACH	Q4xfq2 plasmodium	817	5	55.6	2	Q8PJ59_XANAC	Q8pj59 xanthomonas
745	5	55.6	611	2	Q3Q0P3_9GAMM	Q3q0p3 shewanella	818	5	55.6	2	Q7RUR8_NEURC	Q7rur8 neurospora
746	5	55.6	613	2	Q4QBF9_LEIMA	Q4qbf9 leishmania	819	5	55.6	2	Q3AG94_SYNSC	Q3ag94 synecococc
747	5	55.6	613	2	Q9VBJ6_DROME	Q9vbj6 drosophila	820	5	55.6	2	Q6LRA0_PHOPR	Q6lra0 photobacter
748	5	55.6	615	2	Q7NFU9_GLOVI	Q7nfu9 gloeobacter	821	5	55.6	2	Q852G7_ORYSA	Q852g7 oryza sativ
749	5	55.6	616	2	Q8VXX2_ARATH	Q8vxx2 arabidopsis	822	5	55.6	2	Q852G7_ORYSA	Q852g7 oryza sativ
750	5	55.6	616	2	Q9FF13_ARATH	Q9ff13 arabidopsis	823	5	55.6	2	Q47XQ9_COLP3	Q47xq9 colwellia p
751	5	55.6	616	2	Q5ZL71_CHICK	Q5z171 gallus gall	824	5	55.6	2	Q4U9R3_THEAN	Q4u9r3 theileria a
752	5	55.6	617	1	VF33B_HUMAN	Q9h267 homo sapien	825	5	55.6	2	Q6LQ86_PHOPR	Q6lq86 photobacter
753	5	55.6	617	1	VF33B_MOUSE	P59016 mus musculu	826	5	55.6	2	Q9B107_ENTHI	Q9b107 entamoeba h
754	5	55.6	617	1	VF33B_RAT	Q63616 rattus norv	827	5	55.6	2	Q54D68_DICDI	Q54d68 dictyosteli
755	5	55.6	617	2	Q8C076_MOUSE	Q8c076 mus musculu	828	5	55.6	2	Q4LBI5_PSESH	Q4lb15 pseudomonas
756	5	55.6	620	1	ACE1_CAEER	Q8c076 mus musculu	829	5	55.6	2	Q4ZMG8_PSEU2	Q4zmg8 pseudomonas
757	5	55.6	622	2	Q8AN85_CANAL	Q27459 caenorhabdi	830	5	55.6	2	Q3TIM6_MOUSE	Q3tim6 mus musculu
758	5	55.6	623	2	Q7UFX6_RHOBA	Q58n5 candida alb	831	5	55.6	2	P87541_9POTY	P87541 barley mild
759	5	55.6	624	2	Q9QSK5_IRV6	Q7uix6 rhodopirell	832	5	55.6	2	Q4CS27_TRYCR	Q4cs27 trypanosoma
760	5	55.6	625	2	Q3QEQ8_9GAMM	Q9qek5 chilo iride	833	5	55.6	2	Q4E4F4_TRYCR	Q4e4f4 trypanosoma
761	5	55.6	628	2	Q2TY93_ASPOR	Q3qeq8 shewanella	834	5	55.6	2	Q3JA75_NITOC	Q3ja75 nitrococc
						Q2cy93 aspergillus					Q5FTK2_GLUOX	Q5ftk2 gluconobact

835	5	55.6	724	1	KS6A1_MOUSE	P18653	mus musculus	908	5	55.6	869	2	Q87ZB5_PSESM	Q87ZB5 pseudomonas
836	5	55.6	724	2	Q4YS78_PLABE	Q4YS78	plasmidium	909	5	55.6	869	2	Q88KZ9_PSEPK	Q88KZ9 pseudomonas
837	5	55.6	724	2	Q60C15_METCA	Q60C15	methylococc	910	5	55.6	870	2	Q76NP4_CABEL	Q76NP4 caenorhabdi
838	5	55.6	727	2	Q4N2E9_THEPA	Q4N2E9	theileria p	911	5	55.6	870	2	Q86S28_CABEL	Q86S28 caenorhabdi
839	5	55.6	729	2	Q5QLC6_ORYSA	Q5QLC6	oryza sativ	912	5	55.6	870	2	Q48GW6_PSE14	Q48GW6 pseudomonas
840	5	55.6	732	2	Q4RME1_TETNG	Q4RME1	tetraodon n	913	5	55.6	870	2	Q4ZRA3_PSE02	Q4ZRA3 pseudomonas
841	5	55.6	732	2	Q7ZVH8_BRAZE	Q7ZVH8	brachydanio	914	5	55.6	879	2	Q36KV0_MARHY	Q36KV0 marinobacte
842	5	55.6	735	1	KS6A1_HUMAN	Q15418	homo sapien	915	5	55.6	880	2	Q4DYN0_TRYCR	Q4DYN0 trypanosoma
843	5	55.6	735	1	KS6A1_RAT	Q63531	rattus norv	916	5	55.6	882	2	Q8BPJ3_XANAC	Q8BPJ3 mus musculu
844	5	55.6	735	2	Q5SVN8_HUMAN	Q5SVN8	homo sapien	917	5	55.6	885	2	Q8BPJ3_XANAC	Q8BPJ3 xanthomonas
845	5	55.6	735	2	Q2RUL9_RHOUR	Q2RUL9	rhodospiril	918	5	55.6	889	2	Q8BL87_MOUSE	Q8BL87 mus musculu
846	5	55.6	735	2	Q3UPZ5_MOUSE	Q3UPZ5	mus musculus	919	5	55.6	893	2	Q832P7_ENTFA	Q832P7 enterococcu
847	5	55.6	735	2	Q50SN6_MOUSE	Q50SN6	mus musculus	920	5	55.6	896	2	Q6BR11_DBBHA	Q6BR11 debaryomyce
848	5	55.6	736	2	Q6YVY5_ORYSA	Q6YVY5	oryza sativ	921	5	55.6	896	2	Q8DH74_SYNEL	Q8DH74 synecchococ
849	5	55.6	738	2	Q8TBG4_ASTPE	Q8TBG4	asterina pe	922	5	55.6	897	2	Q3C661_9CLOT	Q3C661 alkaliphilu
850	5	55.6	738	2	Q4HFMA_CAMCO	Q4HFMA	campylobact	923	5	55.6	897	2	Q5NIG1_PPRAT	Q5NIG1 francisella
851	5	55.6	739	2	Q7KRQ2_DROME	Q7KRQ2	drosophila	924	5	55.6	898	2	Q7RJ73_PLAYO	Q7RJ73 plasmidium
852	5	55.6	739	2	Q9PIZ8_CAMJE	Q9PIZ8	campylobact	925	5	55.6	898	2	Q6MRC8_DBBBA	Q6MRC8 bdellovibri
853	5	55.6	741	2	Q8SX87_DROME	Q8SX87	drosophila	926	5	55.6	901	1	GLR21_ARATH	Q04660 arabidopsis
854	5	55.6	742	2	Q6FX80_CANGA	Q6FX80	candida gla	927	5	55.6	901	1	GLR21_ARATH	Q04660 arabidopsis
855	5	55.6	752	1	KS6AA_CHICK	P18652	gallus gall	928	5	55.6	902	2	Q8PXK1_9POXV	Q8PXK1 myxoma viru
856	5	55.6	752	2	Q9UIV9_CABEL	Q9UIV9	caenorhabdi	929	5	55.6	902	2	Q9Q8X9_9POXV	Q9Q8X9 rabbit fibr
857	5	55.6	756	2	Q751Y0_ASHGO	Q751Y0	ashbya goss	930	5	55.6	907	2	Q3JNG1_BURP1	Q3JNG1 burkholderi
858	5	55.6	756	2	Q86S27_CABEL	Q86S27	caenorhabdi	931	5	55.6	907	2	Q62A11_BURP1	Q62A11 burkholderi
859	5	55.6	759	2	Q5W1J6_XENLA	Q5W1J6	xenopus lae	932	5	55.6	907	2	Q3JNG1_BURP1	Q3JNG1 burkholderi
860	5	55.6	760	2	Q7S1T3_NEUCR	Q7S1T3	neurospora	933	5	55.6	909	2	Q3QJH5_BURPS	Q3QJH5 burkholderi
861	5	55.6	760	2	Q60X52_CABEL	Q60X52	caenorhabdi	934	5	55.6	916	2	Q2T710_BURTH	Q2T710 burkholderi
862	5	55.6	767	2	Q4XY12_PLACH	Q4XY12	plasmidium	935	5	55.6	917	2	Q3H993_TRIER	Q3H993 trichodeemi
863	5	55.6	769	2	Q647S8_9ARCH	Q647S8	uncultured	936	5	55.6	919	2	Q4REZ5_TETNG	Q4REZ5 tetraodon n
864	5	55.6	771	2	Q4A675_MYCS5	Q4A675	mycoplasma	937	5	55.6	920	2	Q4AC93_HUMAN	Q4AC93 homo sapien
865	5	55.6	773	2	Q810V8_MOUSE	Q810V8	mus musculus	938	5	55.6	921	2	Q8IK22_PLAP7	Q8IK22 plasmidium
866	5	55.6	777	2	Q7RBN5_PLAYO	Q7RBN5	plasmidium	939	5	55.6	924	2	Q988G5_RHIOU	Q988G5 rhizobium 1
867	5	55.6	778	2	Q86JF9_DICDI	Q86JF9	dictyosteli	940	5	55.6	936	2	Q60UX1_CABER	Q60UX1 caenorhabdi
868	5	55.6	778	2	Q3PRZ3_NITHA	Q3PRZ3	nitrobacter	941	5	55.6	936	2	Q9W365_DROME	Q9W365 drosophila
869	5	55.6	780	2	Q3A744_PELCD	Q3A744	pelobacter	942	5	55.6	937	2	Q2ZYD7_STRSU	Q2ZYD7 streptococc
870	5	55.6	783	2	Q7UHE0_RHOBA	Q7UHE0	rhodospirell	943	5	55.6	940	2	Q2ZYD7_STRSU	Q2ZYD7 streptococc
871	5	55.6	784	2	Q5AK17_CANAL	Q5AK17	candida alb	944	5	55.6	940	2	Q2ZYD7_STRSU	Q2ZYD7 streptococc
872	5	55.6	785	2	Q2XQA9_PSEPU	Q2XQA9	pseudomonas	945	5	55.6	942	2	Q3S8A4_9ADEN	Q3S8A4 human adeno
873	5	55.6	789	2	Q7RTK8_SCHMA	Q7RTK8	schistosoma	946	5	55.6	942	2	Q8TJ74_METAC	Q8TJ74 methanosaer
874	5	55.6	791	2	Q38B12_9TRYP	Q38B12	trypanosoma	947	5	55.6	947	2	Q6YVX3_ORYSA	Q6YVX3 oryza sativ
875	5	55.6	792	2	Q45019_9BURK	Q45019	burkholderi	948	5	55.6	948	2	Q7R7T5_PLAYO	Q7R7T5 plasmidium
876	5	55.6	796	2	Q4LPG2_9BURK	Q4LPG2	burkholderi	949	5	55.6	950	2	Q8VZ08_ARATH	Q8VZ08 arabidopsis
877	5	55.6	797	2	Q4CS75_TRYCR	Q4CS75	trypanosoma	950	5	55.6	953	1	IF2_STRP1	Q8VZ08 arabidopsis
878	5	55.6	798	2	Q4BKX4_BURVI	Q4BKX4	burkholderi	951	5	55.6	953	1	IF2_STRP3	Q8VZ08 arabidopsis
879	5	55.6	800	2	Q5AV46_EMENI	Q5AV46	aspergillus	952	5	55.6	953	1	IF2_STRP6	Q8VZ08 arabidopsis
880	5	55.6	800	2	Q73IS7_WOLPM	Q73IS7	wolbachia p	953	5	55.6	953	1	IF2_STRP8	Q8VZ08 arabidopsis
881	5	55.6	807	2	Q48724_ARATH	Q48724	arabidopsis	954	5	55.6	953	2	Q48E08_STRPM	Q48E08 streptococc
882	5	55.6	812	2	Q61V33_CABER	Q61V33	caenorhabdi	955	5	55.6	956	2	Q3KKN5_CHLTA	Q3KKN5 chlamydia t
883	5	55.6	813	2	Q6ASW7_ORYSA	Q6ASW7	oryza sativ	956	5	55.6	956	2	Q84812_CHLTA	Q84812 chlamydia t
884	5	55.6	817	2	Q98KX1_RHIOU	Q98KX1	rhizobium 1	957	5	55.6	957	2	Q60J73_CABER	Q60J73 caenorhabdi
885	5	55.6	820	2	Q5B0F8_EMENI	Q5B0F8	aspergillus	958	5	55.6	971	1	SWI1_SCHPO	Q9UUM2 schizosacch
886	5	55.6	821	2	Q966D4_CABEL	Q966D4	caenorhabdi	959	5	55.6	976	2	Q73S36_MYCPA	Q73S36 mycobacteri
887	5	55.6	826	1	VP91_NPVEP	VP91	npvep	960	5	55.6	979	2	Q4DKR7_TRYCR	Q4DKR7 trypanosoma
888	5	55.6	829	2	Q5SAU1_DICDI	Q5SAU1	dictyosteli	961	5	55.6	981	2	Q5AQL1_EMENI	Q5AQL1 aspergillus
889	5	55.6	833	2	Q4DLW0_TRYCR	Q4DLW0	trypanosoma	962	5	55.6	982	2	Q54ZK5_DICDI	Q54ZK5 dictyosteli
890	5	55.6	833	2	Q4SVN6_TETNG	Q4SVN6	tetraodon n	963	5	55.6	982	2	Q2WC39_VIRCU	Q2WC39 enterobacte
891	5	55.6	835	2	Q2QNH1_ORYSA	Q2QNH1	oryza sativ	964	5	55.6	982	2	Q6UGD2_BPSPP	Q6UGD2 enterobacte
892	5	55.6	837	2	Q55176_CRYNE	Q55176	cryptococcu	965	5	55.6	989	2	Q4UGM0_THEAN	Q4UGM0 theileria a
893	5	55.6	837	2	Q5K7R1_CRYNE	Q5K7R1	cryptococcu	966	5	55.6	991	2	Q72SC6_LEPIC	Q72SC6 leptospira
894	5	55.6	837	2	Q8G518_BIFLO	Q8G518	bifidobacte	967	5	55.6	991	2	Q8F398_LEPIN	Q8F398 leptospira
895	5	55.6	841	1	PSPI_YEAST	PSPI	yeast	968	5	55.6	994	2	Q6CHE0_YARLI	Q6CHE0 yarrowia li
896	5	55.6	844	2	Q4BCV2_BURVI	Q4BCV2	burkholderi	969	5	55.6	1002	2	Q8EFG0_SHEON	Q8EFG0 shewanella
897	5	55.6	846	2	Q7R2T7_GIALA	Q7R2T7	giardia lam	970	5	55.6	1002	2	Q9AHP2_9ACTO	Q9AHP2 arcanobacte
898	5	55.6	849	2	Q8ZTP7_PYRAE	Q8ZTP7	pyrobaculum	971	5	55.6	1014	2	Q4Q946_LEIMA	Q4Q946 leishmania
899	5	55.6	851	2	Q81IE2_PLAP7	Q81IE2	plasmidium	972	5	55.6	1019	2	Q6Y7Z8_9CAUD	Q6Y7Z8 bacterioph
900	5	55.6	851	2	Q44E08_CHRSL	Q44E08	chromohalob	973	5	55.6	1019	2	Q2PJW0_ENTFC	Q2PJW0 enterococcu
901	5	55.6	855	2	Q4CCN3_CLOIM	Q4CCN3	clostridium	974	5	55.6	1019	2	Q61907_CABEL	Q61907 caenorhabdi
902	5	55.6	861	2	Q3ZVJ3_SPICI	Q3ZVJ3	spiroplasma	975	5	55.6	1022	2	Q2T7E3_BURTH	Q2T7E3 burkholderi
903	5	55.6	863	2	Q3FQJ8_9BURK	Q3FQJ8	wiggleswort	976	5	55.6	1023	2	Q5TML1_ANGOA	Q5TML1 anopheles g
904	5	55.6	864	1	SYL_WIGBR	SYL	wigbr	977	5	55.6	1028	2	Q6CKS6_KULUA	Q6CKS6 kluyveromyc
905	5	55.6	865	2	Q2JG16_9ACTO	Q2JG16	frankia sp.	978	5	55.6	1034	2	Q6CKS6_KULUA	Q6CKS6 kluyveromyc
906	5	55.6	865	2	Q2M0U7_DROPS	Q2M0U7	drosophila	979	5	55.6	1042	2	Q9D806_ERWAT	Q9D806 erwinia car
907	5	55.6	869	2	Q755W6_ASHGO	Q755W6	ashbya goss	980	5	55.6	1044	2	Q9ZH24_PSEAE	Q9ZH24 pseudomonas


```

DR EMBL; U94848; AAB96405.1; -; Genomic DNA.
DR EMBL; AY603355; AAT10416.1; -; Genomic DNA.
DR PIR; A33348; WZVZB1.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
KW Early protein.
FT CHAIN 1 150 Host range protein 2.
FT SEQUENCE 150 AA; 17999 MW; 47CDF841D563COA4 CRC64;
SQ
Query Match 100.0%; Score 9; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYV 9
Db 74 KVDDTFYV 82

RESULT 4
VHR2_VACCC
ID VHR2_VACCC STANDARD; PRT; 150 AA.
AC P68599; P17363;
DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.
DT 07-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Host range protein 2.
DE ORFNames=C7L;
OS Vaccinia virus (strain Copenhagen) (VACV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10249;
RN [1]
RP MEDLINE=91021027; PubMed=2219722;
RX Goebel S.J., Johnson G.P., Perkus M.E., Winslow J.P.,
RA Paoletti E.;
RT "The complete DNA sequence of vaccinia virus.";
RL Virology 179:247-266(1990).
RN [2]
RP COMPLETE GENOME.
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
RA Paoletti E.;
RT "Appendix to 'The complete DNA sequence of vaccinia virus'.";
RL Virology 179:517-563(1990).
CC -!- FUNCTION: Plays a role for multiplication of the virus in
CC different cell types (By similarity).
CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; M35027; AAA47993.1; -; Genomic DNA.
DR PIR; A33348; WZVZB1.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
KW Early protein.
FT CHAIN 1 150 Host range protein 2.
FT SEQUENCE 150 AA; 17999 MW; 47CDF841D563COA4 CRC64;
SQ
Query Match 100.0%; Score 9; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYV 9
Db 74 KVDDTFYV 82

RESULT 5
VHR2_VARY
ID VHR2_VARY STANDARD; PRT; 150 AA.
AC P33860;
DT 01-FEB-1994, integrated into UniProtKB/Swiss-Prot.

```

```

VHR2_VACCV
ID VHR2_VACCV STANDARD; PRT; 150 AA.
AC P68600; P17363; Q76ZY7;
DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.
DT 07-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Host range protein 2.
DE OrderedLocNames=VACWR021; ORFNames=C7L;
OS Vaccinia virus (strain Western Reserve / WR) (VACV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10254;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=89073756; PubMed=2849238;
RA Kotwal G.J., Moss B.;
RT "Analysis of a large cluster of nonessential genes deleted from a
RT vaccinia virus terminal transposition mutant.";
RL Virology 167:524-537(1988).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Esposito J.J., Frace A.M., Sammons S.A., Olsen-Rasmussen M.,
RA Osborne J., Wohlhueter R.;
RT "Sequencing of the coding region of Vaccinia-WR to an average 9-fold
RT redundancy and an error rate of 0.16/10kb.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION.
RX MEDLINE=91021030; PubMed=2171207;
RA Perkus M.E., Goebel S.J., Davis S.W., Johnson G.P., Limbach K.,
RA Norton E.K., Paoletti E.;
RT "Vaccinia virus host range genes.";
RL Virology 179:276-286(1990).
RN [4]
RP FUNCTION.
RX MEDLINE=93329391; PubMed=8336123;
RA Ogutira N., Spehner D., Drillicien R.;
RT "Detection of a protein encoded by the vaccinia virus C7L open reading
RT frame and study of its effect on virus multiplication in different
RT cell lines.";
RL J. Gen. Virol. 74:1409-1413(1993).
CC -!- FUNCTION: Plays a role for multiplication of the virus in
CC different cell types.
CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; M22812; AAA69601.1; -; Genomic DNA.
DR EMBL; AY243312; AAO89300.1; -; Genomic DNA.
DR PIR; A33348; WZVZB1.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
KW Early protein.
FT CHAIN 1 150 Host range protein 2.
FT SEQUENCE 150 AA; 17999 MW; 47CDF841D563COA4 CRC64;
SQ
Query Match 100.0%; Score 9; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYV 9
Db 74 KVDDTFYV 82

RESULT 6
VHR2_VARV
ID VHR2_VARV STANDARD; PRT; 150 AA.
AC P33860;
DT 01-FEB-1994, integrated into UniProtKB/Swiss-Prot.

```

```

DT 01-FEB-1994, sequence version 1.
DT 07-FEB-2006, entry version 30.
DE Host range protein 2.
GN ORFNames=C7L, B15L, D8L;
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]_TaxID=10255;
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=India-1967 / isolate Ind3;
RA MEDLINE=93202281; PubMed=8384139; DOI=10.1016/0014-5793(93)80041-R;
RX Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RA "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms.";
RL FEBS Lett. 319:80-83(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=Bangladesh-1975;
RX MEDLINE=94088747; PubMed=8264798; DOI=10.1038/366748a0;
RA Massung R.F., Eposito J.J., Liu L.I., Qi J., Uterback T.R.,
RA Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
RA Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
RA Venter C.J.;
RT "Potential virulence determinants in terminal regions of variola
RT smallpox virus genome.";
RL Nature 366:748-751(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=Congo-1965, Garcia-1966, and Somalia-1977;
RA Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
RA Totmenin A.V., Shchelkunov S.N., Eposito J.J.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays a role for multiplication of the virus in
CC different cell types (By similarity).
CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; X69198; CAA48949.1; -; Genomic DNA.
DR EMBL; L22579; AAA60756.1; -; Genomic DNA.
DR EMBL; U18340; AAA69419.1; -; Genomic DNA.
DR EMBL; U18337; AAA69313.1; -; Genomic DNA.
DR EMBL; U18338; AAA69354.1; -; Genomic DNA.
DR PIR; F72151; F72151.
DR PIR; H36837; H36837.
DR PIR; T28446; T28446.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
FT CHAIN 1 150 Host range protein 2.
FT /FTID=PRO_0000099389.
SQ SEQUENCE 150 AA; 18027 MW; 50DFD841C253CE94 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYYV 9
DB 74 KVDDTFYYV 82

RESULT 7
Q49QR1_9POXV
ID Q49QR1_9POXV PRELIMINARY; PRT; 150 AA.
AC Q49QR1;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Hypothetical protein.
GN ORFNames=ms020L, ms020L;

```

```

OS Vaccinia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10245;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=L16m8, and L16m0;
RX PubMed=16140764; DOI=10.1128/JVI.79.18.11873-11891.2005;
RA Morikawa S., Sakiyama T., Hasegawa H., Saijo M., Maeda A., Kurane I.,
RA Maeno G., Kimura J., Hirama C., Yoshida T., Asahi-Ozaki Y., Sata T.,
RA Kurata T., Komjima A.;
RT "An attenuated L16m8 smallpox vaccine: analysis of full-genome
RT sequence and induction of immune protection.";
RL J. Virol. 79:11873-11891(2005).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; AY678275; AAW23413.1; -; Genomic DNA.
DR EMBL; AY678277; AAW23695.1; -; Genomic DNA.
DR GO; GO:0016032; P:Viral life cycle; IEA.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
KW Hypothetical protein.
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYYV 9
DB 74 KVDDTFYYV 82

RESULT 8
Q6RZS8_9POXV
ID Q6RZS8_9POXV PRELIMINARY; PRT; 150 AA.
AC Q6RZS8;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE RPXV013.
GN ORFNames=RPXV013;
OS Rabbitpox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=32606;
RN [1]_TaxID=32606;
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16227218; DOI=10.1099/vir.0.81331-0;
RA Li G., Chen N., Roper R.L., Feng Z., Hunter A., Danila M.,
RA Lefkowitz E.J., Buller R.M., Upton C.;
RT "Complete coding sequences of the rabbitpox virus genome.";
RL J. Gen. Virol. 86:2969-2977(2005).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; AY484669; AAS49726.1; -; Genomic DNA.
DR GO; GO:0016032; P:Viral life cycle; IEA.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYYV 9
DB 74 KVDDTFYYV 82

```

```
Db          74 KVDDTFYV 82

RESULT 9
Q76066 VARV PRELIMINARY; PRT; 150 AA.
ID Q76066
AC Q76066
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE B14L protein.
DE Name=B14L;
GN Variola minor virus.
OS Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=53258;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Garcia-1966.
RA Shchelkunov S.N., Totmenin A.V., Gutorov V.V., Safronov P.F.,
RA Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
RA Reposito J.J., Sosnovtsev S.;
RA Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
-----
EMBL; Y16780; CAB54608.1; -; Genomic DNA.
DR GO; GO:0016032; P:Viral life cycle; IEA.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
SQ SEQUENCE 150 AA; 18027 MW; 50DF841C253CE94 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYV 9
Db          74 KVDDTFYV 82

RESULT 10
Q760L6 COMPX PRELIMINARY; PRT; 150 AA.
ID Q760L6_COMPX
AC Q760L6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE C13L protein.
DE Name=C13L;
GN Cowpox virus (CPV).
OS Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GRI-90;
RX MEDLINE=97068532; PubMed=8963248;
RA Safronov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V.,
RA Shchelkunov S.N., Gutorov V.V., Sandakhchiev L.S.;
RA "Genes of a circle of hosts for the cowpox virus.";
RL Dokl. Akad. Nauk SSSR 349:829-833(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GRI-90;
RX MEDLINE=98229462; PubMed=9568042; DOI=10.1006/viro.1998.9039;
RA Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
RA Ryzankina O.I., Gutorov V.V., Kotwal G.J.;
RA "The genomic sequence analysis of the left and right species-specific
RT terminal region of a cowpox virus strain reveals unique sequences and
RT a cluster of intact ORFs for immunomodulatory and host range
```

```
RT proteins.";
RL Virology 243:432-460(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GRI-90;
RA Shchelkunov S.N., Safronov P.F., Totmenin A.V., Miheev M.V.,
RA Ryzankina O.I., Petrov N.A., Gutorov V.V., Kotwal G.J.,
RA Sandakhchiev L.S.;
RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
-----
EMBL; X94355; CAA64098.1; -; Genomic DNA.
DR GO; GO:0016032; P:Viral life cycle; IEA.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563COA4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYV 9
Db          74 KVDDTFYV 82

RESULT 11
Q77TN9 VACCT PRELIMINARY; PRT; 150 AA.
ID Q77TN9_VACCT
AC Q77TN9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE TC7L.
OS Vaccinia virus (strain Tian Tan) (VACV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10253;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Tian Tan;
RA Jin Q., Hou Y.D., Cheng N.H., Yao E.M., Cheng S.X., Yang X.K.,
RA Jing D.Y., Yu W.H., Yuan J.S., Ma X.J.;
RA Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
-----
EMBL; AF095689; AAF33872.1; -; Genomic DNA.
DR GO; GO:0016032; P:Viral life cycle; IEA.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563COA4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYV 9
Db          74 KVDDTFYV 82

RESULT 12
Q8JLI7 9POXV PRELIMINARY; PRT; 150 AA.
ID Q8JLI7_9POXV
AC Q8JLI7;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
```

```

07-FEB-2006, entry version 12.
DE EVM015.
GN Name=EVM015;
OS Ectromelia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=12643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Moscow;
RX MEDLINE=95266283; PubMed=7747448;
RA Mossman K., Upton C., Buller R.M., McPadden G.;
RT "Species specificity of ectromelia virus and vaccinia virus
interferon-gamma binding proteins.";
RL Virology 208:762-769(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Moscow;
RX MEDLINE=20192152; PubMed=10725549; DOI=10.1016/S0168-1702(99)00135-5;
RA Chen N., Buller R.M., Wall E.M., Upton C.;
RT "Analysis of host response modifier ORFs of ectromelia virus, the
causative agent of mousepox.";
RL Virus Res. 66:155-173(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Moscow;
RX MEDLINE=98154919; PubMed=9495531; DOI=10.1016/S0168-1702(97)00122-6;
RA Wall E.M., Cao J.X., Chen N., Buller R.M.L., Upton C.;
RT "A novel poxvirus gene and its human homolog are similar to an E. coli
lysophospholipase.";
RL Virus Res. 52:157-167(1997).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Moscow;
RA Chen N., Dania M.I., Feng Z., Buller M.L., Wang C., Han X.,
Lefkowitz E., Upton C.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
EMBL; AF012825; AAM92321.1; -; Genomic DNA.
DR GO; GO:0016032; P:viral life cycle; IEA.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
SQ SEQUENCE 150 AA; 18130 MW; 4DD4FC55F62422BE CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYV 9
Db 74 KVDDTFYV 82

RESULT 13
QBQN33_COMPX PRELIMINARY; PRT; 150 AA.
AC QBQN33;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE CPXV029 protein.
GN Name=CPXV029 CDS;
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Brighton Red;

```

```

RX MEDLINE=83117629; PubMed=6961398;
RA Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;
RT "Sequence of terminal regions of cowpox virus DNA: arrangement of
repeated and unique sequence elements.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Brighton Red;
RX MEDLINE=90177240; PubMed=2309453;
RA Parsons B.L., Pickup D.J.;
RT "Transcription of orthopoxvirus telomeres at late times during
infection.";
RL Virology 175:69-80(1990).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Brighton Red;
RX MEDLINE=91196263; PubMed=2014645;
RA Hu F.Q., Pickup D.J.;
RT "Transcription of the terminal loop region of vaccinia virus DNA is
initiated from the telomere sequences directing DNA resolution.";
RL Virology 181:716-720(1991).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Brighton Red;
RX MEDLINE=94378510; PubMed=8091665;
RA Hu F.Q., Smith C.A., Pickup D.J.;
RT "Cowpox virus contains two copies of an early gene encoding a soluble
secreted form of the type II TNF receptor.";
RL Virology 204:343-356(1994).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Brighton Red;
RA Dietrich F.S., Ray C.A., Sharma D.A., Allen A., Pickup D.J.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
EMBL; AF482758; AAM13476.1; -; Genomic DNA.
DR GO; GO:0016032; P:viral life cycle; IEA.
DR InterPro; IPR004967; Pox_C7_F8A.
DR Pfam; PF03287; Pox_C7_F8A; 1.
DR PIRSF; PIRSF003779; VAC_C7L; 1.
SQ SEQUENCE 150 AA; 17954 MW; 6B5C029714B02944 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYV 9
Db 74 KVDDTFYV 82

RESULT 14
QBQWIR3_ASFFU PRELIMINARY; PRT; 512 AA.
AC QBQWIR3;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-MAR-2006, entry version 6.
DE Possible beta-xylosidase, family 43 of glycosyl hydrolases.
GN ORFNames=Afu2g00930;
OS Aspergillus fumigatus (Sartorya fumigata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5085;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AF293 / CBS 101355 / FGSC A1100;
RX PubMed=16372009; DOI=10.1038/nature04332;
RA Nierman W.C., Pain A., Anderson M.J., Wortman J.R., Kim H.S.,
Arroyo J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.W.,

```

RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
 RA Farman N., Fedorova N.D., Fedorova N.D., Feldblyum T.V., Fischer R.,
 RA Fokker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
 RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.J.,
 RA Haas H., Harris D.E., Horiuchi H., Huang J., Humphray S., Jimenez J.,
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Konzack S.,
 RA Kulkarni R., Kumagai T., Lafton A., Latge J.-P., Li W., Lord A.,
 Lu C., Majors W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,
 RA Monod M., Mouyina I., Mulligan S., Murphy L.D., O'Neill S., Paulsen I.,
 RA Penalta M.A., Perte M., Price C., Pritchard B.L., Quail M.A.,
 RA Rabinowitsch E., Rawlins N., Rajadream M.A., Reichard U.,
 RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
 RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
 RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
 RA White O., Woodward J.R., Yu J.-H., Fraser C.M., Galagan J.E., Asai K.,
 RA Machida M., Hall N., Barrall B.G., Denning D.W.,
 RA "Genomic sequence of the pathogenic and allergenic filamentous fungus
 RT *Aspergillus fumigatus*,"
 RL Nature 438:1151-1156(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL; AAH01000008; EAL87192.1; -; Genomic DNA.
 DR DR GO: 0016787; F:hydrolase activity; IEA_
 DR DR GO: 0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR DR GO: 0005975; P:carbohydrate metabolism; IEA.
 KW Complete proteome; Hydrolase.
 SQ SEQUENCE 512 AA; 55648 MW; 5E174A037C55B830 CRC64;
 Query Match 77.8%; Score 7; DB 2; Length 512;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTFY 8
 Db 26 VDDTFY 32
 |||||
 [1]
 RESULT 15
 ID Q2U7D1 ASPOR PRELIMINARY; PRT; 515 AA.
 AC Q2U7D1;
 DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
 DT 24-JAN-2006, sequence version 1.
 DT 07-MAR-2006, entry version 3.
 DE Beta-xylosidase.
 GN ORFNames=AO090701000886;
 OS *Aspergillus oryzae*.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.
 OX NCBI_TaxID=5062;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RIB 40;
 RX PubMed=16372010; DOI=10.1038/nature04300;
 RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,
 RA Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,
 RA Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,
 RA Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,
 RA Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotch O., Horikawa H.,
 RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juvvadi P.R.,
 RA Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,
 RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,
 RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,
 RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,
 RA Komori T., Kovama Y., Minetoki T., Suhanan S., Tanaka A., Isono K.,
 RA Kuwara S., Ogasawara N., Kikuchi H.;
 RT "Genome sequencing and analysis of *Aspergillus oryzae*."

RL Nature 438:1157-1161(2005).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL; AP007164; BA662534.1; -; Genomic DNA.
 SQ SEQUENCE 515 AA; 56635 MW; 3EDFD2B09FF52176 CRC64;
 Query Match 77.8%; Score 7; DB 2; Length 515;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTFY 8
 Db 39 VDDTFY 45
 |||||
 [1]
 RESULT 16
 ID P73845 SYNY3 PRELIMINARY; PRT; 770 AA.
 AC P73845;
 DT 01-FEB-1997, integrated into UniProtKB/TrEMBL.
 DT 01-FEB-1997, sequence version 1.
 DT 07-FEB-2006, entry version 26.
 DE S111608 protein.
 GN OrderedLocusNames=s111608;
 OS *Synechocystis* sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; *Synechocystis*.
 OX NCBI_TaxID=1148;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=97061201; PubMed=8905231; DOI=10.1093/dnares/3.3.109;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hiroseawa M., Sugiyama M., Sasaki M., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimizu S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT *Synechocystis* sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL; BA000022; BAA17904.1; -; Genomic DNA.
 DR PIR; S75042; S75042.
 DR BioCyc; SSPI148:SLL1608-MONOMER; -;
 DR InterPro; IPR002931; Trnsglutase like.
 DR Pfam; PF01841; Transglut core; 1.
 DR SMART; SM00460; Tgc; 1.
 KW Complete proteome.
 SQ SEQUENCE 770 AA; 87815 MW; F58C2EA34EC8873C CRC64;
 Query Match 77.8%; Score 7; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VDDTFY 8
 Db 286 VDDTFY 292
 |||||
 [1]
 RESULT 17
 ID Q8VUM8 STAHO PRELIMINARY; PRT; 103 AA.
 AC Q8VUM8;
 DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2002, sequence version 1.
 DT 07-FEB-2006, entry version 9.
 DE ORF19.
 OS *Staphylococcus hominis*.
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.

```

OX NCBI_TaxID=1290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-GIFU12263;
RX MEDLINE=22586405; PubMed=12700250;
RX DOI=10.1128/JB.185.9.2711-2722.2003;
RA Kobayashi Y., Takeuchi F., Ito T., Ma X.X., Ui-Mizutani Y.,
RA Koyayashi I., Hiramatsu K.;
RT "Identification in methicillin-susceptible Staphylococcus hominis of
RT an active primordial mobile genetic element for the staphylococcal
RT cassette chromosome mec of methicillin-resistant Staphylococcus
RT aureus.";
RL J. Bacteriol. 185:2711-2722(2003).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AB063171; BAB83490.1; -; Genomic_DNA.
DR InterPro; IPR009303; DUF960_STA_app.
DR Pfam; PF06124; DUF960; 1.
SQ SEQUENCE 103 AA; 12599 MW; 13194326CCE4617D CRC64;

Query Match 66.7%; Score 6; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
DB 91 DTFYV 96
|||||

RESULT 18
Q38248 9CAUD
ID Q38248_9CAUD PRELIMINARY; PRT; 126 AA.
AC Q38248;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DE 07-FEB-2006, entry version 16.
DE DNA polymerase subunit.
OS Lactococcus phage bIL67.
OC Viruses; gDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC c2-like viruses.
OX NCBI_TaxID=36343;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95111629; PubMed=7812447;
RA Schouler C., Ehrlich S.D., Chopin M.C.;
RT "Sequence and organization of the lactococcal prolate-headed bIL67
RT phage genome.";
RL Microbiology 140:3061-3069(1994).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; L33769; AAA74342.1; -; Genomic_DNA.
SQ SEQUENCE 126 AA; 14843 MW; 1768C9622ED7749B CRC64;

Query Match 66.7%; Score 6; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDTTF 6
DB 100 KVDTTF 105
|||||

RESULT 19
Q5A2T5 CANAL
ID Q5A2T5_CANAL PRELIMINARY; PRT; 176 AA.
AC Q5A2T5;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
```

```

DE Hypothetical protein.
GN ORFNames=CaO19.2181, CaO19.9727;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AACQ01000075; EAK97013.1; -; Genomic_DNA.
DR EMBL; AACQ01000076; EAK96954.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 176 AA; 19448 MW; D04B9BE79CA86853 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
DB 117 VDDTFY 122
|||||

RESULT 20
RAS3 RHIRA
ID _RAS3 RHIRA STANDARD; PRT; 205 AA.
AC P22280;
DT 01-AUG-1991, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1991, sequence version 1.
DT 07-MAR-2006, entry version 37.
DE Ras-like protein 3.
GN Name=RAS3;
OS Rhizomucor racemosus (Mucor circinelloides f. lusitanicus).
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC Mucor.
OX NCBI_TaxID=4841;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN-ATCC 1216B; PubMed=1701021;
RX MEDLINE=91061774; PubMed=1701021;
RA Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.;
RT "Expression of a gene family in the dimorphic fungus Mucor racemosus
RT which exhibits striking similarity to human ras genes.";
RL Mol. Cell. Biol. 10:6654-6663(1990).
CC -!- ENZYME REGULATION: Alternate between an inactive form bound to GDP
CC and an active form bound to GTP. Activated by a guanine
CC nucleotide-exchange factor (GEF) and inactivated by a GTPase-
CC activating protein (GAP).
CC -!- SUBCELLULAR LOCATION: Cell membrane; lipid-anchor.
CC -!- DEVELOPMENTAL STAGE: In sporulating mycelium and much less in
CC germling and yeast.
CC -!- SIMILARITY: Belongs to the small GTPase superfamily. Ras family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; M55177; AAA83379.1; -; Genomic_DNA.
DR PIR; C36365; C36365.
DR HSSP; P01112; 1PLL.
DR InterPro; IPR003579; GTPase_Fab.
```

```

DR InterPro: IPR003577; GTPase_Ras.
DR InterPro: IPR003578; GTPase_Rho.
DR InterPro: IPR001806; Ras_trnsfrmg.
DR InterPro: IPR005225; Small_GTP_bd.
DR Pfam: PF00071; Ras; 1.
DR PRINTS; PR00449; RASTRNSFRMNG.
DR SMART; SM00173; Ras; 1.
DR TIGRFAMs; TIGR00231; small GTP; 1.
KW GTP-binding; Lipoprotein; Nucleotide-binding; Prenylation.
FT CHAIN 1 205
FT NP BIND 16 23 /FTID=PRO_0000082681.
FT NP_BIND 63 67 GTP (By similarity).
FT NP_BIND 122 125 GTP (By similarity).
FT MOTIF 38 46 GTP (By similarity).
FT LIPID 202 202 Effector region (Probable).
SQ SEQUENCE 205 AA; 23408 MW; 23408 MW; DBF086466F090F50 CRC64;

Query Match 66.7%; Score 6; DB 1; Length 205;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
DB 159 VDDTFY 164

RESULT 21
Q8T5E9 RICFL PRELIMINARY; PRT; 231 AA.
AC Q8T5E9
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Green fluorescent protein-like protein.
OS Ricordea florida (Soft coral).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Hexacorallia;
OC Corallimorpharia; Ricordeidae; Ricordea.
OX NCBI_TaxID=165100;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21927629; PubMed=11929996; DOI=10.1073/pnas.062552299;
RA Labas Y.A., Gurskaya N.G., Yanushevich Y.G., Fradkov A.F.,
RA Lukyanov K.A., Lukyanov S.A., Matz M.V.;
RT "Diversity and evolution of the green fluorescent protein family.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4256-4261(2002).
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
-----
DEMBL; AY037772; AAK71338.1; -; mRNA.
DR HSP; Q8U6Y8; 1GGX.
DR GO; GO:0008218; P:bioluminescence; IEA.
DR InterPro: IPR011584; GFP_related.
DR Pfam; PF01353; GFP; 1.
SQ SEQUENCE 231 AA; 26014 MW; 2AC3A356695B42B7E CRC64;

Query Match 66.7%; Score 6; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
DB 115 DTFYV 120

RESULT 22
Q5TOR6 ANOGA PRELIMINARY; PRT; 232 AA.
AC Q5TOR6;
DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.

```

```

DE ENSANGP00000029666.
GN ORFNames=ENSANGG00000022851.
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
-----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
-----
DEMBL; AAB01008962; EAL39783.1; -; Genomic_DNA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR001985; Znf_PHD.
DR Pfam; PF00628; PHD; 1.
DR SMART; SM00249; PHD; 1.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
DR PROSITE; PS50016; ZF_PHD_2; 1.
SQ SEQUENCE 232 AA; 25290 MW; 78A98241F2283718 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
DB 16 VDDTFY 21

RESULT 23
Q9CAE4 ARATH PRELIMINARY; PRT; 261 AA.
AC Q9CAE4;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Hypothetical protein Fl3M14.33 (At3g10400).
GN Name=Fl3M14.33; OrderedLocustNames=At3g10400;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Town C.D., Kaul S.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Ecker J.R.;
RT "Arabidopsis cDNA clones."

```

```
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Kim C.J., Chen H., Cheuk R., Shinn P., Ecker J.R.;
RT "Arabidopsis ORF clones.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AC011560; AAG51392.1; -; Genomic DNA.
DR EMBL; BT015938; AAV31168.1; -; mRNA.
DR EMBL; BT021922; AAX49371.1; -; mRNA.
DR HSSP; O08583; INO8.
DR TAIR; At3g10400; -.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR012677; a_b_plait_nuc_bd.
DR InterPro; IPR000504; RNPI_RNA_bd.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00076; RRM_1; 1.
DR Pfam; PF00098; Zf-CCHC; 1.
DR PRINTS; PR00939; C2HCZFINGER.
DR SMART; SM00360; RRM; 1.
DR SMART; SM00343; Znf_C2HC; 1.
DR PROSITE; PS0102; RRM; 1.
DR PROSITE; PS0158; Zf_CCHC; 1.
KW Hypothetical protein; Metal-binding; zinc; zinc-finger.
SQ SEQUENCE 261 AA; 29367 MW; 4A37767C92819D22 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFFY 8
Db 14 DDTFFY 19

RESULT 24
Q2NEH9_9EURY PRELIMINARY; PRT; 298 AA.
AC Q2NEH9.
DT 07-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DT 07-FEB-2006, entry version 1.
DE CofD.
GN Name=cofD; ORFName=Msp 1403;
OS Methanospaera stadmanae DSM 3091.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanospaera.
OX NCBI_TaxID=339860;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 3091;
RX PubMed=16385054; DOI=10.1128/JB.188.2.642-658.2006;
RA Fricke W.F., Seedorf H., Henne A., Krueer M., Liesegang H.,
RA Hedderich R., Gottschalk G., Thauer R.K.;
RT "The Genome Sequence of Methanospaera stadmanae Reveals Why This
RT Human Intestinal Archaeon Is Restricted to Methanol and H2 for Methane
RT Formation and ATP Synthesis.";
RL J. Bacteriol. 188:642-658(2006).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000102; ABC57774.1; -; Genomic DNA.
SQ SEQUENCE 298 AA; 33234 MW; FFE70D402A75C4C8 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
Db 68 VDDTFY 73

RESULT 25
Q4K6A8_PSEF5 PRELIMINARY; PRT; 311 AA.
ID Q4K6A8_PSEF5.
AC Q4K6A8;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Transcriptional regulator, MerR family.
GN OrderedLocustNames=PFL_5146;
OS Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=220664;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15980861; DOI=10.1038/nbt1110;
RA Paulsen I.T., Press C.M., Ravel J., Kobayashi D.Y., Myers G.S.A.,
RA Mavrodi I.V., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA Durkin A.S., Brinkac L.M., Daugherty S.C., Sullivan S.A.,
RA Rosovitz M.J., Gwinn M.B., Zhou L., Schneider D.J., Cartinhour S.W.,
RA Nelson W.C., Weidman J., Watkins K., Tran K., Khouri H., Pierson E.A.,
RA Pierson L.S. III, Thomashow L.S., Loper J.E.;
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5.";
RL Nat. Biotechnol. 23:873-878(2005).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000076; AAY94368.1; -; Genomic DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000551; HTH_MerR.
DR Pfam; PF00376; MerR; 1.
DR SMART; SM00422; HTH_MER; 1.
DR PROSITE; PS0937; HTH_MER_2; 1.
KW Complete proteome; DNA-binding.
SQ SEQUENCE 311 AA; 34959 MW; AB8C46F939674EFF CRC64;

Query Match 66.7%; Score 6; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTF 6
Db 122 KVDDTF 127

RESULT 26
Q6DB07_ERWCT PRELIMINARY; PRT; 330 AA.
ID Q6DB07_ERWCT.
AC Q6DB07.
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Putative membrane protein.
GN OrderedLocustNames=ECA0095;
OS Erwinia carotovora subsp. atroseptica (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
```



```

RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holvea M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.,
RA "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BX950851; CAG73015.1; -; Genomic DNA.
DR GO; GO:0016747; F:transferase activity, transferring groups o. . .; IEA.
DR InterPro; IPR002656; Acyl_transf_3.
DR Pfam; PF01757; Acyl_transf_3; 1.
DR Complete proteome.
SQ SEQUENCE 330 AA; 36965 MW; D8F8B183D34D1D09 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 330;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
DB 179 DTFYV 184
|||||

RESULT 27
Q5WC87_BACSK PRELIMINARY; PRT; 376 AA.
ID Q5WC87;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Hypothetical protein.
GN OrderedLocNames=ABC3490;
OS Bacillus clausii (strain KSM-K16).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=66692;
RN [1]

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Takaki Y., Kageyama Y., Shimamura S., Suzuki H., Nishi S., Hatada Y.,
RA Kawai S., Ito S., Horikoshi K.;
RT "The complete genome sequence of the alkaliphilic Bacillus clausii
RT KSM-K16.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AP006627; BAD66023.1; -; Genomic DNA.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 376 AA; 42123 MW; FC8A63EA03CD4362 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
DB 172 VDDTFY 177
|||||

RESULT 28
Q5WX32_LEGPL PRELIMINARY; PRT; 399 AA.
ID Q5WX32;
AC Q5WX32;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 14.

```

```

DE Tryptophan synthase beta subunit.
GN Name-trpB; OrderedLocNames=lp11267;
OS Legionella pneumophila (strain Lens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297245;
RN [1]

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA Etienne J., Glaser P., Buchrieser C.;
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CR628337; CAH15507.1; -; Genomic DNA.
DR Legiolist; lp11267; -
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004834; F:tryptophan synthase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006568; P:tryptophan metabolism; IEA.
DR InterPro; IPR001926; B6 enzyme beta.
DR InterPro; IPR006653; Trp synth_b rel.
DR InterPro; IPR006654; Trp_synth_beta.
DR Pfam; PF00291; PALP; 1.
DR TIGRFAMs; TIGR00283; trpB; 1.
DR PROSITE; PS00168; TRP SYNTHASE_BETA; 1.
DR Complete proteome; Pyridoxal phosphate.
SQ SEQUENCE 399 AA; 43301 MW; 25720A677000BAA0 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
DB 186 VDDTFY 191
|||||

RESULT 29
Q5XSQ2_LEGPA PRELIMINARY; PRT; 399 AA.
ID Q5XSQ2;
AC Q5XSQ2;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Tryptophan synthase beta subunit.
GN Name-trpB; OrderedLocNames=lp1268;
OS Legionella pneumophila (strain Paris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297246;
RN [1]

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA Etienne J., Glaser P., Buchrieser C.;
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CR628336; CAH12419.1; -; Genomic DNA.
DR Legiolist; lp1268; -
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004834; F:tryptophan synthase activity; IEA.

```

```

DR GO: GO:0008152; P:metabolism; IEA.
DR GO: GO:0006568; P:tryptophan metabolism; IEA.
DR InterPro: IPR001926; B6_enzyme_beta.
DR InterPro: IPR006653; Trp_synth_beta.
DR InterPro: IPR006654; Trp_synth_beta.
DR Pfam: PF00291; PALP; 1.
DR TIGRFAMs: TIGR00263; trpB; 1.
DR PROSITE: PS00168; TRP SYNTHASE BETA; 1.
KW Complete proteome; Pyridoxal phosphate.
SQ SEQUENCE 399 AA; 43301 MW; 25720A677000BAA0 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
DB 186 VDDTFY 191

RESULT 30
ID Q5ZVY4_LEGPH PRELIMINARY; PRT; 399 AA.
AC Q5ZVY4;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Tryptophan synthetase, beta subunit (EC 4.2.1.20).
GN OrderedLocNames=lp1304;
OS Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 / ATCC 33152).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=272624;

RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15448271; DOI=10.1126/science.1099776;
RA Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
RA Asanani G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J.,
RA Stehenko V., Park S.H., Zhao B., Teplickaya E., Edwards J.R.,
RA Pampou S., Gerghiou A., Chou I.-C., Iannuccilli W., Ulz M.E.,
RA Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
RA Segal G., Qu X., Rzhetsky A., Zhang P., Cayanis E., De Jong P.J.,
RA Ju J., Kalachikov S., Shuman H.A., Russo J.J.;
RT "The genomic sequence of the accidental pathogen Legionella pneumophila.";
RL Science 305:1966-1968(2004).

CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: AE017354; AAU27387.1; -; Genomic_DNA.
DR GO: GO:0016829; F:lyase activity; IEA.
DR GO: GO:0004834; F:tryptophan synthase activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR GO: GO:0006568; P:tryptophan metabolism; IEA.
DR InterPro: IPR001926; B6_enzyme_beta.
DR InterPro: IPR006653; Trp_synth_beta.
DR Pfam: PF00291; PALP; 1.
DR TIGRFAMs: TIGR00263; trpB; 1.
DR PROSITE: PS00168; TRP SYNTHASE BETA; 1.
KW Complete proteome; Lyase; Pyridoxal phosphate.
SQ SEQUENCE 399 AA; 43300 MW; E5BFCB1A797EE32 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
DB 186 VDDTFY 191

```

```

RESULT 31
TRPB_NEIGO
ID TRPB_NEIGO STANDARD; PRT; 400 AA.
AC Q84GT9;
DT 22-AUG-2003, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Tryptophan synthase beta chain (EC 4.2.1.20).
GN Name=trpB;
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;

RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=MS11;
RA Jose J., Otto G.W., Meyer T.F.;
RT "Integration site of the Iga gene in commensal Neisseria sp.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: The beta subunit is responsible for the synthesis of L-tryptophan from indole and L-serine.
CC -!- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate = L-tryptophan + glyceraldehyde 3-phosphate.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate: step 5 [final step].
CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (By similarity).
CC -!- SIMILARITY: Belongs to the trpB family.

CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: AY165022; AAG5176.1; -; Genomic_DNA.
DR HSSP: P00933; 2WSY;
DR HAMAP: MF_00133; -; 1.
DR InterPro: IPR001926; B6_enzyme_beta.
DR InterPro: IPR006653; Trp_synth_beta.
DR Pfam: PF00291; PALP; 1.
DR TIGRFAMs: TIGR00263; trpB; 1.
DR PROSITE: PS00168; TRP SYNTHASE BETA; 1.
KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Lyase;
KW Pyridoxal phosphate; Tryptophan biosynthesis.
FT CHAIN 1 400 Tryptophan synthase beta chain.
FT BINDING 92 92 Pyridoxal phosphate (covalent) (By similarity).
FT SEQUENCE 400 AA; 43549 MW; 3765C02F97627ACA CRC64;

Query Match 66.7%; Score 6; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
DB 186 VDDTFY 191

RESULT 32
TRPB_NEIMA
ID TRPB_NEIMA STANDARD; PRT; 400 AA.
AC Q9JVC0;
DT 19-OCT-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2000, sequence version 1.
DT 07-MAR-2006, entry version 28.
DE Tryptophan synthase beta chain (EC 4.2.1.20).
GN Name=trpB; OrderedLocNames=NNA0904;
OS Neisseria meningitidis serogroup A.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;

```

```

RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moulé S., Murgall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491."
RL Nature 404:502-506(2000).
CC
CC -1- FUNCTION: The beta subunit is responsible for the synthesis of L-
CC tryptophan from indole and L-serine.
CC -1- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate
CC = L-tryptophan + glyceraldehyde 3-phosphate.
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC -1- PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-
CC tryptophan from chorismate; step 5 [final step].
CC -1- SUBUNIT: Tetramer of two alpha and two beta chains (By
CC similarity).
CC
CC -1- SIMILARITY: Belongs to the trpB family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AL162754; CAB84181.1; -; Genomic_DNA.
CC PIR; H81936; H81936.
CC HSSP; P00933; 2WSY.
CC GenomeReviews; AL157959; GR; NMA0904.
CC BioCyc; NMEN65699:NMA0904-MONOMER; -.
CC HAMAP; MF_00133; -; 1.
CC InterPro; IPR001926; B6 enzyme beta.
CC InterPro; IPR006653; Trp synth_b rel.
CC Pfam; PF00291; PALP; 1.
CC TIGRFAMs; TIGR00263; trpB; 1.
CC PROSITE; PS00168; TRP SYNTHASE BETA; 1.
KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
KW Complete proteome; Lyase; Pyridoxal phosphate;
KW Tryptophan biosynthesis.
FT CHAIN 1 400 Tryptophan synthase beta chain.
FT FTId=PRO_0000098972.
FT BINDING 92 92 Pyridoxal phosphate (covalent) (By
FT similarity).
SQ SEQUENCE 400 AA; 43193 MW; 82001AE125A99F80 CRC64;

Query Match 66.7%; Score 6; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
Db 186 VDDTFY 191

RESULT 33
TRPB_NEIMB
ID TRPB_NEIMB STANDARD; PRT; 400 AA.
AC Q9K05;
DT 19-OCT-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2000, sequence version 1.
DT 07-MAR-2006, entry version 29.
DE Tryptophan synthase beta chain (EC 4.2.1.20).
GN Name=trpB; OrderedLocNames=NMB0699;
OS Neisseria meningitidis serogroup B.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=MC58 / Serogroup B;

```

```

RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson E.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,
RA Qin H., Vanathevan J.J., Gill J., Scarlato V., Massignani V., Pizza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
CC
CC -1- FUNCTION: The beta subunit is responsible for the synthesis of L-
CC tryptophan from indole and L-serine.
CC -1- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate
CC = L-tryptophan + glyceraldehyde 3-phosphate.
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC -1- PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-
CC tryptophan from chorismate; step 5 [final step].
CC -1- SUBUNIT: Tetramer of two alpha and two beta chains (By
CC similarity).
CC
CC -1- SIMILARITY: Belongs to the trpB family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AE002098; AAF41116.1; -; Genomic_DNA.
CC PIR; B81169; B81169.
CC HSSP; P00933; 2WSY.
CC GenomeReviews; AE002098; GR; NMB0699.
CC TIGR; NMB0699; -.
CC BioCyc; NMEN491:NMB0699-MONOMER; -.
CC HAMAP; MF_00133; -; 1.
CC InterPro; IPR001926; B6 enzyme beta.
CC InterPro; IPR006653; Trp synth_b rel.
CC Pfam; PF00291; PALP; 1.
CC TIGRFAMs; TIGR00263; trpB; 1.
CC PROSITE; PS00168; TRP SYNTHASE BETA; 1.
KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
KW Complete proteome; Lyase; Pyridoxal phosphate;
KW Tryptophan biosynthesis.
FT CHAIN 1 400 Tryptophan synthase beta chain.
FT FTId=PRO_0000098973.
FT BINDING 92 92 Pyridoxal phosphate (covalent) (By
FT similarity).
SQ SEQUENCE 400 AA; 43209 MW; 86FCC42EF6F64210 CRC64;

Query Match 66.7%; Score 6; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
Db 186 VDDTFY 191

RESULT 34
QSF9W3_NEIG1
ID QSF9W3_NEIG1 PRELIMINARY; PRT; 400 AA.
AC QSF9W3;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Putative tryptophan synthase (EC 4.2.1.20).
GN OrderedLocNames=NGO0274;
OS Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=242231;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

```

```

RA Lewis L.A., Gillaespy A.F., McLaughlin R.E., Gipson M., Ducey T.F.,
RA Ownbey T., Hartman K., Nydick C., Carlson M.B., Vaughn J., Thomson C.,
RA Song L., Lin S., Yuan X., Najjar P., Zhan M., Ren Q., Zhu H., Qi S.,
RA Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;
RT "The complete genome sequence of Neisseria gonorrhoeae.";
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; A5004969; AAW89024.1; -; Genomic DNA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0004834; F:tryptophan synthase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006568; P:tryptophan metabolism; IEA.
DR InterPro; IPR001926; B6 enzyme beta.
DR InterPro; IPR006653; Trp synth b rel.
DR InterPro; IPR006654; Trp synth_beta.
DR Pfam; PF00291; PALP; 1.
DR TIGRFAMs; TIGR00263; trpB; 1.
DR PROSITE; PS00168; TRP_SYNTHASE_BETA; 1.
KW Complete proteome; Lyase; Pyridoxal phosphate.
SQ SEQUENCE 400 AA; 43459 MW; C31E408696C60AE7 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
Db 186 VDDTFY 191

RESULT 35
Q31HH4 THICR
ID Q31HH4 THICR PRELIMINARY; PRT; 401 AA.
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 07-MAR-2006, entry version 1.
DE Tryptophan synthase, beta subunit.
GN ORFNames=trc_0803;
OC Thiomicrospira crunogena (strain XCL-2).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Thiotrichales;
OC Piscirickettsiaceae; Thiomicrospira.
OX NCBI_TaxID=317025;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC US DOE Joint Genome Institute.
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M.,
RA Vergez L., Schmutz J., Larimer F., Land M., Kyrpides N., Lykidis A.,
RA Richardson P.;
RT "Complete sequence of Thiomicrospira crunogena XCL-2.";
RT Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; CP000109; ABB41399.1; -; Genomic DNA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004834; F:tryptophan synthase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006568; P:tryptophan metabolism; IEA.
DR Pyridoxal phosphate.
SQ SEQUENCE 401 AA; 43363 MW; A98F7BF3778EDC2B CRC64;

Query Match 66.7%; Score 6; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7

```

```

Db 198 VDDTFY 193

RESULT 36
Q44BZ8 CHRSL
ID Q44BZ8 CHRSL PRELIMINARY; PRT; 404 AA.
AC Q44BZ8_
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 17-FEB-2006, entry version 1.
DE Tryptophan synthase, beta chain.
GN ORFNames=CaalDRAFT_0124;
OS Chromohalobacter salexigens DSM 3043.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
OC Halomonadaceae; Chromohalobacter.
OX NCBI_TaxID=290398;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 3043;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Chromohalobacter
RT salexigens DSM 3043.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 3043;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Chromohalobacter
RT salexigens DSM 3043.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; AAH201000035; EAM22248.1; -; Genomic DNA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004834; F:tryptophan synthase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006568; P:tryptophan metabolism; IEA.
DR InterPro; IPR001926; B6 enzyme beta.
DR InterPro; IPR006653; Trp synth b rel.
DR InterPro; IPR006654; Trp synth_beta.
DR Pfam; PF00291; PALP; 1.
DR TIGRFAMs; TIGR00263; trpB; 1.
DR PROSITE; PS00168; TRP_SYNTHASE_BETA; 1.
KW Pyridoxal phosphate.
SQ SEQUENCE 404 AA; 43777 MW; FECB7C0B2BD168AE CRC64;

Query Match 66.7%; Score 6; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
Db 190 VDDTFY 195

RESULT 37
Q604P3 METCA
ID Q604P3 METCA PRELIMINARY; PRT; 405 AA.
AC Q604P3_
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Tryptophan synthase, beta subunit (EC 4.2.1.20).
GN Name=trpB; OrderedLocusNames=MCA2495;

```

```

RA Larimer F., Land M.;
RT "Annotation of the draft genome of Marinobacter aquaeolei VT8.";
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AALG01000004; EAO99973.1; -; Genomic_DNA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004834; F:tryptophan synthase activity; IEA.
DR DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006568; P:tryptophan metabolism; IEA.
DR Pyridoxal phosphate.
KW SEQUENCE 406 AA; 43944 MW; 6853FD2DE57F5OA6 CRC64;
SQ
    Query Match          66.7%; Score 6; DB 2; Length 406;
    Best Local Similarity 100.0%; Pred. No. 88;
    Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps
QY      2 VDDTFV 7
Db       193 VDDTFV 198
        |||||
RESULT 39
TRPB PSFH
ID TRPB PSFH STANDARD; PRT; 409 AA.
AC Q849P2;
DT 31-OCT-2003, integrated into UniProtKB/Swiss-Prot.
DC 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Tryptophan synthase beta chain (EC 4.2.1.20).
OS Name=trpB;
OS Pseudomonas syringae pv. phaseolicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=319;
[1]
NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=1449 / Race 7;
TSaltas D.;
RA "Biochemical, structural and molecular characterization of resistant
RT interactions between Pseudomonas syringae pv. phaseolicola and
RT Phaeoelus vulgaris."
RT Thesis (2003), University of London, United Kingdom.
CC -! FUNCTION: The beta subunit is responsible for the synthesis of L-
CC tryptophan from indole and L-serine.
CC -! CATALYTIC ACTIVITY: L-serine + l-(indol-3-yl)glycerol 3-phosphate
CC = L-tryptophan + glyceraldehyde 3-phosphate.
CC -! COFACTOR: Pyridoxal phosphate (By similarity).
CC -! PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-
CC tryptophan from chorismate; step 5 [final step].
CC -! SUBUNIT: Tetramer of two alpha and two beta chains (By
CC similarity).
CC -! SIMILARITY: Belongs to the trpB family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
EMBL; AY210847; AAOS0076.1; -; Genomic_DNA.
HSSP; P00933; 2WSY.
HAMAP; MF_00133; -.
InterPro; IPR001926; B6 enzyme beta.
InterPro; IPR006653; Trp_synth_b_rel.
InterPro; IPR006654; Trp_synth_beta.
Pfam; PF00291; PALP; 1.
TIGRFAMs; TIGR00263; trpB; 1.
PROSITE; PS00168; TRP SYNTHASE BETA; 1.
AMINO-ACID BIOSYNTHESIS; Aromatic amino acid biosynthesis; Lyase;
Pyridoxal phosphate; Tryptophan biosynthesis

```

FT CHAIN 1 409 Tryptophan synthase beta chain.
 FT FTID=PRO_0000098984.
 FT BINDING 95 95 Pyridoxal_phosphate (covalent) (By
 FT similarity).
 SQ SEQUENCE 409 AA; 44542 MW; D6311A4BB6C9BABF CRC64;

Query Match 66.7%; Score 6; DB 1; Length 409;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
 |||||
 Db 189 VDDTFY 194

RESULT 40

TRPB_PSESM
 ID TRPB_PSESM STANDARD; PRT; 409 AA.
 AC Q88B61;
 DT 31-OCT-2003, integrated into UniProtKB/Swiss-Prot.
 DT 01-JUN-2003, sequence version 1.
 DT 07-MAR-2006, entry version 21.
 DE Tryptophan synthase beta chain (EC 4.2.1.20).
 GN Name=trpB; OrderedLocusNames=PSPT00158;
 OS Pseudomonas syringae pv. tomato.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=323;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=DC3000;
 RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
 RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
 RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
 RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
 RA Nelson W.C., Davidovitz T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
 RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
 RA Uterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
 RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
 RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
 RA Bender C.L., White O., Fraser C.M., Collmer A.;
 RT "The complete genome sequence of the Arabidopsis and tomato pathogen
 Pseudomonas syringae pv. tomato DC3000.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
 CC -!- FUNCTION: The beta subunit is responsible for the synthesis of L-
 tryptophan from indole and L-serine.
 CC -!- CATALYTIC ACTIVITY: L-serine + L-(indol-3-yl)glycerol 3-phosphate
 = L-tryptophan + glyceraldehyde 3-phosphate.
 CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -!- PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-
 tryptophan from chorismate; step 5 [final step].
 CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (By
 similarity).
 CC -!- SIMILARITY: Belongs to the trpB family.
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License

EMBL; AE016853; AA053712.1; -; Genomic_DNA.
 HSSP; P00933; 2WSY.
 DR GenomeReviews; AE016853_GR; PSPT00158.
 DR TIGR; PSPT00158; -.
 DR BioCyc; PSYR223283:PSPT00158-MONOMER; -.
 DR HAMAP; MF_00133; -; 1.
 DR InterPro; IPR001926; B6_enzyme_beta.
 DR InterPro; IPR006653; Trp_synth_b_rel.
 DR InterPro; IPR006654; Trp_synth_beta.
 DR Pfam; PF00291; PALP; 1.
 DR TIGRFAMs; TIGR00263; trpB; 1.
 DR PROSITE; PS00168; TRP_SYNTHASE_BETA; 1.
 DR Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
 KW Complete proteome; Lyase; Pyridoxal phosphate;
 KW Tryptophan biosynthesis.

FT CHAIN 1 409 Tryptophan synthase beta chain.
 FT FTID=PRO_0000098985.
 FT BINDING 95 95 Pyridoxal_phosphate (covalent) (By
 FT similarity).
 SQ SEQUENCE 409 AA; 44547 MW; 25A56962380CC284 CRC64;

Query Match 66.7%; Score 6; DB 1; Length 409;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
 |||||
 Db 189 VDDTFY 194

RESULT 41

Q48QG6_PSE14
 ID Q48QG6_PSE14 PRELIMINARY; PRT; 409 AA.
 AC Q48QG6;
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Tryptophan synthase, beta subunit (EC 4.2.1.20).
 GN Name=trpB; OrderedLocusNames=PSPPH_0036;
 OS Pseudomonas syringae pv. phaseolicola (strain 1448A / Race 6).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=264730;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=16159782; DOI=10.1128/JB.187.18.6488-6498.2005;
 RA Joardar V., Lindeberg M., Jackson R., Selengut J., Dodson R.,
 RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Gwinn Giglio M., Madupu R., Nelson W.C., Rosovitz M.J., Sullivan S.A.,
 RA Crabtree J., Creasy T., Davidson T.M., Haft D.H., Zafar N., Zhou L.,
 RA Halpin R., Holley T., Khouri H.M., Feldblyum T.V., White O.,
 RA Fraser C.M., Chatterjee A.K., Cartinhour S., Schneider D.,
 RA Mansfield J., Collmer A., Buell R.;
 RA "Whole-genome sequence analysis of Pseudomonas syringae pv.
 phaseolicola 1448A reveals divergence among pathogens in genes
 involved in virulence and transposition.";
 RL J. Bacteriol. 187:6488-6498(2005).
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License

EMBL; CP000058; AA234189.1; -; Genomic DNA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0004834; F:tryptophan synthase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR GO; GO:0006588; P:tryptophan metabolism; IEA.
 DR InterPro; IPR001926; B6_enzyme_beta.
 DR InterPro; IPR006653; Trp_synth_b_rel.
 DR InterPro; IPR006654; Trp_synth_beta.
 DR Pfam; PF00291; PALP; 1.
 DR TIGRFAMs; TIGR00263; trpB; 1.
 DR PROSITE; PS00168; TRP_SYNTHASE_BETA; 1.
 DR Complete proteome; Lyase; Pyridoxal phosphate.
 SQ SEQUENCE 409 AA; 44516 MW; C2604B0EA298BFA CRC64;

Query Match 66.7%; Score 6; DB 2; Length 409;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
 |||||
 Db 189 VDDTFY 194

RESULT 42

Q500R4_PSEU2
 ID Q500R4_PSEU2 PRELIMINARY; PRT; 409 AA.
 AC Q500R4;

DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DE Tryptophan synthase, entry version 8.
GN OrderedLocusNames=Pyv1_0034;
OS Pseudomonas syringae pv. syringae (strain B728a).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=205918;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16043691; DOI=10.1073/pnas.0504930102;
RA Feil H., Feil W.S., Chain P., Larimer F., Dibartolo G., Copeland A.,
RA Lykidis A., Trong S., Nolan M., Goldsman E., Thiel J., Malfatti S.,
RA Loper J.E., Lapidus A., Detter J.C., Land M., Richardson P.M.,
RA Kyrpides N.C., Ivanova N., Lindow S.E.;
RT "Comparison of the complete genome sequences of Pseudomonas syringae
pv. syringae B728a and pv. tomato DC3000".
RL Proc. Natl. Acad. Sci. U.S.A. 102:11064-11069(2005).
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; CP000075; AAY35108.1; -; Genomic DNA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0004834; F:tryptophan synthase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006568; P:tryptophan metabolism; IEA.
DR InterPro; IPR001926; B6 enzyme beta.
DR InterPro; IPR006653; Trp_synth_beta.
DR InterPro; IPR006654; Trp_synth_beta.
DR Pfam; PF00291; PALP; 1.
DR TIGRFAMs; TIGR00263; trpB; 1.
DR PROSITE; PS00168; TRP SYNTHASE BETA; 1.
DR Complete proteome; Lyase; Pyridoxal phosphate.
KW SEQUENCE 409 AA; 44452 MW; D6B775F530D7E4B CRC64;
SQ
Query Match 66.7%; Score 6; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTFY 7
Db 189 VDDTFY 194
RESULT 43
ID Q2SJD1_9GAMM PRELIMINARY; PRT; 410 AA.
AC Q2SJD1;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DE Tryptophan synthase, entry version 3.
DE Tryptophan synthase, beta subunit (EC 4.2.1.20).
GN Name=trpB1; ORFNames=HCH_02436;
OS Haella chejuensis KCTC 2396.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
OC Haellaceae; Haella.
OX NCBI_TaxID=349521;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KCTC 2396;
RX PubMed=16352867; DOI=10.1093/nar/gki1016;
RA Jeong H., Yim J.H., Lee C., Choi S.-H., Park Y.K., Yoon S.H.,
RA Hur C.-G., Kang H.-Y., Kim D., Lee H.H., Park K.H., Park S.-H.,
RA Park H.-S., Lee H.K., Oh T.K., Kim J.P.;
RT "Genomic blueprint of Haella chejuensis, a marine microbe producing
an algicidal agent".
RL Nucleic Acids Res. 33:7066-7073(2005).
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC

DR EMBL; CP000155; ABC29243.1; -; Genomic DNA.
DR GO; GO:0016829; F:lyase activity; IEA.
KW Lyase; Pyridoxal phosphate.
SQ SEQUENCE 410 AA; 45093 MW; 2389625857C5E998 CRC64;
Query Match 66.7%; Score 6; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTFY 7
Db 197 VDDTFY 202
RESULT 44
ID Q352W5_9GAMM PRELIMINARY; PRT; 411 AA.
AC Q352W5;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DE Tryptophan synthase, entry version 4.
DE Tryptophan synthase, beta chain (EC 4.2.1.20).
GN ORFNames=MIGDRAFT_2774;
OS Alkalilimnicola ehrlichei MLHE-1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC Ectothiorhodospiraceae; Alkalilimnicola.
OX NCBI_TaxID=187272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MLHE-1;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Alkalilimnicola
ehrichtei MLHE-1".
RT Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
RL [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MLHE-1;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome of Alkalilimnicola ehrlichei MLHE-1".
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AALK01000001; EAP35688.1; -; Genomic DNA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0004834; F:tryptophan synthase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006568; P:tryptophan metabolism; IEA.
KW Lyase; Pyridoxal phosphate.
SQ SEQUENCE 411 AA; 44619 MW; B8952DA9644A4C26 CRC64;
Query Match 66.7%; Score 6; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDDTFY 7
Db 198 VDDTFY 203
RESULT 45
ID Q3MWU8_9DELT PRELIMINARY; PRT; 416 AA.
AC Q3MWU8;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.

```
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORFNames=SfumdRAFT_0032;
OS Syntrophobacter fumaroxidans MPOB.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Syntrophobacterales;
OC Syntrophobacteraceae; Syntrophobacter.
OX NCBI_TaxID=335543;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MPOB;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Syntrophobacter
RT fumaroxidans MPOB.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MPOB;
RG US DOE Joint Genome Institute (JGI_ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Syntrophobacter
RT fumaroxidans MPOB.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAJF01000066; EAO19414.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 416 AA; 46643 MW; CE2F7754D4B3F249 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTF 6
Db 136 KVDDTF 141

RESULT 46
Q3EM85 BACTI PRELIMINARY; PRT; 474 AA.
ID Q3EM85_BACTI
AC Q3EM85;
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Phosphoenolpyruvate synthase [EC 2.7.9.2].
GN ORFNames=RBTH_02591;
OS Bacillus thuringiensis serovar israelensis ATCC 35646.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=339854;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 35646;
RA Anderson I., Sorokin A., Kapatral V., Reznik G., Bhattacharya A.,
RA Mikhailova N., Burd H., Joukov V., Kaznadzey D., Walunas T.,
RA D'Souza M., Larsen N., Pusch G., Liolios K., Grechkin Y., Lapidus A.,
RA Goltzman E., Chu L., Fonstein M., Ehrlich D., Overbeek R.,
RA Kyrpides N., Ivanova N.;
RT "Comparative genome analysis of Bacillus cereus group genomes with
RT Bacillus subtilis.";
RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
```

```
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAJW01000430; EAO52421.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008986; F:pyruvate, water dikinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0016310; P:phosphorylation; IEA.
DR InterPro; IPR002192; PPK_PEP_bd.
DR Pfam; PF01326; PPK_N; 1.
KW Pyruvate; Transferase.
SQ SEQUENCE 474 AA; 52575 MW; 1C0A641BE2374B57 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7
Db 300 VDDTFY 305

RESULT 47
Q60051 THEVU PRELIMINARY; PRT; 482 AA.
ID Q60051_THEVU
AC Q60051;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 27.
DE Alpha-amylase precursor [EC 3.2.1.1].
GN Name=amyTV;
OS Thermoactinomyces vulgaris.
OC Bacteria; Firmicutes; Bacillales; Thermoactinomycetaceae;
OC Thermoactinomycetes.
OX NCBI_TaxID=2026;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K94;
RX MEDLINE=95031040; PubMed=7944369;
RA Hofemeister B., Koenig S., Hoang V., Engel J., Mayer G., Hansen G.,
RA Hofemeister J.;
RT "The gene amyE(TV1) codes for a nonglucogenic alpha-amylase from
RT Thermoactinomyces vulgaris 94-2A in Bacillus subtilis.";
RL Appl. Environ. Microbiol. 60:3381-3389(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K94;
RA Hofemeister J.W.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; X69807; CAA49465.1; -; Genomic_DNA.
DR PIR; S31478; S31478.
DR HSSP; P10529; 7TAA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016738; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006048; Alpha_amy1_C.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR Pfam; PF00128; Alpha-amylase; 13.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy; C; 1.
KW Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 29 potential.
FT CHAIN 30 482 alpha-amylase.
SQ SEQUENCE 482 AA; 54483 MW; D8F98C370B579025 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 482;
Best Local Similarity 100.0%; Pred. No. 1e+02;
```


Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTFY 7

Db 409 VDDTFY 414

RESULT 48

Q9L9B9 ARATH PRELIMINARY; PRT; 485 AA.
ID Q9L9B9 ARATH
AC Q9L9B9
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Chloroplast nucleoid DNA binding protein, putative.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22088475; PubMed=12093376;
RA Haas B.J., Volkovsky N., Town C.D., Troughan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
CC [2]

CC NUCLEOTIDE SEQUENCE.
RA Brover V., Troughan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AY085528; AAM66061.1; -; mRNA.
DR HSSP; P42210; IQDM.
DR GO; GO:0004194; F:pepsin A activity; IEA.
DR GO; GO:006508; P:proteolysis; IEA.
DR InterPro; IPR001969; Pept_Asp_AS.
DR InterPro; IPR009007; Pept_Aspartc_cat.
DR InterPro; IPR001461; Peptidase_A1.
DR PANTHER; PTHR13683; Peptidase_A1; 2.
DR Pfam; PF00026; Asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 2.
SQ SEQUENCE 485 AA; 52314 MW; D205E7EA9B283787 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 485;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9

Db 327 DTFYV 332

RESULT 49

Q9LNU3 ARATH PRELIMINARY; PRT; 485 AA.
ID Q9LNU3 ARATH
AC Q9LNU3
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE F6F3.10 protein (Chloroplast nucleoid DNA binding protein, putative)
DE (At1g01300).
GN Name=F6F3.10; OrderedLocNames=At1g01300;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;

RN [1]

NUCLEOTIDE SEQUENCE.

RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
RA Buehler E., Chao Q., Chin C., Chlou J., Choi E., Gonzalez A.,
RA Hwang B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
RA Lenz C., Liu A., Liu S., Mukharly N., Pham P., Sakano H., Shinn P.,
RA Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]

NUCLEOTIDE SEQUENCE.

RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Barh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [3]

NUCLEOTIDE SEQUENCE.

RA Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,
RA Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AC023628; AAF97328.1; -; Genomic_DNA.
DR EMBL; AY128344; AAM91547.1; -; mRNA.
DR EMBL; BT006619; AAP31963.1; -; mRNA.
DR FIR; C86143; C86143.
DR HSSP; P42210; IQDM.
DR TAIR; At1g01300; -.

DR GO; GO:0009505; C:cell wall (sensu Magnoliophyta); IDA.

DR InterPro; IPR001969; Pept_Asp_AS.

DR InterPro; IPR009007; Pept_Aspartc_cat.

DR InterPro; IPR001461; Peptidase_A1.

DR PANTHER; PTHR13683; Peptidase_A1; 2.

DR Pfam; PF00026; Asp; 1.

DR PRINTS; PR00792; PEPSIN.

DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 2.

SQ SEQUENCE 485 AA; 52175 MW; 1A1782027531709 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 485;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9

Db 327 DTFYV 332

RESULT 50

Q2V3N3 ARATH PRELIMINARY; PRT; 499 AA.
ID Q2V3N3 ARATH
AC Q2V3N3
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Protein At3g59080.
GN OrderedLocNames=At3g59080;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].


```

DR InterPro; IPR009007; Pept_Aspartic_cat.
DR InterPro; IPR001461; Peptidase_A1.
DR PANTHER; PTHR13683; Peptidase_A1; 1.
DR Pfam; PF00026; Asp; 1.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
KW DNA-binding.
SQ SEQUENCE 500 AA; 53234 MW; F5DF2E1CF9CB306C CRC64;

Query Match 66.7%; Score 6; DB 2; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVV 9
DB 342 DTFYVV 347

RESULT 53
Q63GZ3_BACCZ
ID Q63GZ3_BACCZ PRELIMINARY; PRT; 512 AA.
AC Q63GZ3
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Hypothetical protein.
GN OrderedLocusNames=BCE33L0203;
OS Bacillus cereus (strain ZK / E33L).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK ";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 512 AA; 58358 MW; DC9F2EFDDA617B50 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 1.e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVV 9
DB 299 DTFYVV 304

RESULT 54
Q6HPG6_BACHK
ID Q6HPG6_BACHK PRELIMINARY; PRT; 512 AA.
AC Q6HPG6;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Hypothetical protein.
GN OrderedLocusNames=BT9727_0199;
OS Bacillus thuringiensis subsp. konkukian.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=180856;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=97-27;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;

"Complete genome sequence of Bacillus thuringiensis 97-27.";
Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
EMBL; AB017355; AAT58945.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 512 AA; 58358 MW; 4FBB111563856EBB CRC64;

Query Match 66.7%; Score 6; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 1.e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVV 9
DB 299 DTFYVV 304

RESULT 55
Q6Z6Q8_ORYSA
ID Q6Z6Q8_ORYSA PRELIMINARY; PRT; 514 AA.
AC Q6Z6Q8;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Putative chloroplast nucleoid DNA binding protein.
GN Names=P0705A04.34;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, PAC
clone:P0705A04.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
EMBL; AF004891; BAD15987.1; -; Genomic DNA.
DR Gramene; Q6Z6Q8; -;
DR GO; GO:0004194; P:pepsin A activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR009007; Pept_Aspartic_cat.
DR InterPro; IPR001461; Peptidase_A1.
DR PANTHER; PTHR13683; Peptidase_A1; 2.
DR Pfam; PF00026; Asp; 1.
DR PRINTS; PR00792; PEPSIN.
SQ SEQUENCE 514 AA; 54891 MW; 77653ACBD68094E1 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 514;
Best Local Similarity 100.0%; Pred. No. 1.e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVV 9
DB 352 DTFYVV 357

RESULT 56
Q9LYS8_ARATH
ID Q9LYS8_ARATH PRELIMINARY; PRT; 535 AA.
AC Q9LYS8;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Hypothetical protein F17J16_130 (AT3G59080/F17J16_130) (Hypothetical
protein At3g59080).
GN Name=F17J16_130; OrderedLocusNames=At3g59080;

```

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA D'Angelo M., Vezzi A., Modesto D., Pigazzi M., Valle G., Mewes H.W.,
 RA Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
 RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RN NUCLEOTIDE SEQUENCE.
 RA EU Arabidopsis sequencing project;
 RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
 RA Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.;
 RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RL [5]
 RP NUCLEOTIDE SEQUENCE.
 RA Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.;
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RL [6]
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 DR EMBL; AL163527; CAB86936.1; -; Genomic_DNA.
 DR EMBL; AF424562; AAL11556.1; -; mRNA.
 DR EMBL; BT000326; AAN15645.1; -; mRNA.
 DR EMBL; AV099818; AAM20669.1; -; mRNA.
 DR PIR; T47790; T47790.
 DR HSP; P07267; IFMX.
 DR TAIR; AT3G59080; -.
 DR GO; GO:0004194; F:pepsin A activity; IEA.
 DR GO; GO:0006508; P:proteolysis; IEA.
 DR InterPro; IPR001969; Pept_Asp_AS.
 DR InterPro; IPR009007; Pept_Aspartc_cat.
 DR InterPro; IPR001461; Peptidase_A1.
 DR PANTHER; PTHR13683; Peptidase_A1; 2.
 DR Pfam; PF00026; Asp; 1.
 DR PRINTS; PS00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 535 AA; 59242 MW; 4C20AF382B66472 CRC64;
 Query Match 66.7%; Score 6; DB 2; Length 535;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 DTFYV 9
 DB 374 DTFYV 379

RESULT 57
 ID Q50EJ4 LACRE PRELIMINARY; PRT; 567 AA.
 AC Q50EJ4;
 DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
 DT 07-JUN-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE ATP-dependent nuclease subunit B (Fragment).
 OS Lactobacillus neuteri.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1598;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CRL1098;
 RA Vera J.L., Santos F., Sesma F.J.M., Font de Valdez G., Hugenholtz J.;
 RA Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 DR EMBL; AY780645; AAX14552.1; -; Genomic_DNA.
 DR NON_TER 567 567
 SQ SEQUENCE 567 AA; 64982 MW; E5AA0430AC8C53AC CRC64;
 Query Match 66.7%; Score 6; DB 2; Length 567;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 DDTFY 8
 DB 33 DDTFY 38
 RESULT 58
 ID Q70Q68 PERMR PRELIMINARY; PRT; 671 AA.
 AC Q70Q68;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE Hemocyanin subunit 2 precursor.
 GN Name=hc2;
 OS Perla marginata (Stonefly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Plecoptera; Perlodea; Perlidae; Perlinae;
 OX NCBI_TaxID=227363;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=14715904; DOI=10.1073/pnas.0305872101;
 RA Hagner-Holler S., Schoen A., Erker W., Marden J.;
 RT "A respiratory hemocyanin from an insect."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:871-874(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Burmester I.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 DR EMBL; AJ555404; CAD87763.1; -; mRNA.
 DR GO; GO:0005344; F:oxygen transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000896; Hemocyanin.
 DR InterPro; IPR005203; hemocyanin_C.
 DR InterPro; IPR005204; hemocyanin_N.
 DR InterPro; IPR002227; Tyrosinase.
 DR PANTHER; PTHR11511; Hemocyanin; 1.
 DR Pfam; PF03723; Hemocyanin_C; 1.
 DR Pfam; PF00372; Hemocyanin_M; 1.

```

DR Pfam: PF03722; Hemocyanin N; 1.
DR PRINTS: PR00187; HAEMOCYANIN.
DR PROSITE: PS00209; HEMOCYANIN_1; 1.
DR PROSITE: PS00210; HEMOCYANIN_2; UNKNOWN_1.
DR PROSITE: PS00498; TYROSINASE_2; UNKNOWN_1.
KW SIGNAL.
FT CHAIN 1 16 Potential.
FT CHAIN 17 671 hemocyanin subunit 2.
SQ SEQUENCE 671 AA; 77870 MW; 39A84D01C1D98AD CRC64;

Query Match
Best Local Similarity 66.7%; Score 6; DB 2; Length 671;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTFY 7
Db 19 VDDTFY 24

RESULT 59
Q8FLC6_ECOL6
ID Q8FLC6_ECOL6 PRELIMINARY; PRT; 678 AA.
AC Q8FLC6;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 21-FEB-2006, entry version 11.
DE Putative glutamate dehydrogenase.
GN ORFNames=c_0018;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: AE014075; AN78518.1; -; Genomic_DNA.
DR BLOCYC; ECOL199310:C0018-MONOMER; -.
KW Complete proteome.
SQ SEQUENCE 678 AA; 78223 MW; C9329675AC896AE9 CRC64;

Query Match
Best Local Similarity 66.7%; Score 6; DB 2; Length 678;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTFY 7
Db 496 VDDTFY 501

RESULT 60
Q7XJX7_ORYSA
ID Q7XJX7_ORYSA PRELIMINARY; PRT; 731 AA.
AC Q7XJX7; Q7X732;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2004, entry version 14.
DE OSJNBa0063C18.16 protein (OSJNBa0033G05.2 protein).
GN Name=OSJNBa0063C18.16; Synonyms=OSJNBa0033G05.2;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;

```

```

OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2237377; PubMed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Wang Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320 (2002).
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: AL731607; CA05975.2; -; Genomic_DNA.
DR EMBL: AL606454; CAD41901.2; -; Genomic_DNA.
GR Gramene; Q7XJX7; -.
DR GO; GO:0007049; P:cell cycle; IEA.
DR InterPro; IPR001373; Cullin.
DR Pfam; PF00888; Cullin; 1.
DR SMART; SM00182; CULLIN; 1.
DR PROSITE; PS00669; CULLIN_2; 1.
SQ SEQUENCE 731 AA; 84804 MW; 6A02220495C5048B CRC64;

Query Match
Best Local Similarity 66.7%; Score 6; DB 2; Length 731;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFFY 8
Db 620 DDTFFY 625

RESULT 61
Q2Z173_9CAUD
ID Q2Z173_9CAUD PRELIMINARY; PRT; 870 AA.
AC Q2Z173;
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
OS Pseudomonas phage phiEL.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=273133;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22684572; PubMed=12798231; DOI=10.1016/S0923-2508(03)00070-6;
RA Krylov V.N., Pleteneva E.A., Bourkalsteva M.V., Shaburova O.V.,
RA Volckaert G., Sykylinda N.N., Kurochkina L.P., Mesyanzhinov V.V.;
RT "Myoviridae bacteriophages of Pseudomonas aeruginosa: a long and
complex evolutionary pathway.";
RL Res. Microbiol. 154:269-275 (2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22389089; PubMed=12500672;
RA Burkal'tseva M.V., Krylov V.N., Pleteneva E.A., Shaburova O.V.,
RA Krylov S.V., Volckaert G., Sykylinda N.N., Kurochkina L.P.,
RA Mesyanzhinov V.V.;
RT "Phenogenetic characterization of a group of giant Phi KZ-like
bacteriophages of Pseudomonas aeruginosa.";
RL Genetika 38:1470-1479 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15033869; DOI=10.1093/bioinformatics/btg456;
RA Lavigne R., Sun W.D., Volckaert G.;
RT "PHIRE, a deterministic approach to reveal regulatory elements in

```

```

RT bacteriophage genomes." ;
RL Bioinformatics 20:629-635(2004).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16256135;
RA Hertveldt K., Lavigne R., Pleteneva E., Sernova N., Kurochkina L.,
RA Korchevskii R., Robben J., Mesyanzhinov V., Krylov V.N., Volckaert G.;
RT "Genome Comparison of Pseudomonas aeruginosa Large Phages.";
RL J. Mol. Biol. 354:536-545(2005).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: AJ679769; CAG27102.1; -; Genomic_DNA.
DK Hypothetical protein.
KW
SQ SEQUENCE 870 AA; 100611 MW; 57347C918488C432 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 870;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
DB 60 DTFYV 65

RESULT 62
Q9S9U5 ARATH PRELIMINARY; PRT; 892 AA.
AC Q9S9U5;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE F15P11.3 protein.
GN Name=F15P11.3;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Washu;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA McPherson C., Wohldmann P., Scronce D.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: AF160760; RAD48936.1; -; Genomic_DNA.
DR InterPro; IPR006595; CTLH_C.
DR InterPro; IPR006594; LISH.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 4.
DR SMART; SM00668; CTLH; 1.
DR SMART; SM00667; LISH; 1.
DR SMART; SM00320; WD40; 2.
DR PROSITE; PS50897; CTLH; 1.
DR PROSITE; PS50896; LISH; 1.
DR PROSITE; PS50082; WD REPEATS 2; 1.
SQ SEQUENCE 892 AA; 39780 MW; 2487A7C97E027AEF CRC64;

Query Match 66.7%; Score 6; DB 2; Length 892;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 KVDDTF 6
DB 520 KVDDTF 525

RESULT 63
Q8T043 DROME PRELIMINARY; PRT; 894 AA.
AC Q8T043; Q9V9B3;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 21-FEB-2006, entry version 24.
DE LD30953p (CG3409-PA)
ORFName=CG3409; Dmel_CG3409;
GN Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

```

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Swirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [4]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Swirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [5]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [6]
RN NUCLEOTIDE SEQUENCE.
RX Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Swirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RN NUCLEOTIDE SEQUENCE.
RX FlyBase;
RG FlyBase;
RA Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
CC similarity).
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AY069571; AL39716.1; -; mRNA.
DR EMBL; AY069571; AL39716.1; -; Genomic_DNA.
DR FlyBase; FBgn0033095; CG3409.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; MFS_1; 1.
DR PROSITE; PS00850; MFS; 1.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 894 AA; 98864 MW; E7515205F19EC998 CRC64;
Query Match 66.7%; Score 6; DB 2; Length 894;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 DDTFFY 8
DB 849 DDTFFY 854
|||||
RESULT 64
Q9VPH1_DROME

ID Q9VPH1_DROME PRELIMINARY; PRT; 900 AA.
AC Q9VPH1;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE CG5528-PA, entry version 25.
DE Names:roll-9; ORFNames=Dmel CG5528;
GN Drosophila melanogaster [fruit fly].
OS Drosophila melanogaster (Insecta; Pterygota;
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OX Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiot E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smet T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhan M., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Swirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Swirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective";

Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).

RA NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminer J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celnik S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celnik S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RP NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
 CC EMBL; AEO03591; AAF51581.1; -; Genomic_DNA.
 DR HSP; Q15399; 1FYV.
 DR FlyBase; FBgn0036978; Toll-9.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR003591; LRR typ.
 DR InterPro; IPR00157; TIR.
 DR Pfam; PF00560; LRR_1; 6.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00369; LRR_TYP; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS0104; TIR; 1.
 SQ SEQUENCE 900 AA; 104013 MW; 627062202C192062 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 900;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
 |||||
 Db 304 DTFYV 309

RESULT 65
 Q41709 GIBZE PRELIMINARY; PRT; 1080 AA.
 AC Q41709 GIBZE PRELIMINARY; PRT; 1080 AA.
 DT 16-AUG-2005, integrated into UniProtKB/TrEMBL.
 DT 16-AUG-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Hypothetical protein.
 GN ORFNames=FG06999.1;
 OS Gibberella zeae (Fusarium graminearum).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 OX NCBI_TaxID=5518;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=PH-1 / NRRL 31084;
 RA Birren B.W., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,

RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D.,
 RA Galagan J.E., Gardyna S., Gnerre S., Graham L., Grand-Pierre N.,
 RA Hafez N., Hagopian D., Hagos B., Hall J., Horton L., Hulme W.,
 RA Iliev I., Jaffe D., Johnson R., Jones C., Kamal M., Kamat A.,
 RA Karatas A., Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G.,
 RA Lui A., Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J.,
 RA Manning J., Matthews C., Mauceli E., McCarthy M., Meldrim J.,
 RA Menes L., Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C.,
 RA Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P.,
 RA O'Neil D., Oliver J., Peterson K., Phunkhang P., Pierre N.,
 RA Purcell S., Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C.,
 RA Rogov P., Roman J., Schauer S., Schupack R., Seaman S., Severy P.,
 RA Smirnov S., Smith C., Spencer B., Stange-Thomann N., Stojanovic N.,
 RA Stubbins M., Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Willson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.S.;
 RT "Fusarium graminearum genome sequence";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC !- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC EMBL; AACM01000290; EAA75944.1; -; Genomic_DNA.
 DR GO; GO:0000145; C:exocyst; IEA.
 DR GO; GO:0015031; P:protein transport; IEA.
 DR GO; GO:0006904; P:vesicle docking during exocytosis; IEA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 1080 AA; 121264 MW; E8310A2DE90F998B CRC64;

Query Match 66.7%; Score 6; DB 2; Length 1080;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYV 9
 |||||
 Db 340 DTFYV 345

RESULT 66
 SEC8 NEUCR STANDARD; PRT; 1111 AA.
 AC Q9HE88; O7S707;
 DT 25-OCT-2002, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAR-2001, sequence version 1.
 DT 07-FEB-2006, entry version 29.
 DE Probable exocyst complex component sec8.
 GN Name=sec-8; ORFNames=B13020.150, NCU04190;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=74-OR23-1A / FGSC 987;
 EX MEDLINE=22542210; PubMed=12655011; DOI=10.1093/nar/gkg293;
 RA Mannhaupt G., Montrone C., Haase D., Mewes H.-W., Aign V.,
 RA Hoheisel J.D., Fartmann B., Nyakatura G., Kempken F., Maier J.,
 RA Schulte U.;
 RT "What's in the genome of a filamentous fungus? Analysis of the
 RT Neurospora genome sequence";
 RL Neurospora genome sequence.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=74-OR23-1A / FGSC 987;
 RX MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A.,
RA Werner-Washburne M., Sellitrennikoff C.P., Kinsey J.A., Braun E.L.,
RA Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA Stange-Thomann N., Barrett R., Gnerre S., Kamal M., Kamvysellis M.,
RA Mauceli E., Bielke C., Rudd S., Frishman D., Kryzstofova S.,
RA Ramussen C., Metzberg R.L., Perkins D.D., Kroken S., Cogoni C.,
RA Macino G., Catcheside D.E.A., Li W., Pratt R.J., Osmari S.A.,
RA DeSouza C.P.C., Glass N.L., Orbach M.J., Berglund J.A., Voelker R.,
RA Yarden O., Plamann M., Siller S., Dunlap J.C., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbel D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.W.;
RT "The genome sequence of the filamentous fungus *Neurospora crassa*.";
RL Nature 422:859-868(2003).
CC -!- FUNCTION: Component of the exocyst complex involved in the docking
CC of exocystic vesicles with fusions site on the plasma membrane (By
CC similarity).
CC -!- SUBUNIT: The exocyst complex is composed of SEC3, SEC5, SEC6,
CC SEC8, SEC10, SEC15, EXO70 and EXO84 (By similarity).
CC -!- SIMILARITY: Belongs to the SEC8 family.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC ENBL; AL451015; CAC18205.1; -; Genomic DNA.
CC EMBL; ABX01000274; EAA31914.1; -; Genomic DNA.
CC BioCyc; NCRA-XX3-01:NCRA-XX3-01-007938-MONOMER; -;
CC InterPro; IPR007191; Sec8 exocyst.
CC Pfam; PF04048; Sec8_exocyst; 1.
CC Exocytosis; Protein transport; Transport.
FT CHAIN 1 llll
FT PROBABLE exocyst complex component sec8.
SQ SEQUENCE 1111 AA; 124417 MW; 6AC72D46750E7D0B CRC64;

Query Match 66.7%; Score 6; DB 1; Length 1111;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVV 9
DB 338 DTFYVV 343

RESULT 67
ID Q9XVH4 CAEBL PRELIMINARY; PRT; 1256 AA.
AC Q9XVH4
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 32.
DE Hypothetical protein.
GN ORFNames=W02B8.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=Bristol N2;
RA MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RX The C. elegans sequencing consortium;
RG "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- SIMILARITY: Contains 1 PH domain.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; Z81136; CAB03458.1; -; Genomic DNA.
CC FIR; T26101; T26101.

DR Ensembl; W02B8.2; Caenorhabditis elegans.
DR WormBase; WBGene00012198; W02B8.2.
DR WormBep; W02B8.2; CE20131.
DR GO; GO:0005083; F:small GTPase regulator activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001180; Citron.
DR InterPro; IPR002219; DAG_PE_bd.
DR InterPro; IPR011849; PH.
DR InterPro; IPR011993; PH_type.
DR Pfam; PF001130; Cl.1; 1.
DR Pfam; PF00780; CNH; 1.
DR Pfam; PF001189; PH; 1.
DR SMART; SM00109; Cl; 1.
DR SMART; SM00036; CNH; 1.
DR SMART; SM00233; PH; 1.
DR PROSITE; PS50081; ZF_DAG_PE_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1256 AA; 144854 MW; 3036E19D668CBB2 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 1256;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVV 9
DB 1096 DTFYVV 1101

RESULT 68
ID Q61VN1 CAEBR PRELIMINARY; PRT; 1284 AA.
AC Q61VN1;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Hypothetical protein CBG04771.
GN Name=CBG04771;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=AF16;
RX PubMed=14624247; DOI=10.1371/journal.pbio.0000045;
RA Stein L.D., Bao Z., Blasiar D., Blumenthal T., Brent M.R., Chen N.,
RA Chinwalla A., Clarke L., Clee C., Coghlan A., Coulson A.,
RA D'Eustachio P., Fitch D.H.A., Fulton L.A., Fulton R.E.,
RA Griffiths-Jones S., Harris T.W., Hillier L.W., Kamath R.,
RA Kuwabara P.E., Mardis E.R., Marra M.A., Miner T.L., Minx P.,
RA Mullikin J.C., Plumb R.W., Rogers J., Schein J.E., Sohrmann M.,
RA Spieth J., Stajich J.E., Wei C., Willey D., Wilson R.K., Durbin R.,
RA Waterston R.H.;
RT "The genome sequence of *Caenorhabditis briggsae*: a platform for
RT comparative genomics.";
RL PLOS Biol. 1:166-192(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; CAAC01000021; CAE61028.1; -; Genomic DNA.
DR GO; GO:0005083; F:small GTPase regulator activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001180; Citron.
DR InterPro; IPR002219; DAG_PE_bd.
DR InterPro; IPR011993; PH_type.
DR Pfam; PF00780; CNH; 1.
DR SMART; SM00109; Cl; 1.
DR SMART; SM00036; CNH; 1.

```

DR PROSITE; P850081; ZF DAG PE 2; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1284 AA; 148578 MW; 8C34675D3535D450 CRC64;

Query Match      66.7%; Score 6; DB 2; Length 1284;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVV 9
Db 1123 DTFYVV 1128

RESULT 69
Q21025 CAEEL
ID Q21025_CAEEL PRELIMINARY; PRT; 1286 AA.
AC Q21025;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 36.
DE Hypothetical protein.
DE ORFNames=F59A6.5;
GN Caenorhabditis elegans.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
ON NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=9069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- SIMILARITY: Contains 1 PH domain.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; U01994; AK31526.1; -; Genomic DNA.
DR F1R; T16507; T16507.
DR Ensembl; F59A6.5; Caenorhabditis elegans.
DR WormBase; WBGene00019087; F59A6.5.
DR WormPep; F59A6.5; CE02790.
DR GO; GO:0005083; F.small GTPase regulator activity; IEA.
DR GO; GO:0007242; P.intracellular signaling cascade; IEA.
DR InterPro; IPR001180; Citron.
DR InterPro; IPR002219; DAG_PE_bd.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH_type.
DR Pfam; PF00130; CL_1; 1.
DR Pfam; PF00780; CNH; 1.
DR Pfam; PF00169; PH; 1.
DR SMART; SM00109; CL; 1.
DR SMART; SM00036; CNH; 1.
DR SMART; SM00233; PH; 1.
DR PROSITE; P850003; PH_DOMAIN; 1.
DR PROSITE; P850081; ZF DAG PE 2; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1286 AA; 148667 MW; 1402C3A80DC12BE4 CRC64;

Query Match      66.7%; Score 6; DB 2; Length 1286;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYVV 9
Db 1120 DTFYVV 1125

RESULT 70
Q73C85_BACCI
ID Q73C85_BACCI PRELIMINARY; PRT; 51 AA.

```

```

AC Q73C85;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Hypothetical protein.
DE ORFNames=BCE1181;
GN Bacillus cereus (strain ATCC 10987).
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
ON NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Raeko D.A., Ravel J., Oekstad O.A., Helsen E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AE017194; AA040111.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 51 AA; 5976 MW; E259DD9994414B92 CRC64;

Query Match      55.6%; Score 5; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFFYVV 9
Db 43 TFFYVV 47

RESULT 71
Q838E6_ENTFA
ID Q838E6_ENTFA PRELIMINARY; PRT; 56 AA.
AC Q838E6;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Hypothetical protein.
DE ORFNames=EF_0621;
GN Enterococcus faecalis (Streptococcus faecalis).
OS Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
ON NCBI_TaxID=1351;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umavayam L.A., Brinkac L.M., Beanan M.J.,
RA Dougherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 299:2071-2074(2003).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AE016830; AA080448.1; -; Genomic DNA.
DR TIGR; EF0621; -.
DR BioCyc; EF0621:185; EF0621-MONOMER; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 56 AA; 6873 MW; B513B3961BFDD83B CRC64;

Query Match      55.6%; Score 5; DB 2; Length 56;

```



```

RESULT 75
RS27A_LYCES
ID RS27A_LYCES STANDARD; PRT; 80 AA.
AC P62980; P27083;
DT 31-AUG-2004, integrated into UniProtKB/Swiss-Prot.
DT 31-AUG-2004, sequence version 1.
DT 07-MAR-2006, entry version 11.
DE 40S ribosomal protein S27a.
GN Name=UBI3; Synonyms=RPS27a;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
OX NCBI_TaxID=4081;
RN [1]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA] (UBI3).
RC STRAIN=cv. Lemhi Russet; TISSUE=Tuber;
RX MEDLINE=92032784; PubMed=1657246;
RA Hoffman N.E., Ko K., Milkowski D., Pichersky E.;
RT "Isolation and characterization of tomato cDNA and genomic clones
RT encoding the ubiquitin gene ubi3.";
RL Plant Mol. Biol. 17:1189-1201(1991).
CC -!- MISCELLANEOUS: This ribosomal protein is synthesized as a C-
CC terminal extension protein (CEP) of ubiquitin.
CC -!- SIMILARITY: Belongs to the ribosomal protein S27Ae family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; X59253; CAA41207.1; ALT_INIT; Genomic_DNA.
DR PIR; S18351; UQO7A.
DR InterPro; IPR002906; Ribosomal_S27a.
DR Pfam; PF01599; Ribosomal_S27; 1.
DR Metal-binding; Ribonucleoprotein; Ribosomal protein; Zinc;
KW Zinc-finger.
FT CHAIN 1 80 40S ribosomal protein S27a.
FT ZN_FING 45 68 C4-type.
FT COMEBIAS 1 23 Lys-rich (highly basic).
SQ SEQUENCE 80 AA; 9195 MW; 89FD2DC98B1E55B7 CRC64;

Query Match 55.6%; Score 5; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVDDT 5
DB 31 KVVDDT 35

RESULT 76
RS27A_SOLTU
ID RS27A_SOLTU STANDARD; PRT; 80 AA.
AC P62981; P27083;
DT 31-AUG-2004, integrated into UniProtKB/Swiss-Prot.
DT 31-AUG-2004, sequence version 1.
DT 07-MAR-2006, entry version 11.
DE 40S ribosomal protein S27a.
GN Name=UBI3; Synonyms=RPS27a;
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RN NUCLEOTIDE SEQUENCE [MRNA] (UBI3).
RC STRAIN=cv. Lemhi Russet; TISSUE=Tuber;
RX MEDLINE=93004476; PubMed=1327270;
RA Garbarino J.E., Rockhold D.R., Belknap W.R.;
RT "Expression of stress-responsive ubiquitin genes in potato tubers.";
RL Plant Mol. Biol. 20:235-244 (1992).
RN [2]

```

```

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] (UBI3).
RC STRAIN=cv. Lemhi Russet; TISSUE=Tuber;
RX MEDLINE=94154225; PubMed=8111011;
RA Garbarino J.E., Belknap W.R.;
RT "Isolation of a ubiquitin-ribosomal protein gene (ubi3) from potato
RT and expression of its promoter in transgenic plants.";
RL Plant Mol. Biol. 24:119-127(1994).
CC -!- MISCELLANEOUS: This ribosomal protein is synthesized as a C-
CC terminal extension protein (CEP) of ubiquitin.
CC -!- SIMILARITY: Belongs to the ribosomal protein S27Ae family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; Z11659; CAA77735.1; ALT_INIT; mRNA.
DR EMBL; U22576; AAA19247.1; ALT_INIT; Unassigned_DNA.
DR InterPro; IPR002906; Ribosomal_S27a.
DR Pfam; PF01599; Ribosomal_S27; 1.
DR Metal-binding; Ribonucleoprotein; Ribosomal protein; Zinc;
KW Zinc-finger.
FT CHAIN 1 80 40S ribosomal protein S27a.
FT ZN_FING 45 68 C4-type.
FT COMEBIAS 1 23 Lys-rich (highly basic).
SQ SEQUENCE 80 AA; 9195 MW; 89FD2DC98B1E55B7 CRC64;

Query Match 55.6%; Score 5; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVDDT 5
DB 31 KVVDDT 35

RESULT 77
Q3GRU9_9GAMM
ID Q3GRU9_9GAMM PRELIMINARY; PRT; 80 AA.
AC Q3GRU9;
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Twin-arginine translocation protein TatA/E.
GN ORFNames=PcrvODRAFT_2424;
OS Psychrobacter cryohalolentis K5.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Psychrobacter.
OX NCBI_TaxID=335284;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=K5;
RC US DOE Joint Genome Institute (JGI-PGF);
RG Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Psychrobacter
RT cryohalolentis K5.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=K5;
RC US DOE Joint Genome Institute (JGI-ORNL);
RG Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Psychrobacter
RT cryohalolentis K5.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AAJ01000001; EA012126.1; -; Genomic_DNA.

```

DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0008565; F:protein transporter activity; IEA.
 DR GO; GO:0015031; P:protein transport; IEA.
 DR InterPro; IPR003369; MtaA_Hcf106.
 DR InterPro; IPR006312; TATA_E.
 DR Pfam; PF02416; MtaA_Hcf106; 1.
 DR TIGRFAMs; TIGR01411_tataE; 1.
 SQ SEQUENCE 80 AA; 8738 MW; 04992A211384B965 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 73 KVDDT 77

RESULT 78

Q48Q06 STRPM PRELIMINARY; PRT; 81 AA.
 AC Q48Q06;
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Phase protein.
 GN OrderedLocNames=M28_Spy1844;
 OS Streptococcus pyogenes serotype M28.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OC NCBI_TaxID=319700;
 RN [1]

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=MGAS6180 / Serotype M28;
 RX PubMed=16088825; DOI=10.1086/430618;
 RA Green N.M., Zhang S., Porcella S.F., Nagiec M.J., Barbican K.D.,
 RA Beres S.B., Lefebvre R.B., Mueser J.M.;
 RT "Genome sequence of a serotype M28 strain of group A Streptococcus:
 RT potential new insights into puerperal sepsis and bacterial disease
 RT specificity.";
 RL J. Infect. Dis. 192:760-770(2005).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; CP000056; AAX72954.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 81 AA; 9636 MW; 23DC6107C6B34810 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 81;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 42 KVDDT 46

RESULT 79

Q4F061 PSYAR PRELIMINARY; PRT; 87 AA.
 AC Q4F061;
 DT 30-AUG-2005, integrated into UniProtKB/TrEMBL.
 DT 30-AUG-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Twin-arginine translocation protein TATA/E.
 GN Name=tatA; OrderedLocNames=Psyc_2000;
 OS Psychrobacter arcticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Psychrobacter.
 OC NCBI_TaxID=334543;
 RN [1]

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=273-4;
 RG NASA Astrobiology Institute;
 RA Ayala-del-Rio H.L., Chain P., Ponder M.A., Di Bartolo G., Ivanova N.,
 RA Bergholz P.W., Hauser L., Land M., Bakermans C., Rodrigues D.,
 RA Klappenbach J.A., Zarka D., Larimer F., Richardson P., Thomasow M.F.,
 RA Tiedje J.M.;
 RT "Complete sequence of Psychrobacter arcticus 273-4.";
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; CP000082; AAZ19847.1; -; Genomic_DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0008565; F:protein transporter activity; IEA.
 DR GO; GO:0015031; P:protein transport; IEA.
 DR InterPro; IPR006312; TATA_E.
 DR Pfam; PF02416; MtaA_Hcf106; 1.
 DR TIGRFAMs; TIGR01411; tataE; 1.
 KW Complete proteome.
 SQ SEQUENCE 87 AA; 9280 MW; 5240B1E656680D60 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
 Db 80 KVDDT 84

RESULT 80

Y3711 CLOAB STANDARD; PRT; 90 AA.
 AC Q4353;
 DT 01-FEB-1994, integrated into UniProtKB/Swiss-Prot.
 DT 29-AUG-2001, sequence version 2.
 DT 07-MAR-2006, entry version 25.
 DE Hypothetical protein CAC3711.
 GN OrderedLocNames=CAC3711;
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OC NCBI_TaxID=1488;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=93273706; PubMed=8501044;
 RA Sauer U., Duerre P.;
 RT "Sequence and molecular characterization of a DNA region encoding a
 RT small heat shock protein of Clostridium acetobutylicum.";
 RL J. Bacteriol. 175:3394-3400(1993).
 RN [2]

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RX DOI=10.1128/JB.183.16.4823-4838.2001;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
 RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 183:4823-4838(2001).

CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; X65276; CAA46377.1; ALT INIT; Genomic_DNA.
 DR EMBL; AE007866; AAK81631.1; -; Genomic_DNA.
 DR FIR; D97355; D97355.
 DR GenomeReviews; AE001437.GR; CAC3711.
 DR BioCyc; CAC3711-MONOMER; -.

KW Complete proteome; Hypothetical protein.
FT CHAIN 1 90 Hypothetical protein CAC3711.
/FTID=PRO_0000207115.
SQ SEQUENCE 90 AA; 10302 MW; DDDDE0F5C2FDD3C3C CRC64;

Query Match 55.6%; Score 5; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
|||||
Db 56 KVDDT 60

RESULT 81
Q8JM27_9NUCL PRELIMINARY; PRT; 91 AA.
AC Q8JM27; integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Hypothetical protein.
OS Mamestra configurata NPV-B.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=204440;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22080411; PubMed=12083822; DOI=10.1006/viro.2002.1411;
RA Li L., Donly C., Li Q., Willis L.G., Keddle B.A., Erlandson M.A.,
RA Theilmann D.A.;
RT "Identification and genomic analysis of a second species of
RT nucleopolyhedrovirus isolated from Mamestra configurata";
RL Virology 297:226-244 (2002).

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License

EMBL; AV126275; AAM95113.1; -; Genomic_DNA.
DR InterPro: IPR009317; Chab.
DR Pfam: PF06150; Chab; 1.
KW Hypothetical protein.
SQ SEQUENCE 91 AA; 10720 MW; B34A44F5A99C02FB CRC64;

Query Match 55.6%; Score 5; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 85 DDTFY 89

RESULT 82
Q63CD4_BACCZ PRELIMINARY; PRT; 92 AA.
AC Q63CD4;
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DE Hypothetical protein.
DE Hypothetical protein.
GN OrderedLocusNames=BCE33311838;
OS Bacillus cereus (strain ZK / E33L).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License

DR EMBL; CP000001; AAU18407.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 92 AA; 10293 MW; AB488CFBD09699D1 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
|||||
Db 52 DDTFY 56

RESULT 83
Q81RL2_BACAN PRELIMINARY; PRT; 92 AA.
AC Q81RL2_Q6HZT8; O6KTS2;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Conserved domain protein.
GN OrderedLocusNames=BA2031, BAS1886, GBAA2031; ORFNames=BA_2031;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=1271629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Ostad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria";
RL Nature 423:81-86 (2003).

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License

DR EMBL; AE016879; AAP25920.1; -; Genomic_DNA.
DR EMBL; AE017334; AAT31148.1; -; Genomic_DNA.
DR EMBL; AE017225; AAT54201.1; -; Genomic_DNA.
DR MEROPS; M73.001; -.
DR TIGR; BA2031; -.

DR TIGR: GBAA2031; --
 KW Complete proteome.
 SQ SEQUENCE 92 AA; 10279 MW; AB4C57DBD09699D1 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
 DB 52 DDTFY 56
 |||||

RESULT 84
 Q220L6_9ADEN PRELIMINARY; PRT; 92 AA.
 AC Q220L6;
 DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
 DT 20-DEC-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Hexon capsid protein (Fragment).
 GN Name=hexon;
 OS Human adenovirus type 38.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=46943;
 RN [1]

NUCLEOTIDE SEQUENCE.
 RA Madisch I., Harste G., Pommer H., Helm A.;
 RT "Phylogenetic Analysis of Main Neutralization (epsilon) and
 Hemagglutination(Gamma) Determinants of all Human Adenovirus
 RT Prototypes as a Basis for Molecular Classification and Taxonomy.";
 RL J. Virol. 0:0-0(2005).
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 CC EMBL; AJ745893; CAG34210.2; --; Genomic_DNA.
 DR NON_TER 1
 FT NON_TER 92
 SQ SEQUENCE 92 AA; 10228 MW; 680705BC73BC3A16 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDVT 5
 DB 71 KVDVT 75
 |||||

RESULT 85
 Q2WLY5_CLOBE PRELIMINARY; PRT; 94 AA.
 AC Q2WLY5;
 DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
 DT 10-JAN-2006, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Hypothetical protein.
 GN ORFNames=CbeiDRAFT_1625;
 OS Clostridium beijerinckii NCIMB 8052.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=290402;
 RN [1]

NUCLEOTIDE SEQUENCE.
 RP STRAIN=NCIMB 8052;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Richardson P.;
 RA "Sequencing of the draft genome and assembly of Clostridium
 RT beijerinckii NCIMB 8052";
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NCIMB 8052;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of Clostridium beijerinckii
 RT NCIMB 8052";
 RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 CC EMBL; AALQ01000023; EAP59102.1; --; Genomic_DNA.
 DR Hypothetical protein.
 KW SEQUENCE 94 AA; 10807 MW; 65A52A20B248AE6C CRC64;

Query Match 55.6%; Score 5; DB 2; Length 94;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDVT 5
 DB 8 KVDVT 12
 |||||

RESULT 86
 Q4DFB0_TRYCR PRELIMINARY; PRT; 100 AA.
 ID Q4DFB0_TRYCR
 AC Q4DFB0;
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE 10 kDa heat shock protein, putative.
 GN ORFNames=rc00.1047053508209.100, Tc00.1047053508209.90,
 GN Tc00.1047053509505.30, Tc00.1047053509505.70;
 OS Trypanosoma cruzi.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
 OC Schizotrypanum.
 OX NCBI_TaxID=5693;
 RN [1]

NUCLEOTIDE SEQUENCE.
 RP STRAIN=CL Brenner;
 RC El-Sayed N.M.A., Myler P.J., Bartholomeu D.C., Nilsson D.,
 RA Aggarwal G., Tran A.-N., Ghedin E., Worthey E.A., Delcher A.L.,
 RA Blandin G., Westenberger S.J., Caler E., Cerqueira G.C., Branche C.,
 RA Haas B., Anapuma A., Arner E., Aslund L., Attipoe P., Bontempi E.,
 RA Bringaud F., Burton P., Cadag E., Campbell D.A., Carrington M.,
 RA Crabtree J., Darban H., da Silveira J.F., de Jong P., Edwards K.,
 RA Englund P.T., Fazelina G., Feldblyum T., Ferella M., Frasch A.C.,
 RA Gull K., Horn D., Hou L., Huang Y., Kindlund E., Klingbeil M.,
 RA Kluge S., Koo H., Lacerda D., Levin M.J., Lorenzi H., Louie T.,
 RA Machado C.R., McCulloch R., McKenna A., Mizuno Y., Mottram J.C.,
 RA Nelson S., Ochaya S., Osoegawa K., Pai G., Parsons M., Pentony M.,
 RA Pettersson U., Pop M., Ramirez J.L., Rinta J., Robertson L.,
 RA Salzberg S.L., Sanchez D.O., Seyler A., Sharma R., Shetty J.,
 RA Simpson A.J., Sisk E., Tammi M.T., Tarleton R., Teixeira S.,
 RA Van Aken S., Vogt C., Ward P.N., Wickstead B., Wortman J., White O.,
 RA Fraser C.M., Stuart K.D., Andersson B.;
 RA "The Genome Sequence of Trypanosoma cruzi, Etiologic Agent of Chagas'
 RT Disease";
 RL Science 0:0-0(2005).
 RN [2]

NUCLEOTIDE SEQUENCE.
 RP STRAIN=CL Brenner;
 RC El-Sayed N.M.A., Myler P.J., Blandin G., Berriman M., Crabtree J.,
 RA Aggarwal G., Caler E., Renauld H., Worthey E.A., Hertz-Fowler C.,
 RA Ghedin E., Peacock C., Bartholomeu D.C., Haas B.J., Tran A.-N.,
 RA Wortman J.R., Alsmark U.C.M., Angiuoli S., Anupama A., Badger J.,
 RA Bringaud F., Cadag E., Carlton J.M., Cerqueira G.C., Creasy T.,
 RA Delcher A.L., Djikeng A., Embley T.M., Hauser C., Ivans A.C.,
 RA Kummerfeld S.K., Persira-Leal J.B., Nilsson D., Peterson J.,

RA Salzberg S.L., Shallom J., Silva J.C., Sundaram J., Westenberger S.,
 RA White O., Melville S.E., Donelson J.E., Andersson B., Stuart K.D.,
 RA Hall N.;
 RT "Comparative Genomics of Trypanosomatid Parasitic Protozoa."; Science 0:0-0(2005).
 RN [3]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=CL Brenner;
 RC El-Sayed N., Bartholomeu D., Haas B.;
 RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AAHK01000544; EAN91212.1; -; Genomic DNA.
 DR EMBL; AAHK01001336; EAN85850.1; -; Genomic DNA.
 DR EMBL; AAHK01000544; EAN91211.1; -; Genomic DNA.
 DR EMBL; AAHK01001336; EAN85854.1; -; Genomic DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0051082; F:unfolded protein binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR001476; Chaprinin_Cpn10.
 DR Pfam; PF00166; Cpn10; 1.
 DR PRINTS; PR00297; CHAPERONIN10.
 DR ProDom; PD000566; Chaprinin_Cpn10; 1.
 KW Chaperone; Heat shock.
 SQ SEQUENCE 100 AA; 10700 MW; 436B56AEDAF1B354 CRC64;
 Query Match 55.6%; Score 5; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVDDT 5
 DB 64 KVVDDT 68
 |||||

 RESULT 87
 ID Q2JOA0 RHOPA PRELIMINARY; PRT; 104 AA.
 AC Q2JOA0;
 DT 07-MAR-2006, integrated into UniProtKB/TrEMBL.
 DT 07-MAR-2006, sequence version 1.
 DT 07-MAR-2006, entry version 1.
 DE Hypothetical protein.
 GN ORFNames=RPB 1400;
 OS Rhodopseudomonas palustris Haa2.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodopseudomonas.
 OX NCBI_TaxID=316058;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Haa2;
 RG US DOE Joint Genome Institute;
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M.,
 RA Vergez L., Schmutz J., Larimer P., Land M., Hauser L., Pelletier D.A.,
 RA Kyrtides N., Anderson I., Oda Y., Harwood C.S., Richardson P.;
 RT "Complete sequence of Rhodopseudomonas palustris Haa2."; Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; CP000250; ABD06110.1; -; Genomic DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 104 AA; 10889 MW; F2169AB4F2FE7F CRC64;
 Query Match 55.6%; Score 5; DB 2; Length 104;
 QY 1 KVVDDT 5
 DB 64 KVVDDT 68
 |||||

Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVDDT 5
 DB 75 KVVDDT 79
 |||||

 RESULT 88
 Q65G18 BACLD PRELIMINARY; PRT; 106 AA.
 ID Q65G18 BACLD PRELIMINARY; PRT; 106 AA.
 AC Q65G18; Q62RH3;
 DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
 DT 25-OCT-2004, sequence version 1.
 DT 07-FEB-2006, entry version 15.
 DE Putative thioredoxin Ytpp.
 GN Name=Ytpp; OrderedLocusNames=BL00046, BLi03135;
 OS Bacillus licheniformis (strain DSM 13 / ATCC 14580).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=279010;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15383718; DOI=10.1159/000079829;
 RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
 RA Ehrenreich P., Baumeier S., Henne A., Liesegang H., Merkl R.,
 RA Ehrenreich A., Gottschalk G.;
 RT "The complete genome sequence of Bacillus licheniformis DSM13, an organism with great industrial potential."; J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15461803; DOI=10.1186/gb-2004-5-10-r77;
 RA Rey M.W., Ramaia P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
 RA Tang M., Lopez de Leon A., Xiang H., Gusti V., Clausen I.G.,
 RA Olsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L.,
 RA Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N.,
 RA Ehrlich S.D., Berka R.M.;
 RT "Complete genome sequence of the industrial bacterium Bacillus licheniformis and comparisons with closely related Bacillus species."; Genome Biol. 5:RESEARCH077.1-RESEARCH077.12(2004).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AE017333; AAU41996.1; -; Genomic DNA.
 DR EMBL; CP000002; AAU24637.1; -; Genomic DNA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR012336; Thiordxn-like_fd.
 DR InterPro; IPR006662; Thiored.
 DR InterPro; IPR006663; Thioredox_dom2.
 DR InterPro; IPR012335; Thioredoxin_fold.
 DR Pfam; PF00085; Thioredoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 KW Complete proteome.
 SQ SEQUENCE 106 AA; 12625 MW; 63F72F5A999FA8A8 CRC64;
 Query Match 55.6%; Score 5; DB 2; Length 106;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 TFFYV 9
 DB 49 TFFYV 53
 |||||

 RESULT 89
 Q5WEA4 BACSK PRELIMINARY; PRT; 108 AA.
 ID Q5WEA4 BACSK PRELIMINARY; PRT; 108 AA.
 AC Q5WEA4;
 DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
 DT 23-NOV-2004, sequence version 1.
 DT 07-FEB-2006, entry version 9.

DN Thioresdoxin.
GN OrderedLocusNames=ABC2772;
OS Bacillus clausii (strain KSM-K16).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=66692;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Takaki Y., Kageyama Y., Shimamura S., Suzuki H., Nishi S., Hatada Y.,
RA Kawai S., Ito S., Horikoshi K.;
RT "The complete genome sequence of the alkaliphilic Bacillus clausii
RT KSM-K16";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AP006627; BAD5306.1; -; Genomic DNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR012336; Thioridoxn-like_fold.
DR InterPro; IPR006662; Thioridox.
DR InterPro; IPR006663; Thioridox dom2.
DR InterPro; IPR012335; Thioridoxin_fold.
DR Pfam; PF00085; Thioridoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
KW Complete proteome.
SQ SEQUENCE 108 AA; 12516 MW; 0F5925611B113856 CRC64;
Query Match 55.6%; Score 5; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 TFYV 9
Db 49 TFYV 53
RESULT 90
Q4XC7 PLACH PRELIMINARY; PRT; 109 AA.
AC Q4XC7;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN ORFNames=PC403203.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; CAJ01007439; CAH85235.1; -; Genomic_DNA.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 109 AA; 13670 MW; 480F614CD3A2B037 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 TFYV 9
Db 25 TFYV 29
RESULT 91
Q6Y8R4 MYCHO PRELIMINARY; PRT; 116 AA.
AC Q6Y8R4;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Hypothetical conserved protein (Fragment).
OS Mycoplasma hominis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2098;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PG21.
RX PubMed=15616325; DOI=10.1128/AAC.49.1.421-424.2005;
RA Raherison S., Gonzalez P., Renaudin H., Charron A., Bebear C.,
RA Bebear C.M.;
RT "Increased Expression of Two Multidrug Transporter-Like Genes Is
RT Associated with Ethidium Bromide and Ciprofloxacin Resistance in
RT Mycoplasma hominis";
RL Antimicrob. Agents Chemother. 49:421-424(2005).
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AY169817; AAO39417.1; -; Genomic_DNA.
DR Hypothetical protein.
KW NON_TER
PT 1
SQ SEQUENCE 116 AA; 13513 MW; ADC7AC6DC5AAB3A7 CRC64;
Query Match 55.6%; Score 5; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 TFYV 9
Db 33 TFYV 37
RESULT 92
Q63BU1 BACCZ PRELIMINARY; PRT; 119 AA.
AC Q63BU1;
DT 23-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 23-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Acetyltransferase.
GN OrderedLocusNames=BCE333L2034;
OS Bacillus cereus (strain ZK / E33L).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; CP000001; AAU18222.1; -; Genomic_DNA.

```
DR GO: GO:0008080; F:N-acetyltransferase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR InterPro: IPR000182; GCN5acetyl_trans.
DR Pfam: PF00583; Acetyltransf_1; 1.
KW Complete proteome; Transferase.
SQ SEQUENCE 119 AA; 13936 MW; B8CCBE34683CF9DAA CRC64;

Query Match 55.6%; Score 5; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 34 KVDDT 38

RESULT 93
Q6HJB1 BACHK
ID Q6HJB1 BACHK PRELIMINARY; PRT; 119 AA.
AC Q6HJB1
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Acetyltransferase.
GN OrderedLocusNames=BT9727.2036;
OS Bacillus thuringiensis subsp. konkukian.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=180856;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=97-27;
RA Bretkin T.S.; Bruce D.; Challacombe J.F.; Gilna P.; Han C.; Hill K.;
RA Hitchcock P.; Jackson P.; Keim P.; Longmire J.; Lucas S.; Okinaka R.;
RA Richardson P.; Rubin E.; Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AE017355; AAT61224.1; -; Genomic DNA.
DR GO: GO:0008080; F:N-acetyltransferase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR InterPro: IPR000182; GCN5acetyl_trans.
DR Pfam: PF00583; Acetyltransf_1; 1.
KW Complete proteome; Transferase.
SQ SEQUENCE 119 AA; 13948 MW; 5989EED70ACF9DAB CRC64;

Query Match 55.6%; Score 5; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 34 KVDDT 38

RESULT 94
Q81DZ1 BACCR
ID Q81DZ1 BACCR PRELIMINARY; PRT; 119 AA.
AC Q81DZ1
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Acetyltransferase (EC 2.3.1.-).
GN OrderedLocusNames=BC2205; ORFNames=BC 2205;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
```

```
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N.; Sorokin A.; Anderson I.; Galleron N.; Candelon B.;
RA Kapatral V.; Bhattacharyya A.; Reznik G.; Mikhailova N.; Lapidus A.;
RA Chu L.; Mazur M.; Goltsman E.; Larsen N.; D'Souza M.; Walunas T.;
RA Grechkin Y.; Pusch G.; Haselkorn R.; Fonstein M.; Ehrlich S.D.;
RA Overbeek R.; Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AE016877; AAP09171.1; -; Genomic_DNA.
DR BioCyc; BCR226900:BC2205-MONOMER; -.
DR LinkHub; Q81DZ1; -.
DR GO: GO:0008415; F:acetyltransferase activity; IEA.
DR GO: GO:0008080; F:N-acetyltransferase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR InterPro: IPR000182; GCN5acetyl_trans.
DR Pfam: PF00583; Acetyltransf_1; 1.
KW Acyltransferase; Complete proteome; Transferase.
SQ SEQUENCE 119 AA; 14012 MW; BB0A424E269AADBA CRC64;

Query Match 55.6%; Score 5; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 34 KVDDT 38

RESULT 95
Q81R08 BACAN
ID Q81R08 BACAN PRELIMINARY; PRT; 119 AA.
AC Q81R08; Q6HZ79; Q6KT72;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Acetyltransferase, GNAT family.
GN OrderedLocusNames=BA2252, BAS2096, GBAA2252; ORFNames=BA_2252;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D.; Peterson S.N.; Tourasse N.J.; Baillie L.W.; Paulsen I.T.;
RA Nelson K.E.; Tettelin H.; Fouts D.E.; Eisen J.A.; Gill S.R.;
RA Holtzapple E.K.; Okstad O.A.; Helgason E.; Rikstone J.; Wu M.;
RA Kolonay J.F.; Beanan M.J.; Dodson R.J.; Brinkac L.M.; Gwinn M.L.;
RA DeBoy R.T.; Madpu R.; Daugherty S.C.; Durkin A.S.; Haft D.H.;
RA Nelson W.C.; Peterson J.D.; Pop M.; Khouri H.M.; Radune D.;
RA Benton J.L.; Mahamoud Y.; Jiang L.; Hance I.R.; Weidman J.F.;
RA Berry K.J.; Plaut R.D.; Wolf A.M.; Watkins K.L.; Niernan W.C.;
RA Hazen A.; Cline R.T.; Redmond C.; Thwaite J.E.; White O.;
RA Salzberg S.L.; Thomason B.; Friedlander A.M.; Koehler T.M.;
RA Hanna P.C.; Kolstoe A.-B.; Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Ames ancestor;
RA Ravel J.; Rasko D.A.; Shumway M.F.; Jiang L.; Cer R.Z.; Federova N.B.;
RA Wilson M.; Stanley S.; Decker S.; Read T.D.; Salzberg S.L.;
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
```

```

RC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=Sterne;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus anthracis Sterne.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AE016879; AAP26128.1; -; Genomic DNA.
DR EMBL; AE017334; AAT31373.1; -; Genomic DNA.
DR EMBL; AE017225; AAT54410.1; -; Genomic DNA.
DR TIGR; BA2252; -.
DR TIGR; GBAA2252; -.
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000182; GCS5acetyl trans.
DR Pfam; PF00583; Acetyltransf_1; I.
DR Complete proteome; Transferase.
SQ SEQUENCE 119 AA; 13963 MW; 7A85C8D72145B508 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 34 KVDDT 38

RESULT 96
Q738W2_BAC11
ID Q738W2_BAC11 PRELIMINARY; PRT; 119 AA.
AC Q738W2;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Acetyltransferase, GNAT family.
GN ORFNames=BCE 2281;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Raiko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
adaptations and a large plasmid related to Bacillus anthracis pXOI."
RL Nucleic Acids Res. 32:977-988(2004).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AE017194; AAS41200.1; -; Genomic DNA.
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000182; GCS5acetyl trans.
DR Pfam; PF00583; Acetyltransf_1; I.
DR Complete proteome; Transferase.
SQ SEQUENCE 119 AA; 13993 MW; E5AD587DF1503A3 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 34 KVDDT 38

```

```

RESULT 97
Q8U332_PVRFU
ID Q8U332_PVRFU PRELIMINARY; PRT; 120 AA.
AC Q8U332;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Hypothetical protein PF0643.
DE OrderedLocusNames=PF0643;
GN Pyrococcus furiosus.
OS Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AE010185; AAL80767.1; -; Genomic DNA.
DR BioCyc; PFUR186497:PF0643-MONOMER; -.
DR LinkHub; Q8U332; -.
DR Complete proteome.
SQ SEQUENCE 120 AA; 13395 MW; 4B5C2B85C5609085 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
Db 16 VDDTF 20

RESULT 98
Q4MTS5_BACCE
ID Q4MTS5_BACCE PRELIMINARY; PRT; 120 AA.
AC Q4MTS5;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Acetyltransferase.
GN ORFNames=BCE G9241_2217;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Malden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Ralston J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
with an illness resembling inhalation anthrax.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAEK0100006; EAL15572.1; -; Genomic DNA.

```

```

DR GO: GO:0008080; F:N-acetyltransferase activity; IEA.
DR GO: GO:0016740; P:transferase activity; IEA.
KW transferase.
SQ SEQUENCE 120 AA; 14050 MW; 96E8CCE346986E27 CRC64;

Query Match          55.6%; Score 5; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 34 KVDDT 38

RESULT 99
QSDHT7 SCHJA PRELIMINARY; PRT; 126 AA.
AC QSDHT7;
DT 29-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 29-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE SJCCHC02803 protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RT "The full-length cDNA sequences of Schistosoma japonicum genes.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RA Liu F., Lu J., Hu W., Wang S.-Y., Cui S.-J., Chi M., Yan Q.,
RA Wang X.-R., Song H.-D., Xu X.-N., Wang J.-J., Zhang X.-L., Wang Z.-Q.,
RA Xue C.-L., Brindley P.J., McManus D.P., Yang P.-Y., Feng Z., Chen Z.,
RA Han Z.-G.;
RT "New Perspectives on Host-parasite Interplay by Comparative
RT Transcriptomic and Proteomic Analyses of the Human Blood Fluke,
RT Schistosoma japonicum.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY812887; AA264619.1; -; mRNA.
SQ SEQUENCE 126 AA; 14649 MW; F44CAF4F9495A4DC CRC64;

Query Match          55.6%; Score 5; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 22 KVDDT 26

RESULT 100
Q33XT4 9GAMM PRELIMINARY; PRT; 128 AA.
AC Q33XT4;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Membrane protein, putative precursor.
GN ORFNames=ShewDRAFT_2962;
OS Shewanella sp. PV-4.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=323850;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=PV-4;

US DOE Joint Genome Institute (JGI-PGP);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Istrani S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Shewanella sp. PV-4.";
RN Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=PV-4;
US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Shewanella sp. PV-4.";
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AALSO1000003; EAP03875.1; -; Genomic_DNA.
KW Signal.
FT SIGNAL 1 20 Potential.
SQ SEQUENCE 128 AA; 13939 MW; 25FEDA74705A22BB CRC64;

Query Match          55.6%; Score 5; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 78 KVDDT 82

RESULT 101
Q8X3T8 ECO57 PRELIMINARY; PRT; 128 AA.
AC Q8X3T8;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE No significant matches.
GN OrderedLocustNames=z2511;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AE005174; AAG56523.1; -; Genomic_DNA.
DR PIR; G85757; G85757.
KW Complete proteome.
SQ SEQUENCE 128 AA; 14229 MW; DA17C71370F86470 CRC64;

Query Match          55.6%; Score 5; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 78 KVDDT 82

```

```

Db      14 KVDDT 18

RESULT 102
Q7NF95 GLOVI PRELIMINARY; PRT; 130 AA.
AC Q7NF95
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE G113631 protein.
GN OrderedLocusNames=g113631;
OS Gloeobacteria; Gloeobacteriales; Gloeobacter.
OX NCBI_TaxID=33072;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=14621292; DOI=10.1093/dnares/10.4.137;
RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Teuchiya T.,
RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimo S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT cyanobacterium that lacks thylakoids.";
RL DNA Res. 10:137-145(2003).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BA000045; BAC91572.1; -; Genomic_DNA.
DR BioCyc; GVIO251221:G113631-MONOMER; -.
KW Complete proteome.
SQ SEQUENCE 130 AA; 15261 MW; 3BF2C32C890C7F6A CRC64;

Query Match 55.6%; Score 5; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 11 KVDDT 15

RESULT 103
PA2 APICC STANDARD; PRT; 134 AA.
AC Q9BMK4;
DT 01-NOV-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2006, entry version 31.
DE Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase).
OS Apis cerana cerana (Oriental honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=94128;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC Shen L.R., Zhang C.X., Cheng J.A.;
RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RL
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides (By similarity).
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a carboxylate.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted protein (By similarity).
CC -!- ALLERGEN: Causes an allergic reaction in human (By similarity).
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----

```

```

DR EMBL; AF321087; AAK09361.1; -; mRNA.
DR HSSP; P06630; 1POC.
DR SMR; Q9BMK4; 1-134.
DR InterPro; IPR008774; Phospholip_A2.
DR InterPro; IPR013090; Phospholip_A2_AS.
DR InterPro; IPR001211; PhospholipaseA2.
DR PANTHER; PTHR12253; Phospholip_A2; 1.
DR Pfam; PF05826; Phospholip_A2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2_ASP; FALSE_NEG.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Allergen; Calcium; Glycoprotein; Hydrolase; Lipid degradation;
KW Metal-binding.
FT CHAIN 1 134 Phospholipase A2.
FT ACT_SITE 34 34 /FTID=PRO_0000161722.
FT ACT_SITE 64 64 By similarity.
FT METAL 8 8 Calcium (via carbonyl oxygen) (By
FT METAL 10 10 Calcium (via carbonyl oxygen) (By
FT METAL 12 12 Calcium (via carbonyl oxygen) (By
FT METAL 35 35 Calcium (By similarity).
FT CARBOHYD 13 13 N-linked (GlcNAc...) (Potential).
FT DISULFID 9 31 By similarity.
FT DISULFID 30 70 By similarity.
FT DISULFID 37 63 By similarity.
FT DISULFID 61 95 By similarity.
FT DISULFID 105 113 By similarity.
SQ SEQUENCE 134 AA; 15197 MW; CAC19BF92E4EC849 CRC64;

Query Match 55.6%; Score 5; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFY 7
Db 64 DDTFY 68

RESULT 104
Q8ZI74 YERPE PRELIMINARY; PRT; 134 AA.
AC Q8ZI74;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein YPO0641.
GN OrderedLocusNames=YPO0641;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Tittball R.W., Holden M.T.G.,
RA Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdono-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holtroyd S., Jagsels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AJ414143; CAC89494.1; -; Genomic_DNA.
DR PIR; AC0079; AC0079.

```

```

DR BioCyc; YP00641-MONOMER; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 134 AA; 15056 MW; 578A769DC5545ABC CRC64;

Query Match 55.6%; Score 5; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 8
DB 91 DTFY 95

RESULT 105
Q2NCAO_9SPHN PRELIMINARY; PRT; 137 AA.
AC Q2NCAO;
DT 07-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein.
GN ORFNames=ELI_02995;
OS Erythrobacter litoralis HTCC2594.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Erythrobacteraceae; Erythrobacter.
OX NCBI_TaxID=314225;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HTCC2594;
RA Giovannoni S.J., Cho J.-C., Ferriera S., Johnson J., Kravits S.,
RA Halpern A., Remington K., Beeson K., Tran B., Rogers Y.-H.,
RA Friedman R., Venter J.C.;
RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; U23407; AA80225.1; -; mRNA.
DR PIR; I53298; I53298.
DR HSSP; P29373; 1CBS.
DR SMR; P51673; 1-138.
DR Ensembl; ENSRNOG00000022101; Rattus norvegicus.
DR RGD; 62070; Crabp2.
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:0008289; Lipid binding; TAS.
DR GO; GO:0008669; Lipid transport; NAS.
DR GO; GO:0042573; Piretinoid acid metabolism; NAS.
DR InterPro; IPR012674; Calycin.
DR InterPro; IPR000463; Fatty acid bd.
DR InterPro; IPR000566; Lipocalin_cyFABP.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00176; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
DR Transport; Vitamin A.
KW INIT MET 0 By similarity.
FT CHAIN 1 138 Cellular retinoic acid-binding protein 2.
FT /FTId=PRO_0000057417.
FT
SQ SEQUENCE 138 AA; 15802 MW; BD9A90A502FC7841 CRC64;

Query Match 55.6%; Score 5; DB 1; Length 138;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DTFY 7
DB 48 DTFY 52

RESULT 107
Q315F6_DESDG PRELIMINARY; PRT; 138 AA.
ID Q315F6_DESDG AC Q315F6;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 21-FEB-2006, entry version 4.
DE Hypothetical protein.
GN OrderedLocNames=Dde_0639;
OS Desulfovibrio desulfuricans (strain G20).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=207559;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Goodwin L.A., Schmutz J.,
RA Larimer F., Land M., Kyrpides N., Ivanova N., Richardson P.;
RT Complete sequence of Desulfovibrio desulfuricans G20.;
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000112; ABB37440.1; -; Genomic_DNA.
SQ Complete proteome; Hypothetical protein.
KW SEQUENCE 138 AA; 15826 MW; 86C9458336FF3415 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 138;

```


RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=GUTat10.1;
RA	Ghedini E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
RA	Shallon J., Hou L., Djikeng A., Feldblum T., Hostetler J.,
RA	Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
RA	Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
RA	Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=GUTat10.1;
RA	El-Sayed N.M., Khalak H., Adams M.D.;
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=GUTat10.1;
RA	Haas B., Blandin G., El-Sayed N.;
RL	Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC	-----
CC	Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NoDerivs License
CC	-----
DR	EMBL; AC008146; AAX80287.1; -; Genomic_DNA.
DR	GO; GO:0005634; C:nucleus; IEA.
DR	GO; GO:0007530; P:sex determination; IEA.
DR	InterPro; IPR004023; Mago nashi.
DR	PANTHER; PTRH12638; Mago nashi.
DR	Pfam; PF02792; Mago_nashi_1.
SQ	SEQUENCE 147 AA; 17147 MW; 1BFBE46AD03C187 CRC64;
	Query Match 55.6%; Score 5; DB 2; Length 147;
	Best Local Similarity 100.0%; Pred.No.5.5e+02;
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy	4 DTFY 8
Dd	121 DTFY 125
	RESULT 112
ID	Q60DU6 ORYZA PRELIMINARY; PRT; 147 AA.
AC	Q60DU6;
DT	23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT	23-NOV-2004, sequence version 1.
DT	07-FEB-2006, entry version 6.
DE	Hypothetical protein OSUNBA0086E02.8.
OS	Name=OSUNBA0086E02.8;
GN	Oryza sativa (japonica cultivar-group).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP Clade;
OC	Ehrhartodeae; Oryzaceae; Oryza.
OX	NCBI_TaxID=39947;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RA	Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA	Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA	Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA	Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA	Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA	Wu H.-P., Shaw J.-F.;
RT	"Oryza sativa BAC OSUNBA0086E02 genomic sequence.";
RL	Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
CC	-----
CC	Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NoDerivs License
CC	-----
DR	EMBL; AC144741; AAV25237.1; -; Genomic_DNA.
DR	Gramene; Q60DU6; -;
KW	Hypothetical protein.
SQ	SEQUENCE 147 AA; 16892 MW; D89A9A93DCF1A649 CRC64;
	Query Match 55.6%; Score 5; DB 2; Length 147;


```

Best Local Similarity 100.0%; Pred. No. 5.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 KVDDT 5
Db 136 KVDDT 140

RESULT 113
Q72QW4 LEPIC PRELIMINARY; PRT; 148 AA.
AC Q72QW4;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DE Hypothetical protein.
GN OrderedLocusNames=LIC11994; ORFNames=LIC_11994;
OS Leptospira interrogans serogroup Icterohaemorrhagiae serovar
    copenhageni.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiroaceae; Leptospira.
OX NCBI_TaxID=44275;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=Fiocruz LI-130;
RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
RA Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
    Ho P.L., Haake D.A., Verjovsky-Almeida S., Hartseerl R.A.,
    Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,
    Coutinho L.L., Degraeve W.M., Dellagostin O.A., El-Dorri H.,
    Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Gigliotti E.A.,
    Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.,
    Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T.,
    Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
    de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
    Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
    Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.; reveals
    "Comparative genomics of two Leptospira interrogans serovars reveals
    novel insights into physiology and pathogenesis.";
RL J. Bacteriol. 186:2164-2172(2004).
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
EMBL; AB016823; AAS70570.1; -; Genomic DNA.
GO; GO:0003824; F: catalytic activity; IEA.
InterPro; IPR003736; PAAI.
InterPro; IPR006683; Thioestr_supf.
Pfam; PF03061; 4HBT; 1.
TIGRFAMs; TIGR00369; unchar dom_1; 1.
Complete proteome; Hypothetical protein.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 148 AA; 16851 MW; 11B58255C1FC528D CRC64;

Query Match 55.6%; Score 5; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 47 VDDTF 51

RESULT 114
Q8F4Y0 LEPIN PRELIMINARY; PRT; 148 AA.
AC Q8F4Y0;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-MAR-2006, entry version 11.
DE Hypothetical protein.
GN OrderedLocusNames=LA1908; ORFNames=LA_1908;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiroaceae; Leptospira.
OX NCBI_TaxID=173;

```

```

[1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RN STRAIN=56501 / Serogroup Icterohaemorrhagiae / Serovar lai;
RC MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
    Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
    Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
    RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
    Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
    RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
    Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
    intergans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
EMBL; AB010300; AAN49107.1; -; Genomic DNA.
DR GenomeReviews; AB010300 GR; LA1908.
DR BiOCYC; LINT189518:LA1908-MONOMER; -.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR InterPro; IPR003736; PAAI.
DR InterPro; IPR006683; Thioestr_supf.
DR Pfam; PF03061; 4HBT; 1.
DR TIGRFAMs; TIGR00369; unchar dom_1; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 148 AA; 16851 MW; 11B58255C1FC528D CRC64;

Query Match 55.6%; Score 5; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 47 VDDTF 51

RESULT 115
Q5IFZ7_9PROT PRELIMINARY; PRT; 149 AA.
AC Q5IFZ7;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Ammonia monooxygenase subunit A (Fragment).
GN Name=amoA;
OS uncultured ammonia-oxidizing bacterium.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; environmental samples.
OX NCBI_TaxID=152492;
[1] NUCLEOTIDE SEQUENCE.
RN PubMed=15691919; DOI=10.1128/AEM.71.2.697-705.2005;
RX O'Mullan G.D., Ward B.B.;
RT "Relationship of Temporal and Spatial Variabilities of Ammonia-
    Oxidizing Bacteria to Nitrification Rates in Monterey Bay,
    California.";
RL Appl. Environ. Microbiol. 71:697-705(2005).
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
EMBL; AV736858; AAV91797.1; -; Genomic DNA.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0004497; F: monooxygenase activity; IEA.
DR GO; GO:0006807; P: nitrogen compound metabolism; IEA.
DR InterPro; IPR003393; NH3_CH4_mOase_A.
DR Pfam; PF02461; AMO; 1.
DR Monooxygenase.
KW Monooxygenase.
FT NON_TER 149
FT NON_TER 149
SQ SEQUENCE 149 AA; 16678 MW; 79D0C6C5190C30B7 CRC64;

```

Query Match 55.6%; Score 5; DB 2; Length 149;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFFVV 9
 |||||
 Db 128 TFFVV 132

RESULT 116

Q93AM5_9BACT PRELIMINARY; PRT; 150 AA.
 AC Q93AM5;
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 01-DEC-2001, sequence version 1.
 DT 07-FEB-2006, entry version 12.
 DE Ammonia monooxygenase (Fragment).
 GN Name=amoA;
 OS uncultured bacterium.
 OC Bacteria; environmental samples.
 OX NCBI_TaxID=77133;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21633822; PubMed=1172633; DOI=10.1128/AEM.68.1.245-253.2002;
 RA Dionisi H.M., Layton A.C., Harms G., Gregory I.R., Robinson K.G.,
 RA Sayler G.S.,
 RT "Quantification of Nitrosomonas oligotropha-like ammonia-oxidizing
 RT bacteria and Nitrospira spp. from full-scale wastewater treatment
 RT plants by competitive PCR.";
 RL Appl. Environ. Microbiol. 68:245-253 (2002).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL; AF420300; AAL15012.1; -; Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004497; F:monooxygenase activity; IEA.
 DR GO; GO:0006807; P:nitrogen compound metabolism; IEA.
 DR InterPro; IPR003393; NH3_CH4_mOase_A.
 DR Pfam; PF02461; AMO; 1.
 KW Monooxygenase.
 FT NON_TER 1
 FT NON_TER 150
 FT NON_TER 150
 SQ SEQUENCE 150 AA; 16801 MW; 11DC7A7630D1E276 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFFVV 9
 |||||
 Db 129 TFFVV 133

RESULT 117

Q9AF59_9PROT PRELIMINARY; PRT; 151 AA.
 AC Q9AF59;
 DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2001, sequence version 1.
 DT 07-FEB-2006, entry version 13.
 DE Ammonia monooxygenase (Fragment).
 GN Name=amoA;
 OS uncultured bacterium B4-3.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
 OC Nitrosomonadaceae; environmental samples.
 OX NCBI_TaxID=137839;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21141854; PubMed=11229931;
 RX DOI=10.1128/AEM.67.3.1351-1362.2001;
 RA Gieseke A., Purkhold U., Wagner M., Amann R., Schramm A.;

RT "Community structure and activity dynamics of nitrifying bacteria in a
 RT phosphate-removing biofilm.";
 RL Appl. Environ. Microbiol. 67:1351-1362 (2001).
 CC -----

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----

CC EMBL; AY007575; AAG22847.1; -; Genomic_DNA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004497; F:monooxygenase activity; IEA.

DR GO; GO:0006807; P:nitrogen compound metabolism; IEA.

DR InterPro; IPR003393; NH3_CH4_mOase_A.

DR Pfam; PF02461; AMO; 1.

KW Monooxygenase.

FT NON_TER 1

FT NON_TER 151

SQ SEQUENCE 151 AA; 16954 MW; 7638BED3BD9236A1 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TFFVV 9
 |||||
 Db 130 TFFVV 134

RESULT 118

Q665U0_YERPS PRELIMINARY; PRT; 151 AA.
 ID Q665U0_YERPS
 AC Q665U0;
 DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2004, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Hypothetical protein.
 OS Versinia pseudotuberculosis.
 QS OrderedLocustNames=YPTB3420;
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Versinia.
 OX NCBI_TaxID=633;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=IP32953 / Serotype I;
 RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
 RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
 RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
 RA Brubaker R.R., Fowler J., Hinnébusch J., Marceau M., Médigue C.,
 RA Simonet M., Chenail-Francois V., Souza B., Dacheux D., Elliott J.M.,
 RA Derbise A., Hauser L.J., Garcia E.;
 RT "Insights into the evolution of Versinia pseudotuberculosis";
 RT comparison with Versinia pseudotuberculosis";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831 (2004).

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----

CC EMBL; BX936398; CAH23658.1; -; Genomic_DNA.

KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 151 AA; 16976 MW; 7B07E2A6BD70D7C3 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFYY 8
 |||||
 Db 108 DTFYY 112

RESULT 119

Q8CKF9_YERPE PRELIMINARY; PRT; 153 AA.
 ID Q8CKF9_YERPE
 AC Q8CKF9; Q74RR4;

DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DE 07-FEB-2006, entry version 16.
DE Hypothetical.
GN OrderedLocusNames=YF2954, Y3541;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
EX DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=91001 / Biovar Mediaevalis;
RX PubMed=1536893; DOI=10.1093/dnares/11.3.179;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
RT avirulent to humans.";
RL DNA Res. 11:179-197(2004).
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License

DR EMBL; AE013957; AAM87089.1; -; Genomic DNA.
DR EMBL; AE017138; AAS63134.1; -; Genomic DNA.
DR BiOCyc; YPES187410:Y3541-MONOMER; -;
DR BiOCyc; YPES229193:YF2954-MONOMER; -;
KW Hypothetical protein.
SQ SEQUENCE 153 AA; 17263 MW; 0FAD7AF02027BB5A CRC64;

Query Match 55.6%; Score 5; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFY 8
Db 110 DTFY 114

RESULT 120
Q41753 MAIZE
ID Q41753 MAIZE PRELIMINARY; PRT; 155 AA.
AC Q41753;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DE 07-FEB-2006, entry version 26.
DE Ubiquitin fusion protein.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Oh43; TISSUE=Radicle;
RA Liu L., Maillet D.S., Frappier J.H., d'Ailly K., Walden D.B.,
RA Atkinson B.G.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NoDerivs License

DR EMBL; U29160; AAA70104.1; -; Genomic DNA.
DR HSSP; Q862M4; LAAR.
DR SMR; Q41753; 1-76.
DR Gramene; Q41753;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR002906; Ribosomal_S27a.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF01599; Ribosomal_S27; 1.
DR Pfam; PF00240; ubiquitin; 1.
DR PRINTS; PR00348; UBIQUITIN.
DR SMART; SM00213; UBO; 1.
DR PROSITE; PS00299; UBIQUITIN_1; 1.
DR PROSITE; PS00593; UBIQUITIN_2; 1.
SQ SEQUENCE 155 AA; 17732 MW; 8AABCBB92F413C3 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDVT 5
Db 107 KVDVT 111

RESULT 121
Q7MXG7 PORGI
ID Q7MXG7 PORGI PRELIMINARY; PRT; 155 AA.
AC Q7MXG7;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE DNA-binding protein, histone-like family.
GN OrderedLocusNames=PG0222; ORFNames=PG_0222;
OS Porphyromonas gingivalis (Bacteroides_gingivalis).
OC Bacteria; Bacteroidetes; Bacteroidetes (Class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=W83;
RX MEDLINE=22829867; PubMed=12949112;
RX DOI=10.1128/JB.185.18.5591-5601.2003;
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA Dewhirst F.E., Fraser C.M.;
RT "Complete genome sequence of the oral pathogenic bacterium
RT Porphyromonas gingivalis strain W83.";
RL J. Bacteriol. 185:5591-5601(2003).
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License

DR EMBL; AE015924; AAQ65452.1; -; Genomic DNA.
DR TIGR; PG0222;
DR BiOCyc; PGIN242619:PG0222-MONOMER; -;
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR005902; HU_DNA_bd_put.
DR TIGRFAMS; TIGR01201; HU_rel; 1.
KW Complete proteome; DNA-binding.
SQ SEQUENCE 155 AA; 17249 MW; F6832CF5F5B4DA7 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 KVDVT 5
Db 131 KVDVT 135

RESULT 122
ID Q6Q131 RAT PRELIMINARY; PRT; 155 AA.
AC Q6Q131;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DE LRG00177.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Xu C.S., Zhang L., Chang C.F., Han H.P., Wang G.P., Chai L.Q.,
RA Yuan J.Y., Yang K.J., Zhao L.F., Ma H.H., Wang L., Wang S.F., Xing X.K.,
RA Shen G.M., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY539928; AA66268.1; -; mRNA.
DR Ensembl; ENRNOG0000033993; Rattus norvegicus.
SQ SEQUENCE 155 AA; 17255 MW; 1188278B491FADEB CRC64;

Query Match 55.6%; Score 5; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTFY 8
Db 147 DTFY 151

RESULT 123
ID Q9VJR2 DROME PRELIMINARY; PRT; 157 AA.
AC Q9VJR2;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 2.
DT 07-FEB-2006, entry version 18.
DE CG15278-PA.
GN ORFNames=CG15278, Dmel CG15278;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananthanides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers J., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

```

```

RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Waasman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000)
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective."
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacle J., Park S., Svirskaas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence."
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC

```

```

DR EMBL; AE003645; AAF53417.2; -; Genomic_DNA.
DR FlyBase; FBgn0032554; CG15278.
SQ SEQUENCE 157 AA; 18142 MW; 45259692497BFF19 CRC64;

Query Match
Best Local Similarity 55.6%; Score 5; DB 2; Length 157;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TFFYV 9
Db 33 TFFYV 37

RESULT 124
Q70Z72 CANFA
ID Q70Z72 CANFA PRELIMINARY; PRT; 159 AA.
AC Q70Z72;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 21-FEB-2006, entry version 15.
DE Olfactory receptor (fragment).
GN Name=OR16H06;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OC NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Quignon P., Guyon R., Renier C., Cadieu E., Hitte C., Andre C.,
RA Galibert F.;
RT "Comparison of the canine and human olfactory receptor gene
RT repertoire."
RL Genome Biol. 4:R80-R80(2003).
CC -!- FUNCTION: Putative odorant or sperm cell receptor (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
CC similarity).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
EMBL; AJ431547; CAD24257.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0007608; P:sensory perception of smell; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PANTHER; PTHR11398; Olfact_rcpt.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Membrane; Olfaction; Receptor;
KW Sensory transduction; Transducer; Transmembrane.
FT NON_TER 1
FT TER 159
SQ SEQUENCE 159 AA; 18340 MW; 73CDF660C08026D7 CRC64;

Query Match
Best Local Similarity 55.6%; Score 5; DB 2; Length 159;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TFFYV 9
Db 123 TFFYV 127

RESULT 125
Q4UID3_THEAN
ID Q4UID3 THEAN PRELIMINARY; PRT; 161 AA.
AC Q4UID3;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein.
GN ORFNames=TA06515;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC Theileria.
OC NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RX PubMed=15994597; DOI=10.1258/jrsm.98.7.320;
RA Pain A., Renauld H., Berriman M., Murphy L., Yeats C.A., Weir W.,
RA Kethnou A., Aslett M., Bishop R., Bouchier C., Cochet M.,
RA Coulson R.M.R., Cronin A., de Villiers E.P., Fraser A., Fosker N.,
RA Gardner M., Gobie A., Griffiths-Jones S., Harris D.E., Katzer F.,
RA Larke N., Lord A., Maser P., McKellar S., Mooney P., Morton P.,
RA Nene V., O'Neil S., Price C., Quail M.A., Rabinowitch E.,
RA Rawlings N.D., Rutter S., Saunders D., Seeger K., Shah T., Squares R.,
RA Squares S., Tivey A., Walker A.R., Woodward J., Dobbelaere D.A.E.,
RA Langsley G., Rajandream M.A., McKeever D., Shiels B., Tait A.,
RA Barrell B., Hall N.;
RT "Genome of the host-cell transforming parasite Theileria annulata
RT compared with T. parva."
RL Science 309:131-133(2005).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
EMBL; CR940347; CAI73156.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005732; C:small nuclear ribonucleoprotein complex; IEA.
DR GO; GO:0006397; P:mRNA processing; IEA.
DR InterPro; IPR006649; Euk_arc_LSM_core.
DR Pfam; PF01423; LSM; 1.
DR PDom; PD020287; snRNP; 1.
DR SMART; SM00651; Sm; 1.
KW Hypothetical protein.
SQ SEQUENCE 161 AA; 18443 MW; 0FB85E14C75ADF5C CRC64;

Query Match
Best Local Similarity 55.6%; Score 5; DB 2; Length 161;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DDTFY 7
Db 31 DDTFY 35

RESULT 126
Q43W25 SOLUS
ID Q43W25 SOLUS PRELIMINARY; PRT; 161 AA.
AC Q43W25;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
GN ORFNames=AcidDRAFT_3042;
OS Solibacter usitatus Ellin6076.
OC Bacteria; Acidobacteria; Solibacteres; Solibacterales;
OC Solibacteraceae; Solibacter.
OC NCBI_TaxID=234267;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ellin6076;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Solibacter usitatus
RT Ellin6076."

```

```

RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ellin676;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Solibacter usitatus.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AIA01000028; EMB56968.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 161 AA; 18142 MW; C897EB62D14A2A07 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFFY 7
DB 83 DDTFFY 87

RESULT 127
Q4N780 THEPA
ID Q4N780 THEPA PRELIMINARY; PRT; 162 AA.
AC Q4N780;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORFNames=TP01_0940;
OS Theileria parva.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC Theileria.
OC NCBI_TaxID=5875;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RX PubMed=15994558; DOI=10.1126/science.1110439;
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoaibi A., Domingo A.R., Wasawo D.,
RA Crabtree J., Wortman J.R., Haas B., Angioli S.V., Creasy T.H., Lu C.,
RA Suh B., Silva J.C., Uterback T.R., Feldblyum T.V., Pertea M.,
RA Allen J., Niernan W.C., Taracha E.L., Salzberg S.L., White O.R.,
RA Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;
RT "Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms
RT Lymphocytes.";
RL Science 309:134-137(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RX Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
RA Haas B., Angioli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Uterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms

```

```

CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AGK01000001; EAN34178.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005732; C:small nucleolar ribonucleoprotein complex; IEA.
DR GO; GO:0006397; P:mRNA processing; IEA.
DR InterPro; IPR006649; Euk_arc_LSM_core.
DR Pfam; PF01423; LSM; 1.
DR ProDom; PD020287; snRNP; 1.
DR SMART; SM00651; Sm; 1.
KW Hypothetical protein.
SQ SEQUENCE 162 AA; 18708 MW; B5EE7718AE781445 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFFY 7
DB 31 DDTFFY 35

RESULT 128
Q4ZPM6 PSEU2
ID Q4ZPM6 PSEU2 PRELIMINARY; PRT; 163 AA.
AC Q4ZPM6;
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Hypothetical protein precursor.
GN OrderedLocNames=PvYT_3866;
OS Pseudomonas syringae pv. syringae (strain B728a).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OC NCBI_TaxID=205918;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16043691; DOI=10.1073/pnas.0504930102;
RA Feil H., Fell W.S., Chain P., Larimer F., Dibartolo G., Copeland A.,
RA Lykidis A., Trong S., Nolan M., Goltsman E., Thiel J., Malfatti S.,
RA Loper J.E., Lapidus A., Dettler J.C., Land M., Richardson P.M.,
RA Kyriades N.C., Ivanova N., Lindow S.E.;
RT "Comparison of the complete genome sequences of Pseudomonas syringae
RT pv. syringae B728a and pv. tomato DC3000.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:11064-11069(2005).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000075; AAY38896.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein; Signal.
FT SIGNAL 1 32 Potential.
SQ SEQUENCE 163 AA; 18862 MW; E85C44B19B68E332 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
DB 84 VDDTF 88

RESULT 129
Q5SVM6 HUMAN
ID Q5SVM6 HUMAN PRELIMINARY; PRT; 166 AA.
AC Q5SVM6;
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Ribosomal protein S6 kinase, 90kDa, polypeptide 1 (fragment).
GN Name=RP56K1; ORFNames=RP11-492M19.2-007;
OS Homo sapiens (Human).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Carchinhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Harrison E.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 CC EMBL; AL627313; CA114646.1; -; Genomic DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0003735; P:structural constituent of ribosome; IEA.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000961; Pkinase.C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin.AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; Pkinase.1.
 DR Pfam; PF00433; Pkinase.C.1.
 DR ProDom; PD000001; Prot_kinase.1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS0108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding; Ribosomal protein;
 KW Serine/threonine-protein kinase; Transferase.
 FT NON TER 1
 FT NON TER 166
 FT NON TER 166 166
 SQ SEQUENCE 166 AA; 18710 MW; D7089EF1616B6134 CRC64;
 Query Match 55.6%; Score 5; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 DDTFY 7
 Db 4 DDTFY 8
 RESULT 130
 Q51Y06 MONPV
 ID Q51Y06 MONPV PRELIMINARY; PRT; 167 AA.
 AC Q51Y06;
 DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
 DT 15-FEB-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE MPKV-WRAIR013 (Hypothetical protein) (MPKV-SL-013) (MPKV-COP- 013).
 GN ORFNames=MPKV-COP-013, MPKV-SL-013, MPKV-WRAIR013,
 GN MPKV_L1B1970_184_018, MPKV_USA2003_039_018, MPKV_USA2003_044_018;
 OS Monkeypox virus.
 OS Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10244;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=MPKV-WRAIR7-61, Sierra Leone, and COP-58;
 RC PubMed=16023693; DOI=10.1016/j.virol.2005.05.030;
 RX Chen N., Li G., Libzewski M.K., Atkinson J.P., Jahrling P.B., Feng Z.,
 RA Schriewer J., Buck C., Wang C., Lefkowitz B.J., Esposito J.J.,
 RA Harms T., Damon I.K., Roper R.L., Upton C., Buller R.M.;
 RT "Virulence differences between monkeypox virus isolates from West
 RT Africa and the Congo basin."
 RL Virology 340:46-63(2005).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=Liberia 1970 184, USA 2003 039, and USA_2003_044;
 RX PubMed=16186219; DOI=10.1099/vir.0.81215-0;
 RA Likos A.M., Sammons S.A., Olson V.A., Frace A.M., Li Y.,
 RA Olsen-Rasmussen M., Davidson W., Galloway R., Khristova M.L.,

RA Reynolds M.G., Zhao H., Carroll D.S., Curns A., Formenty P.,
 RA Esposito J.J., Regnery R.L., Damon I.K.;
 RT "A tale of two clades: monkeypox viruses."
 RL J. Gen. Virol. 86:2661-2672(2005).
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 CC EMBL; AY603973; AAU01223.1; -; Genomic DNA.
 DR EMBL; DQ011156; AAY97415.1; -; Genomic DNA.
 DR EMBL; DQ011157; AAY97613.1; -; Genomic DNA.
 DR EMBL; AY741551; AAW67771.1; -; Genomic DNA.
 DR EMBL; AY753185; AAX09114.1; -; Genomic DNA.
 DR EMBL; DQ011153; AAY96815.1; -; Genomic DNA.
 DR GO; GO:0016032; P:viral life cycle; IEA.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A.1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 DR Hypothetical protein.
 KW SEQUENCE 167 AA; 19963 MW; 928269D5ADF1352 CRC64;
 Query Match 55.6%; Score 5; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 TFYV 9
 Db 95 TFYV 99
 RESULT 131
 Q5C0Z6 SCHJA
 ID Q5C0Z6 SCHJA PRELIMINARY; PRT; 170 AA.
 AC Q5C0Z6;
 DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
 DT 08-NOV-2005, sequence version 2.
 DT 07-FEB-2006, entry version 5.
 DE SCHGC08507 protein (Fragment).
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
 OC Schistosomatoidea; Schistosomatidae; Schistosoma.
 OX NCBI_TaxID=6182;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RP Liu F., Lu J., Hu W., Wang S.-Y., Cui S.-J., Chi M., Yan Q.,
 RA Wang X.-R., Song H.-D., Xu X.-N., Wang J.-J., Zhang X.-L., Wang Z.-Q.,
 RA Xue C.-L., Brindley P.J., McManus D.P., Yang P.-Y., Feng Z., Chen Z.,
 RA Han Z.-G.;
 RT "New Perspectives on Host-parasite Interplay by Comparative
 RT Transcriptomic and Proteomic Analyses of the Human Blood Fluke,
 RT Schistosoma japonicum."
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 CC EMBL; AY810790; AAX26679.2; -; mRNA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2.1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
 FT NON TER 1
 FT NON TER 170 170
 SQ SEQUENCE 170 AA; 18444 MW; EE79561F108B51EC CRC64;
 Query Match 55.6%; Score 5; DB 2; Length 170;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVDVT 5

```
Db      18 KVDVT 22
|||||
RESULT 132
Q5K255_GUITH PRELIMINARY; PRT; 170 AA.
AC Q5K255;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Putative 29 kDa ribonucleoprotein A (Fragment).
GN Name=riba;
OS Guillardia theta (Cryptomonas phi).
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX NCBI_TaxID=55529;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gould S.B., Sommer M.S., Hadfi K., Zauner S., Maier U.G.;
RT "Transport of proteins into multimeric membranes."
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: AJ821834; CAA25374.1; -; mRNA.
DR GO: GO:0030529; C:ribonucleoprotein complex; IEA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR InterPro: IPR012677; a_b_plait_nuc_bd.
DR InterPro: IPR000504; RNPI_RNA_Bd.
DR Pfam: PF00076; RRM_1; 1.
DR SMART: SM00360; RRM; 1.
DR PROSITE: PS50102; RRM; 1.
KW Ribonucleoprotein; Viral nucleoprotein.
FT NON TER 1
SQ SEQUENCE 170 AA; 18877 MW; E62860E70B167E11 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDVT 5
|||||
Db 70 KVDVT 74

RESULT 133
Q6LVZ2_PHOPR
ID Q6LVZ2_PHOPR PRELIMINARY; PRT; 170 AA.
AC Q6LVZ2;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Hypothetical membrane-fusion protein.
GN Names=CBU1094; OrderedLocNames=PBPR0088;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N.,
RA Lauro F.M., Cestaro A., Malacrida G., Simonati B., Cannata N.,
RA Rinaldi C., Bartlett D.H., Valle G.;
RT "Life at depth: Photobacterium profundum genome sequence and
RT expression analysis."
RL Science 307:1459-1461 (2005).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
```

```
DR EMBL: CR378663; CAG18533.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 170 AA; 18639 MW; 62BC48D6C8E2EB1C CRC64;

Query Match 55.6%; Score 5; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDVT 5
|||||
Db 134 KVDVT 138

RESULT 134
Q7VIT4_HELHP
ID Q7VIT4_HELHP PRELIMINARY; PRT; 171 AA.
AC Q7VIT4;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Hypothetical protein.
GN OrderedLocNames=HH0520; ORFNames=HH_0520;
OS Helicobacter hepaticus.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=32025;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 51449 / 3B1;
RX MEDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;
RA Suerbaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt A.,
RA Bell M., Droege M., Partmann B., Fischer H.-P., Ge Z., Hoerster A.,
RA Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,
RA Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
RT "The complete genome sequence of the carcinogenic bacterium
RT Helicobacter hepaticus."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906 (2003).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: AB017125; AAP77117.1; -; Genomic DNA.
DR BioCyc: HHEP235279:HH0520-MONOMER; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 171 AA; 19782 MW; 9EEF2ADEE1B8DC75 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
|||||
Db 63 VDDTF 67

RESULT 135
Q6WHR4_BPKV4
ID Q6WHR4_BPKV4 PRELIMINARY; PRT; 175 AA.
AC Q6WHR4;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Hypothetical protein.
GN ORFNames=KVP40.0240;
OS Bacteriophage KVP40.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=75320;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22803260; PubMed=12923095;
RX DOI=10.1128/JB.185.17.5220-5233.2003;
RA Miller E., Heidelberg J., Eisen J., Nelson W., Durkin A., Ciecko A.,
```



```

RA Feldblyum T., White O., Paulsen I., Nierman W., Lee J.,
RA Szczybinski B., Fraser C.;
RT "Complete genome sequence of the broad-host-range vibriophage KVP40:
RT comparative genomics of a T4-related bacteriophage.";
RL J. Bacteriol. 185:5220-5233(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Miller E., Lee J., Szczybinski B.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY283928; AAQ64309.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 175 AA; 20874 MW; 2D95DAAA8F5E9B39 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 175;
Best Local Similarity 100.0%; Pred.No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
Db 48 VDDTF 52

RESULT 136
Q9DHU6_YLDV
ID Q9DHU6_YLDV PRELIMINARY; PRT; 176 AA.
AC Q9DHU6;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DE 07-FEB-2006, entry version 10.
DR 16L protein precursor.
GN Name=16L;
OS Yaba-like disease virus (YLDV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Yatapoxvirus.
OC Xatapoxvirus.
OX NCBI_TaxID=132475;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=21176366; PubMed=11277691; DOI=10.1006/viro.2000.0761;
RA Lee H.-J., Essani K., Smith G.L.;
RT "The genome sequence of Yaba-like disease virus, a yatapoxvirus.";
RL Virology 281:170-192(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lee H.J.;
RL Thesis (2000), Sir William Dunn School of Pathology, University of
RL Oxford, Oxford, UNITED KINGDOM.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AJ293568; CAC21254.1; -; Genomic_DNA.
KW Signal.
FT SIGNAL 176 176 Potential.
SQ SEQUENCE 176 AA; 20531 MW; 55B33869B12B09DF CRC64;

Query Match 55.6%; Score 5; DB 2; Length 176;
Best Local Similarity 100.0%; Pred.No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 65 KVDDT 69

RESULT 137
Q5GSE5_WOLTR
ID Q5GSE5_WOLTR PRELIMINARY; PRT; 179 AA.
AC Q5GSE5;
DT 01-MAR-2005, integrated into UniProtKB/TrEMBL.

```

```

DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Cytochrome oxidase assembly factor.
GN OrderedLocusNames=Wb0491;
OS Wolbachia sp. subsp. Brugia malayi (strain TRS).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachiae; Wolbachia.
OX NCBI_TaxID=292805;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15780005; DOI=10.1371/journal.pbio.0030121;
RA Foster J., Ganatra M., Kamal I., Ware J., Makarova K., Ivanova N.,
RA Bhattacharya A., Kapatral V., Kumar S., Posfai J., Vincze T.,
RA Ingram J., Moran L., Lapidus A., Omelchenko M., Kyrpides N.,
RA Ghedin E., Wang S., Goltsman E., Joukov V., Ostrovskaya O.,
RA Tsukerman K., Mazur M., Comb D., Koonin E., Slatko B.;
RT "The Wolbachia genome of Brugia malayi: endosymbiont evolution within
RT a human pathogenic nematode.";
RL PLoS Biol. 3:599-614(2005).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AE017321; AAU71079.1; -; Genomic_DNA.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR InterPro; IPR007533; Ctag_Cox11.
DR PANTHER; PTHR14053; Ctag_Cox11; 1.
DR Pfam; PF04442; Ctag_Cox11; 1.
KW Complete proteome.
SQ SEQUENCE 179 AA; 20337 MW; 07EDCBC372750AC5 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 179;
Best Local Similarity 100.0%; Pred.No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TFFYV 9
Db 96 TFFYV 100

RESULT 138
Q4D000_TRYCR
ID Q4D000_TRYCR PRELIMINARY; PRT; 180 AA.
AC Q4D000;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DE 07-FEB-2006, entry version 5.
DE 10 kDa heat shock protein, putative.
GN ORFNames=Tc00.1047053509505.50;
OS Trypanosoma cruzi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
OC Schizotrypanum.
OX NCBI_TaxID=5693;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CL Brener;
RA El-Sayed N.M.A., Myler P.J., Bartholomew D.C., Nilsson D.,
RA Agarwal G., Tran A.-N., Ghedin E., Worthey E.A., Delcher A.L.,
RA Blandin G., Westenberger S.J., Caler E., Cerqueira G.C., Branche C.,
RA Haas B., Anapuma A., Arner E., Aelund L., Attipoe P., Bontempi E.,
RA Bringsaud F., Burton P., Cadag E., Campbell D.A., Carrington M.,
RA Crabtree J., Darban H., da Silveira J.F., de Jong P., Edwards K.,
RA Englund P.T., Fazellina G., Feldblyum T., Ferella M., Frasch A.C.,
RA Gull K., Horn D., Hou L., Huang Y., Kindlund E., Klingbeil M.,
RA Kluge S., Koo H., Lacerda D., Levin M.J., Lorenzi H., Louie T.,
RA Machado C.R., McCulloch R., McKenna A., Mizuno Y., Mottram J.C.,
RA Nelson S., Ochaya S., Osogawa K., Pai G., Parsons M., Pentony M.,
RA Pettersson U., Pop M., Ramirez J.L., Rinta J., Robertson L.,
RA Salzborg S.L., Sanchez D.O., Seyler A., Sharma R., Shetty J.,
RA Simpson A.J., Sisk E., Tammi M.T., Tarleton R., Teixeira S.,
RA Van Aken S., Vogt C., Ward P.N., Wickstead B., Wortman J., White O.,
RA Fraser C.M., Stuart K.D., Andersson B.;
RT "The Genome Sequence of Trypanosoma cruzi, Etiologic Agent of Chagas'

```

```

RT Disease.";
RL Science 0:0-0(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CL Brenner;
RA El-Sayed N.M.A., Myler P.J., Blandin G., Berriman M., Crabtree J.,
RA Aggarwal G., Caler E., Renaud H., Worthey E.A., Hertz-Powley C.,
RA Ghedin E., Peacock C., Bartholomeu D.C., Haas B.J., Tran A.-N.,
RA Wortman J.R., Alsmark U.C.M., Angiuoli S., Anupama A., Badger J.,
RA Brindaud F., Cadag E., Carleton J.M., Cerqueira G.C., Creasy T.,
RA Delcher A.L., Djikeng A., Embley T.M., Hauser C., Ivans A.C.,
RA Kummerfeld S.K., Pereira-Leal J.B., Nilsson D., Peterson J.,
RA Salzberg S.L., Shalton J., Silva J.C., Sundaram J., Westenberg S.,
RA White O., Melville S.E., Donelson J.E., Andersson B., Stuart K.D.,
RA Hall N.;
RT "Comparative Genomics of Trypanosomatid Parasitic Protozoa.";
RL Science 0:0-0(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CL Brenner;
RA El-Sayed N., Bartholomeu D., Haas B.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAKH01001336; EAN85852.1; -; Genomic DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001476; Chaprin_Cpn10.
DR Pfam; PF001166; Cpn10; 1.
DR PRINTS; PR00297; CHAPERONIN10.
DR ProDom; PD000566; Chaprin_Cpn10; 1.
KW Chaperone; Heat shock.
SQ SEQUENCE 180 AA; 20098 MW; 031E9A1B5742E90A CRC64;

Query Match 55.6%; Score 5; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDT 5
Db 144 KVDDT 148

RESULT 139
Q32EE6_SHIDS PRELIMINARY; PRT; 180 AA.
AC Q32EE6;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Putative transcriptional regulator LYSR-type.
GN Names=yey; OrderedLocusNames=SDY 2224;
OS Shigella dysenteriae serotype 1 (strain Sd197).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=300267;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16275786; DOI=10.1093/nar/gki954;
RA Wang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
RA Yang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
RA Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
RA Qiang B., Hou Y., Yu J., Jin Q.;
RT "Genome dynamics and diversity of Shigella species, the etiologic
RT agents of bacillary dysentery."
RL Nucleic Acids Res. 33:6445-6458 (2005).

```

```

CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000034; ABB62309.1; -; Genomic DNA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Complete proteome.
SQ SEQUENCE 180 AA; 20000 MW; 30ED00DFFADB95BB CRC64;

Query Match 55.6%; Score 5; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDDTF 6
Db 99 VDDTF 103

RESULT 140
Q5FJR3_LACAC PRELIMINARY; PRT; 182 AA.
AC Q5FJR3;
DT 01-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein.
GN OrderedLocusNames=LBA1227;
OS Lactobacillus acidophilus.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1579;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NCFM;
RX PubMed=15671160; DOI=10.1073/pnas.0409188102;
RA Altermann E., Russell W.M., Azcarate-Peril M.A., Barrangou R.,
RA Buck B.L., McAuliffe O., Souther N., Dobson A., Duong T., Callanan M.,
RA Lick S., Hamrick A., Cano R., Klaenhammer T.R.;
RT "Complete genome sequence of the probiotic lactic acid bacterium
RT Lactobacillus acidophilus NCFM."
RL Proc. Natl. Acad. Sci. U.S.A. 102:3906-3912 (2005).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000033; AAV43061.1; -; Genomic DNA.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 182 AA; 21096 MW; 2030DA6DBD7F2C05 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDTFY 7
Db 116 DDTFY 120

RESULT 141
Q64LE1_9ADEN PRELIMINARY; PRT; 183 AA.
AC Q64LE1;
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Hexon (Fragment).
OS Human adenovirus type 38.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=46943;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC VR-988;

```

```

RX PubMed=15364976; DOI=10.1128/JCM.42.9.3963-3969.2004;
RA "Sarantis H., Johnson G., Brown M., Petric M., Tellier R.;
RT "Comprehensive detection and serotyping of human adenoviruses by PCR
RL J. Clin. Microbiol. 42:3963-3969(2004).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY288124; AAQ24013.1; -; Genomic_DNA.
DR SMR; Q64LE1; 1-182.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000736; Adeno_hexon.
DR Pfam; PF01065; Adeno_hexon; 1.
DR ProDom; PD002815; Adeno_hexon; 1.
FT NON_TER 1
FT NON_TER 183
SQ SEQUENCE 183 AA; 20383 MW; 63F0C725BE3A82C1 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 96 KVDDT 100

RESULT 142
Q5CNC5 CRYHO PRELIMINARY; PRT; 186 AA.
ID Q5CNC5 CRYHO PRELIMINARY; PRT; 186 AA.
AC Q5CNC5;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 12-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE NAC domain protein.
GN ORFNames=Chro.60282;
OS Cryptosporidium hominis.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=237895;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TU502;
RX PubMed=15510150; DOI=10.1038/nature02977;
RA Xu P., Widmer G., Wang Y., Ozaki L.S., Alves J.M., Serrano M.G.,
RA Puiu D., Manque P., Akiyoshi D., Mackey A.J., Pearson W.R., Dear P.H.,
RA Bankier A.T., Peterson D.L., Abrahamsen M.S., Kapur V., Tzipori S.,
RA Buck G.A.;
RT "The genome of Cryptosporidium hominis.";
RL Nature 431:1107-1112(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAEL01000012; EAL38115.1; -; Genomic_DNA.
DR GO; GO:0003779; F:actin binding; IEA.
DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; IEA.
DR InterPro; IPR002715; NAC.
DR InterPro; IPR003128; VHP.
DR Pfam; PF01849; NAC; 1.
SQ SEQUENCE 186 AA; 21326 MW; 7AE6C179CBB887B9 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 186;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 96 KVDDT 100

```

```

Db 30 KVDDT 34

RESULT 143
Q7YF2 CRYPV PRELIMINARY; PRT; 186 AA.
AC Q7YF2;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Conserved NAC domain protein (BTF domain, basal transcription factor).
GN ORFNames=IMB.263, C96_2430;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Bimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Iowa;
RA Bankier A.T., Spriggs H.F., Fartmann B., Konfortov B.A., Madera M.,
RA Vogel C., Teichmann S.A., Ivens A., Dear P.H.;
RT "Integrated mapping, chromosomal sequencing and sequence analysis of
RT Cryptosporidium parvum.";
RL Genome Res. 0:0-0(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Iowa type II;
RX PubMed=15044751; DOI=10.1126/science.1094786;
RA Abrahamsen M.S., Templeton T.J., Enomoto S., Abrahante J.E., Zhu G.,
RA Lantto C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu P.,
RA Bankier A.T., Dear P.H., Konfortov B.A., Spriggs H.F., Iyer L.,
RA Anantharaman V., Aravind L., Kapur V.;
RT "Complete genome sequence of the apicomplexan, Cryptosporidium
RT parvum.";
RL Science 304:441-445(2004).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BX538351; CAD98533.1; -; Genomic_DNA.
DR EMBL; AAEE01000002; EAK89888.1; -; Genomic_DNA.
DR GO; GO:0003779; F:actin binding; IEA.
DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; IEA.
DR InterPro; IPR002715; NAC.
DR InterPro; IPR003128; VHP.
DR Pfam; PF01849; NAC; 1.
SQ SEQUENCE 186 AA; 21241 MW; 805A07041AFB87A1 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 186;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 30 KVDDT 34

RESULT 144
Q47L35 THEFY PRELIMINARY; PRT; 188 AA.
AC Q47L35;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Putative ATP/GTP-binding protein.
GN OrderedLocNames=Tfu_2804;
OS Thermobifida fusca (strain YX).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptosporangineae; Nocardiopsaceae; Thermobifida.
OX NCBI_TaxID=269800;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC US DOE Joint Genome Institute;

```

```
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Di Bartolo G., Chain P., Schmutz J.,
RA Larimer F., Land M., Lykidis A., Richardson P.,
RT "Complete sequence of Thermobifida fusca YK.",
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000088; AA256837.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR001806; Ras trnsfrmg.
DR Pfam; PF03029; ATP bind 1; 1.
DR PRINTS; PR00449; RASTNSFRMG.
DR Complete proteome.
SQ SEQUENCE 188 AA; 20464 MW; 9BAC9AEA219FB6F5 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTF 6
Db 71 VDDTF 75

RESULT 145
Q3Y144_ENTFC
ID Q3Y144_ENTFC PRELIMINARY; PRT; 189 AA.
AC Q3Y144;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Transferase hexapeptide repeat.
GN ORFNames=EfaeDRAFT_1650;
OS Enterococcus faecium DO.
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=333849;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DO;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.,
RT "Sequencing of the draft genome and assembly of Enterococcus faecium
RT DO.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DO;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Enterococcus faecium DO.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DO;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAK03000013; EBN10199.1; -; Genomic_DNA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR001451; Hexapep_transf.
```

```
DR Pfam; PF00132; Hexapep; 2.
DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
KW Transferase.
SQ SEQUENCE 189 AA; 20753 MW; AC49EF58AF3D26A8 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 59 KVDDT 63

RESULT 146
Q5MJW8_TOBAC
ID Q5MJW8_TOBAC PRELIMINARY; PRT; 191 AA.
AC Q5MJW8;
DT 01-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 01-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Avr9/Cf-9 rapidly elicited protein 36 (Fragment).
GN Name=ACRE36;
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15598806; DOI=10.1105/tpc.104.026013;
RA Rowland O., Ludwig A.A., Merrick C.J., Baillieul F., Tracy F.E.,
RA Durrant W.E., Fritz-Laylin L., Nekrasov V., Sjolander K., Yoshioka H.,
RA Jones J.D.;
RT "Functional Analysis of Avr9/Cf-9 Rapidly Elicited Genes Identifies a
RT Protein Kinase, AC1K1, That Is Essential for Full Cf-9-Dependent
RT Disease Resistance in Tomato.";
RL Plant Cell 17:295-310 (2005).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY750333; AAV92892.1; -; mRNA.
DR GO; GO:0004194; F:pepsin A activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR009007; Pept_Aspartc_cat.
DR InterPro; IPR001461; Peptidase_A1.
DR PANTHER; PTHR13683; Peptidase_A1; 1.
FT NON TER 1
SQ SEQUENCE 191 AA; 21454 MW; B6CAFD141916CFB1 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TFYVV 9
Db 31 TFYVV 35

RESULT 147
Q6C1O6_YARLI
ID Q6C1O6_YARLI PRELIMINARY; PRT; 192 AA.
AC Q6C1O6;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Similarity.
GN OrderedLocNames=YALI0F142899;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
```

[1]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=CLIB 122 / E 150;
 RX PubMed:15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boissane L., Boyer J., Cattolico L., Confaniolero F., de Daruvar A.,
 RA Despons A., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.;
 RT "Genome evolution in yeasts";
 RL Nature 430:35-44(2004).
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 CC
 DR EMBL: CR382132; CAG78215.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 192 AA; 21061 MW; 304DA60AA7422FFD9 CRC64;
 Query Match 55.6%; Score 5; DB 2; Length 192;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVDVT 5
 Db 157 KVDVT 161
 RESULT 148
 Q36SQ4_MARHY
 ID Q36SQ4_MARHY PRELIMINARY; PRT; 194 AA.
 AC Q36SQ4;
 DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
 DT 06-DEC-2005, sequence version 1.
 DT 07-MAR-2006, entry version 4.
 DE Hypothetical protein.
 GN ORFNames=MaquidRAFT 1985;
 OS Marinobacter aquaeolei VT8.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 OC Alteromonadaceae; Marinobacter.
 OX NCBI_TaxID=351348;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=VT8;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Richardson P.;
 RT "Sequencing of the draft genome and assembly of Marinobacter aquaeolei
 VT8.";
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=VT8;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RA "Annotation of the draft genome of Marinobacter aquaeolei VT8.";
 RT Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -1- FUNCTION: Repressor involved in choline regulation of the bet
 CC genes (By similarity).
 CC -1- PATHWAY: Betaine biosynthesis from choline; regulation.
 CC

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 CC
 DR EMBL: AALG01000004; EAP00103.1; -; Genomic_DNA.
 DR GO: GO:0003700; P:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 KW DNA-binding; Hypothetical protein; Transcription;
 KW Transcription regulation.
 SQ SEQUENCE 194 AA; 22316 MW; 0196B922CC0ABB47 CRC64;
 Query Match 55.6%; Score 5; DB 2; Length 194;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 TFYTV 9
 Db 58 TFYTV 62
 RESULT 149
 Q9RBX9_PSEIN
 ID Q9RBX9_PSEIN PRELIMINARY; PRT; 195 AA.
 AC Q9RBX9;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 12.
 DE Hypothetical protein (Fragment).
 OS Pseudomonas indigofera.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Vogesella.
 OX NCBI_TaxID=45465;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=ATCC19706;
 RA van de Loo E.J., Keese P., Llewellyn D.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 CC
 DR EMBL: AF088856; AAD54002.1; -; Genomic_DNA.
 DR InterPro: IPR005302; MOSC.
 DR InterPro: IPR005303; MOSC_N.
 DR Pfam: PF03473; MOSC; 1.
 DR Pfam: PF03476; MOSC_N; 1.
 KW Hypothetical protein.
 FT NON_TER 195 195
 SQ SEQUENCE 195 AA; 21939 MW; 726A35252A9DD3F8 CRC64;
 Query Match 55.6%; Score 5; DB 2; Length 195;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 VDDTF 6
 Db 174 VDDTF 178
 RESULT 150
 Q3FPC2_9BURK
 ID Q3FPC2_9BURK PRELIMINARY; PRT; 196 AA.
 AC Q3FPC2;
 DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 08-NOV-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Transport-associated precursor.
 GN ORFNames=RferDRAFT 1177;
 OS Rhodoferrax ferrireducens DSM 15236.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Comamonadaceae; Rhodoferrax.
 OX NCBI_TaxID=338969;
 RN NUCLEOTIDE SEQUENCE.
 RP

```

RC STRAIN=DSM 15236;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Rhodoferrax
RT ferrireducens DSM 15236.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 15236;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Rhodoferrax ferrireducens
RT DSM 15236.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAJK01000016; EAO39974.1; -; Genomic_DNA.
DR InterPro; IPR007055; TAD.
DR Pfam; PFO4972; BON; 2.
DR PROSITE; PS50914; BON; 2.
KW Signal.
FT SIGNAL 1 27 Potential.
SQ SEQUENCE 196 AA; 20013 MW; BD57C939F69A2CD5 CRC64;

Query Match 55.6%; Score 5; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDT 5
Db 126 KVDDT 130

```

Search completed: May 17, 2006, 06:27:38
 Job time : 263 secs